

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 10, 2003, 14:13:55 ; Search time 40.43 Seconds  
(without alignments)  
5279.867 Million cell updates/sec

Title: US-10-090-827-7

Perfect score: 5446

Sequence: 1 MAAGCLALTLTLFQSLIG.....RLIOAEQTSQPCPCDMVK 1036

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL.21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5446	100.0	1091	6 077773	077773 sus scrofa
2	5376.5	98.7	1110	4 09U1U0	09u1u0 homo sapien
3	5325	97.8	1091	11 09ERS3	09ers3 rattus norv
4	5253	96.5	1103	11 008532	008532 mus musculu
5	5229	96.0	1079	11 08VHS9	08vhs9 rattus norv
6	3634	66.7	745	4 09UDQ3	09udq3 homo sapien
7	2965	54.4	1150	4 09NY47	09ny47 homo sapien
8	2937.5	53.9	1143	4 09NY48	09ny48 homo sapien
9	2937.5	53.7	1156	11 09ROG2	09eqg2 mus musculu
10	2924.5	53.7	1164	4 09Y268	09y268 homo sapien
11	2912	53.5	1084	11 09Z0H6	09z0h6 mus musculu
12	2903.5	53.3	1076	4 09UEW0	09uew0 homo sapien
13	2728	50.1	975	4 09NSA6	09nsa6 homo sapien
14	1112	20.4	1091	11 09Z1L5	09z1l5 mus musculu
15	1045	19.2	997	4 09NY16	09ny16 homo sapien
16	1028	18.9	1218	5 0879C3	0879c3 drosophila

17	941.5	17.3	2190	5 09NK64	09nk64 drosophila
18	926.5	17.0	2172	5 09VJMO	09vjmo drosophila
19	901	16.5	1191	5 09VJN7	09vjn7 drosophila
20	899.5	16.5	1255	5 09NK83	09nk83 drosophila
21	875	16.1	170	4 09UDL7	09udl7 homo sapien
22	855	15.7	1022	5 09V6T7	09v6t7 drosophila
23	759.5	13.9	519	4 09NY18	09ny18 homo sapien
24	661	12.1	317	11 09Z0H5	09z0h5 mus musculu
25	571	10.5	1148	5 017517	017517 caenorhabdi
26	555.5	10.2	842	5 095875	095875 drosophila
27	516.5	9.5	104	4 09UD81	09ud81 homo sapien
28	515	9.5	100	6 09GLH1	09glh1 bos taurus
29	496.5	9.1	121	4 09UD82	09ud82 homo sapien
30	479	8.8	98	4 09UD05	09ud05 homo sapien
31	467	8.6	97	4 09UD80	09ud80 homo sapien
32	404	7.4	77	4 095026	095026 homo sapien
33	369.5	6.8	223	11 09R142	09r142 mus musculu
34	350.5	6.1	1185	4 09HC19	09hc19 homo sapien
35	229	4.2	978	6 095KE0	095ke0 macaca fasc
36	218	4.0	1449	5 09V917	09v917 drosophila
37	201.5	3.7	886	11 091WG9	091wg9 mus musculu
38	190.5	3.5	1450	16 09CE07	09ce07 lactococcus
39	177.5	3.3	494	5 09U7P4	09u7p4 eufoiiculi
40	170.5	3.1	1819	16 097K40	097k40 clostridium
41	167	3.1	796	17 09AH3	09ah3 thermoplasm
42	167	3.1	800	17 097AH3	097ah3 thermoplasm
43	165	3.0	459	16 025905	025905 helicobacte
44	164.5	3.0	789	2 045793	045793 bacillus th
45	164	3.0	614	16 08XN21	08xn21 clostridium

## ALIGNMENTS

## RESULT 1

077773 PRELIMINARY: PRT: 1091 AA.

ID 077773  
AC 077773;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE Voltage-dependent calcium channel alpha-2 delta subunit precursor.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN CORTEX;  
RX MEDLINE=98411353; PubMed=9738015;  
RA Brown J.P., Gee N.S.,  
RT Cloning and deletion mutagenesis of the alpha2 delta calcium channel  
RT subunit from porcine cerebral cortex. Expression of a soluble form of  
RT the protein that retains [3H]gabapentin binding activity.";  
RL J. Biol. Chem. 273:25458-25465(1998).  
DR EMBL:AF077665; AAC36289-1-  
DR InterPro: IPR004010; Cache.  
DR InterPro: IPR002035; VWF.A.  
DR Pfam: PF02743; Cache; 1.  
DR SMART: SM00327; VWA; 1.  
DR PROSITE: PS50234; VWFA; 1.  
KW SIGNAL.  
FT SIGNAL. 1 24  
FT CHAIN 25 1091  
SQ SEQUENCE 1091 AA: 123150 MW: 2933DC7BEB9E60E CRC64;

Query Match 100.0%; Score 5446; DB 6; Length 1091;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLALTLTLFQSLIGSPFPPSAVTIKSWDKMQEDLVYLAATKASGVNQLVDI 60

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Db 1 MAAGCLALTLTLFOSLLIGPSSQEPFSAVYIKSMVQKQEDLVTLAKTASGVNQLVDI 60
QY 61 YEKYODLYTEVPNNARQLEIATARDIEKLISRSKALVRLAEAKVOAAHQMEDPASN 120
Db 61 YEKYODLYTEVPNNARQLEIATARDIEKLISRSKALVRLAEAKVOAAHQMEDPASN 120
QY 121 EYVYINAKDDLPEKNDSEPSQRIKPYFIDDANFGROIQOHAHVHPDITGSGTIVL 180
Db 121 EYVYINAKDDLPEKNDSEPSQRIKPYFIDDANFGROIQOHAHVHPDITGSGTIVL 180
QY 181 NELNMTSALDEYFKKREDEPSLLMQVGSATGLARYYPASPMWDNSRTPNKIDLYDVR 240
Db 181 NELNMTSALDEYFKKREDEPSLLMQVGSATGLARYYPASPMWDNSRTPNKIDLYDVR 240
QY 241 RFWYIOGAASPKMDLIVDVGSGVGLTKLIRTSVSMLETTSDDDFVNVASFNSAOD 300
Db 241 RFWYIOGAASPKMDLIVDVGSGVGLTKLIRTSVSMLETTSDDDFVNVASFNSAOD 300
QY 301 VSCFOHLVQAVNRKKVYLKDAVNNITAKGTDYKGFSAFEQLLNTVSRACNKTIML 360
Db 301 VSCFOHLVQAVNRKKVYLKDAVNNITAKGTDYKGFSAFEQLLNTVSRACNKTIML 360
QY 361 FTDGGEERAQEIFAKYKNDKVRFTSVGOHNDRGP IQMACENKGYEIPSTGAIR 420
Db 361 FTDGGEERAQEIFAKYKNDKVRFTSVGOHNDRGP IQMACENKGYEIPSTGAIR 420
QY 421 INTGEYLDVIGRPVYLAGDAKQOVQWNVYLDLLELGLVTTGTLPVFNITGQENKTNL 480
Db 421 INTGEYLDVIGRPVYLAGDAKQOVQWNVYLDLLELGLVTTGTLPVFNITGQENKTNL 480
QY 481 NQLLIGVGVDSLEDIKRLTPRETLCPNGYYPALDPNGVYLHPMLQPKNKPSQEPVTL 540
Db 481 NQLLIGVGVDSLEDIKRLTPRETLCPNGYYPALDPNGVYLHPMLQPKNKPSQEPVTL 540
QY 541 DFLDAELNDIKVEIRNMKIDGSEKTEFTLVKSODERYIDKNGNTYVWTVNCTDSL 600
Db 541 DFLDAELNDIKVEIRNMKIDGSEKTEFTLVKSODERYIDKNGNTYVWTVNCTDSL 600
QY 601 ALVLPYSPFYIKAKIETITQARSKKGMKQSETLKPNFEESGYTFAPRDYCNDLKI 660
Db 601 ALVLPYSPFYIKAKIETITQARSKKGMKQSETLKPNFEESGYTFAPRDYCNDLKI 660
QY 661 SDNTEFLNFEFIDRKTPNNPSCNTDLINRYLDAGFTNLYONVYSKOKNIKGVAR 720
Db 661 SDNTEFLNFEFIDRKTPNNPSCNTDLINRYLDAGFTNLYONVYSKOKNIKGVAR 720
QY 721 FVYTDGIGTRVYKPKAGEMWQENPETYEDSFYKSLDNDNVYFTAPYFNKSGPAGYESGI 780
Db 721 FVYTDGIGTRVYKPKAGEMWQENPETYEDSFYKSLDNDNVYFTAPYFNKSGPAGYESGI 780
QY 781 MYSKAVEIYIOGKILKPAVVGIKIDVNSMIEFVTKSTRDCCAGVCCCKNSVMDCVI 840
Db 781 MYSKAVEIYIOGKILKPAVVGIKIDVNSMIEFVTKSTRDCCAGVCCCKNSVMDCVI 840
QY 841 LDDGGFLMANADDYTNQIGRFGSIDPSLMRHLVNISVAFNKSXYQSCVCEGAPKQ 900
Db 841 LDDGGFLMANADDYTNQIGRFGSIDPSLMRHLVNISVAFNKSXYQSCVCEGAPKQ 900
QY 901 GAGHSASVYPSIADLIHGMWATAAASIILOQFLSLTFPRLAVALVEMEDDFTASLSKQ 960
Db 901 GAGHSASVYPSIADLIHGMWATAAASIILOQFLSLTFPRLAVALVEMEDDFTASLSKQ 960
QY 961 SCITRQOTQYFFDNDKSPSGVLDGNCGRIFPHVEKLMANTNLIIFMWSKGTCCDRFLLI 1020
Db 961 SCITRQOTQYFFDNDKSPSGVLDGNCGRIFPHVEKLMANTNLIIFMWSKGTCCDRFLLI 1020
QY 1021 QAEQTSDEPDCDMVK 1036
Db 1021 QAEQTSDEPDCDMVK 1036

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RESULT 2

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Q99IU0
ID Q99IU0 PRELIMINARY: PRT: 1110 AA.
AC Q99IU0:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Dihydropyridine receptor alpha 2 subunit.
GN CACNA2D1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20005942; PubMed=10534405;
RA Schleithoff L., Mehre G., Reutlinger B., Lehmann-Horn F.;
RT "Genomic structure and functional expression of a human alpha(2)/delta
RL calcium channel subunit gene (CACNA2).";
Genomics 61:201-209(1999).
DR EMBL: AF083854; AAF03259.1; JOINED.
DR EMBL: AF083817; AAF03259.1; JOINED.
DR EMBL: AF083818; AAF03259.1; JOINED.
DR EMBL: AF083819; AAF03259.1; JOINED.
DR EMBL: AF083820; AAF03259.1; JOINED.
DR EMBL: AF083821; AAF03259.1; JOINED.
DR EMBL: AF083822; AAF03259.1; JOINED.
DR EMBL: AF083823; AAF03259.1; JOINED.
DR EMBL: AF083824; AAF03259.1; JOINED.
DR EMBL: AF083825; AAF03259.1; JOINED.
DR EMBL: AF083826; AAF03259.1; JOINED.
DR EMBL: AF083827; AAF03259.1; JOINED.
DR EMBL: AF083828; AAF03259.1; JOINED.
DR EMBL: AF083829; AAF03259.1; JOINED.
DR EMBL: AF083830; AAF03259.1; JOINED.
DR EMBL: AF083831; AAF03259.1; JOINED.
DR EMBL: AF083832; AAF03259.1; JOINED.
DR EMBL: AF083833; AAF03259.1; JOINED.
DR EMBL: AF083834; AAF03259.1; JOINED.
DR EMBL: AF083835; AAF03259.1; JOINED.
DR EMBL: AF083836; AAF03259.1; JOINED.
DR EMBL: AF083837; AAF03259.1; JOINED.
DR EMBL: AF083838; AAF03259.1; JOINED.
DR EMBL: AF083839; AAF03259.1; JOINED.
DR EMBL: AF083840; AAF03259.1; JOINED.
DR EMBL: AF083841; AAF03259.1; JOINED.
DR EMBL: AF083842; AAF03259.1; JOINED.
DR EMBL: AF083843; AAF03259.1; JOINED.
DR EMBL: AF083844; AAF03259.1; JOINED.
DR EMBL: AF083845; AAF03259.1; JOINED.
DR EMBL: AF083846; AAF03259.1; JOINED.
DR EMBL: AF083847; AAF03259.1; JOINED.
DR EMBL: AF083848; AAF03259.1; JOINED.
DR EMBL: AF083849; AAF03259.1; JOINED.
DR EMBL: AF083850; AAF03259.1; JOINED.
DR EMBL: AF083851; AAF03259.1; JOINED.
DR EMBL: AF083852; AAF03259.1; JOINED.
DR EMBL: AF083853; AAF03259.1; JOINED.
DR EMBL: AF083854; AAF03259.1; JOINED.
DR InterPro: IPR004010; Cache.
DR InterPro: IPR002035; WVF_A.
DR Pfam: PF00743; Cache; 1.
DR SMART: SM00327; WMA; 1.
DR PROSITE: PS0234; WFA; 1.
DR KW RECEPTOR.
SQ SEQUENCE 1110 AA; 125307 MW; 83580C6AD489C074 CRC64;

Query Match 98.7%; Score 5376.5; DB 4; Length 1110;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 1026; Conservative 5; Mismatches 5; Indels 19; Gaps 1;
QY 1 MAAGCLALTLTLFOSLLIGPSSQEPFSAVYIKSMVQKQEDLVTLAKTASGVNQLVDI 60
Db 1 MAAGCLALTLTLFOSLLIGPSSQEPFSAVYIKSMVQKQEDLVTLAKTASGVNQLVDI 60

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OY 61 YEKYODLYVEPNNAQOLVEIARDEIKLSNRKALVRLALEAKVOAHOQWREDFASN 120
DB 61 YEKYODLYVEPNNAQOLVEIARDEIKLSNRKALVRLALEAKVOAHOQWREDFASN 120
OY 121 EYVYVNAKDDLDPEKNDSESGSORIKPVIFIDANFGROISYOAHAHVIPTDIYESTIVL 180
DB 121 EYVYVNAKDDLDPEKNDSESGSORIKPVIFIDANFGROISYOAHAHVIPTDIYESTIVL 180
OY 121 EYVYVNAKDDLDPEKNDSESGSORIKPVIFIDANFGROISYOAHAHVIPTDIYESTIVL 180
DB 121 EYVYVNAKDDLDPEKNDSESGSORIKPVIFIDANFGROISYOAHAHVIPTDIYESTIVL 180
OY 181 NELNMTSALDEVEKKNREDDPSLLMOVFGSATGLARYYPASPWVNSRTPKIDLYDVR 240
DB 181 NELNMTSALDEVEKKNREDDPSLLMOVFGSATGLARYYPASPWVNSRTPKIDLYDVR 240
OY 241 RPYVIOGAASPKDMLILVDVSGSVGLTKLRTSYSEMLETLSDDDFVNAFNSNAOD 300
DB 241 RPYVIOGAASPKDMLILVDVSGSVGLTKLRTSYSEMLETLSDDDFVNAFNSNAOD 300
OY 301 VSCFOHLVQANVRNKKVLAQVANNITAKGTDYKKGFSAFQOLNANVSRANCKIIML 360
DB 301 VSCFOHLVQANVRNKKVLAQVANNITAKGTDYKKGFSAFQOLNANVSRANCKIIML 360
OY 361 FTGGEERAOEIFAKYNNKDKRVFTFSVQOHNDRGPIQMACENKGYIYEIPSGAIR 420
DB 361 FTGGEERAOEIFAKYNNKDKRVFTFSVQOHNDRGPIQMACENKGYIYEIPSGAIR 420
OY 421 INTQEVLDVIGRPVNLADGKAKOVOMTNYLDALGLVITGTLPPFNITGONENKTNLK 480
DB 421 INTQEVLDVIGRPVNLADGKAKOVOMTNYLDALGLVITGTLPPFNITGONENKTNLK 480
OY 481 NQILIGVGVVDSLEDIRKLPREFLCNGYFAIDPNGVYLLAPNLOPK ----- 530
DB 481 NQILIGVGVVDSLEDIRKLPREFLCNGYFAIDPNGVYLLAPNLOPK ----- 530
OY 531 ----- NPKSEPTLDFLAELENDIKVEIRNKMIDGSEGETFRILVASQDERI 581
DB 531 ----- NPKSEPTLDFLAELENDIKVEIRNKMIDGSEGETFRILVASQDERI 581
OY 581 LKRRPNIONKRSQEPVTLDFLAELENDIKVEIRNKMIDGSEGETFRILVASQDERI 600
DB 581 LKRRPNIONKRSQEPVTLDFLAELENDIKVEIRNKMIDGSEGETFRILVASQDERI 600
OY 601 DKGNTTYTWTVPVNGTDYSLALVLTPTYSFYIKAKIEETITQARSKKGMKMDSETLKPND 641
DB 601 DKGNTTYTWTVPVNGTDYSLALVLTPTYSFYIKAKIEETITQARSKKGMKMDSETLKPND 641
OY 641 EBSGYTFIAPRDYCNOLKISDNNTFELNNEFIDRKTPNNPSCNDLIRVYLLDGFYN 701
DB 641 EBSGYTFIAPRDYCNOLKISDNNTFELNNEFIDRKTPNNPSCNDLIRVYLLDGFYN 701
OY 701 EBSGYTFIAPRDYCNOLKISDNNTFELNNEFIDRKTPNNPSCNDLIRVYLLDGFYN 720
DB 701 EBSGYTFIAPRDYCNOLKISDNNTFELNNEFIDRKTPNNPSCNDLIRVYLLDGFYN 720
OY 721 ELYOVYMSKOKINIKGVKARFVYTDGSTRVYKPEAGENMOENPETYEDSEYKSLDNDY 761
DB 721 ELYOVYMSKOKINIKGVKARFVYTDGSTRVYKPEAGENMOENPETYEDSEYKSLDNDY 761
OY 761 VFTAPYFNKSGPGAYESGIMVSKAVEIYIQKLLKPAVVGIKIDVNSWIEFTKTSIRDP 821
DB 761 VFTAPYFNKSGPGAYESGIMVSKAVEIYIQKLLKPAVVGIKIDVNSWIEFTKTSIRDP 821
OY 821 CAGPYCCKCRNSDVNDYCYLDDGGLMANHDDYDNOIGREFGIDSLMRHIVNISVYA 881
DB 821 CAGPYCCKCRNSDVNDYCYLDDGGLMANHDDYDNOIGREFGIDSLMRHIVNISVYA 881
OY 881 FPKSYDYOVCPEGAAPKQAGHRSAYVSIADILHIGMATAAAMSTLQOFLSLTFPR 941
DB 881 FPKSYDYOVCPEGAAPKQAGHRSAYVSIADILHIGMATAAAMSTLQOFLSLTFPR 941
OY 941 LLEAVEMEDDDFTASLSKOSCTTEOTQYFPDNDKSFSGVJDCGNCSTIFVEKIAMTNL 1001
DB 941 LLEAVEMEDDDFTASLSKOSCTTEOTQYFPDNDKSFSGVJDCGNCSTIFVEKIAMTNL 1001
OY 1001 IFIMVESKGTCPDTRILIOAOTSDGPPCDMYK 1036
DB 1001 IFIMVESKGTCPDTRILIOAOTSDGPPCDMYK 1036
OY 1021 IFIMVESKGTCPDTRILIOAOTSDGPPCDMYK 1055
DB 1021 IFIMVESKGTCPDTRILIOAOTSDGPPCDMYK 1055

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RESULT 3  
Q9ERS3 PRELIMINARY: PRT: 1091 AA.

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AC Q9ERS3;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE Voltage-gated calcium channel alpha2/delta-1 subunit.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_Taxid-10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-SUPERIOR CERVICAL GANGLIA;
RA Lin Y., Lipscombe D.;
RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF286488; AAG28164.1;
DR InterPro: IPR004010; Cache.
DR InterPro: IPR002035; WVF_A.
DR Pfam: PF02743; Cache; 1.
DR SMART: SM00327; WVF_1.
DR PROSITE: PS50234; WVF_1.
FT VARIANT 209 212 GSAT -> AADR.
FT VARIANT 338 338 S -> T.
FT VARIANT 599 600 SL -> RY.
FT VARIANT 869 869 S -> R.
SQ SEQUENCE 1091 AA: 123467 MW: C155088971628E19 CRC64;

Query Match 97.8%; Score 5325; DB 11; Length 1091;
Best Local Similarity 97.0%; Pred. 1.2e-316;
Matches 1005; Conservative 21; Mismatches 10; Indels 0; Gaps 0;

OY 1 MAAGCLLALTLTFLQSLIGPSSQEPFSAVITKSVNKKQEDLVTLAKTAGVNOYDI 60
DB 1 MAAGCLLALTLTFLQSLIGPSSQEPFSAVITKSVNKKQEDLVTLAKTAGVNOYDI 60
OY 61 YEKYODLYVEPNNAQOLVEIARDEIKLSNRKALVRLALEAKVOAHOQWREDFASN 120
DB 61 YEKYODLYVEPNNAQOLVEIARDEIKLSNRKALVRLALEAKVOAHOQWREDFASN 120
OY 121 EYVYVNAKDDLDPEKNDSESGSORIKPVIFIDANFGROISYOAHAHVIPTDIYESTIVL 180
DB 121 EYVYVNAKDDLDPEKNDSESGSORIKPVIFIDANFGROISYOAHAHVIPTDIYESTIVL 180
OY 121 EYVYVNAKDDLDPEKNDSESGSORIKPVIFIDANFGROISYOAHAHVIPTDIYESTIVL 180
DB 121 EYVYVNAKDDLDPEKNDSESGSORIKPVIFIDANFGROISYOAHAHVIPTDIYESTIVL 180
OY 181 NELNMTSALDEVEKKNREDDPSLLMOVFGSATGLARYYPASPWVNSRTPKIDLYDVR 240
DB 181 NELNMTSALDEVEKKNREDDPSLLMOVFGSATGLARYYPASPWVNSRTPKIDLYDVR 240
OY 181 NELNMTSALDEVEKKNREDDPSLLMOVFGSATGLARYYPASPWVNSRTPKIDLYDVR 240
DB 181 NELNMTSALDEVEKKNREDDPSLLMOVFGSATGLARYYPASPWVNSRTPKIDLYDVR 240
OY 241 RPYVIOGAASPKDMLILVDVSGSVGLTKLRTSYSEMLETLSDDDFVNAFNSNAOD 300
DB 241 RPYVIOGAASPKDMLILVDVSGSVGLTKLRTSYSEMLETLSDDDFVNAFNSNAOD 300
OY 301 VSCFOHLVQANVRNKKVLAQVANNITAKGTDYKKGFSAFQOLNANVSRANCKIIML 360
DB 301 VSCFOHLVQANVRNKKVLAQVANNITAKGTDYKKGFSAFQOLNANVSRANCKIIML 360
OY 361 FTGGEERAOEIFAKYNNKDKRVFTFSVQOHNDRGPIQMACENKGYIYEIPSGAIR 420
DB 361 FTGGEERAOEIFAKYNNKDKRVFTFSVQOHNDRGPIQMACENKGYIYEIPSGAIR 420
OY 421 INTQEVLDVIGRPVNLADGKAKOVOMTNYLDALGLVITGTLPPFNITGONENKTNLK 480
DB 421 INTQEVLDVIGRPVNLADGKAKOVOMTNYLDALGLVITGTLPPFNITGONENKTNLK 480
OY 481 NQILIGVGVVDSLEDIRKLPREFLCNGYFAIDPNGVYLLAPNLOPKNSQEPVTL 540
DB 481 NQILIGVGVVDSLEDIRKLPREFLCNGYFAIDPNGVYLLAPNLOPKNSQEPVTL 540
OY 541 DFLDALENDIKVEIRNKMIDGSEGETFRILVKSQDERYIDKGNRTYTWTVPVNGTDSL 600
DB 541 DFLDALENDIKVEIRNKMIDGSEGETFRILVKSQDERYIDKGNRTYTWTVPVNGTDSL 600
OY 601 ALVLPYTFYIYKAKIEETITQARSKKGMKMDSETLAKDNFESGYTFIAPRDYCNOLKI 660
DB 601 ALVLPYTFYIYKAKIEETITQARSKKGMKMDSETLAKDNFESGYTFIAPRDYCNOLKI 660

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Db 601 ALVLPYSPYIKAKIEITITQARSKKMKSEFLKPDNEEGSYTFLAPREYCNLDLP 660  
 QY 661 SDNTEFLINENEFIDRKTNNPSCNTDLINRVLADGETNELVONYSKOKINGVAR 720  
 Db 661 SUNNTEFLINENEFIDRKTNNPSCNTDLINRVLADGETNELVONYSKOKINGVAR 720  
 QY 721 FVVTGGTIRRYPKRGEWMQENPETYEDSFYKSLDNDNVYFAPYFNKSGPGAYESGI 780  
 Db 721 FVVTGGTIRRYPKRGEWMQENPETYEDSFYKSLDNDNVYFAPYFNKSGPGAYESGI 780  
 QY 781 MYSKAVEITYQGLKLPKPAVVGKIDVNSWIEFTKSIIRDPCAGVCCCKRSDVMDVY 840  
 Db 781 MYSKAVEITYQGLKLPKPAVVGKIDVNSWIEFTKSIIRDPCAGVCCCKRSDVMDVY 840  
 QY 841 LDDGGLLMANHDYTNIGRFFGEIDPSLMRHLNIVSYAFNKSVDYQSCPCAPAKQ 900  
 Db 841 LDDGGLLMANHDYTNIGRFFGEIDPSLMRHLNIVSYAFNKSVDYQSCPCAPAKQ 900  
 QY 901 GAGHSAYVPSIADILHIGWATAAASILDOFLISTFPRLLAEVEMDDFTASLSKQ 960  
 Db 901 GAGHSAYVPSIADILHIGWATAAASILDOFLISTFPRLLAEVEMDDFTASLSKQ 960  
 QY 961 SCITEQOTYFFDNDKSPSGVLDGNCGRIFRHEKIMNTNLIFIMVESKGTCPDTRLI 1020  
 Db 961 SCITEQOTYFFDNDKSPSGVLDGNCGRIFRHEKIMNTNLIFIMVESKGTCPDTRLI 1020  
 QY 1021 QAEOTSDGPDPCDMVK 1036  
 Db 1021 QAEOTSDGPDPCDMVK 1036

## RESULT 4

008532 PRELIMINARY; PRT: 1103 AA.

AC 008532; 008533; 008534; 008535; 008536;  
 DT 01-JUN-1998 (TREMUREL. 06, Created)  
 DT 01-JUN-1998 (TREMUREL. 06, Last sequence update)  
 DT 01-MAR-2002 (TREMUREL. 20, Last annotation update)  
 DE Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta  
 subunits precursor.  
 GN CACNA2D1 OR CACNA2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RX MEDLINE=97113514; PubMed=8955374;  
 RA Angelotti T., Hofmann F.;  
 RL FEBS Lett. 397:331-337(1996).  
 CC -1- FUNCTION: CALCIUM CHANNEL. PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN  
 CC EXCITATION-CONTRACTION COUPLING.  
 CC -1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:  
 CC ALPHA-1, ALPHA-2, BETA AND GAMMA.  
 CC -1- SUBUNIT: ALPHA-2 AND DELTA FORM HETERODIMERS THAT ARE DISULFIDE-  
 CC LINKED.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- ALTERNATIVE PRODUCTS: FIVE FORMS OF THE PROTEIN, ISOFORMS 2A-2E,  
 CC ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THE  
 CC SEQUENCE SHOWN HERE IS THAT OF ISOFORM 2A.  
 CC -1- TISSUE SPECIFICITY: ISOFORM 2A IS EXPRESSED IN SKELETAL MUSCLE AND  
 CC AORTA, 2B IS EXPRESSED IN BRAIN, 2C IS EXPRESSED IN HEART, 2D IS  
 CC EXPRESSED IN HEART AND SMOOTH MUSCLE, AND 2E IS EXPRESSED IN  
 CC SMOOTH MUSCLE. ALL FIVE ISOFORMS ARE EXPRESSED IN THE  
 CC CARDIOVASCULAR SYSTEM.  
 CC -1- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM  
 CC A PRECURSOR FORM.  
 CC -1- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.  
 DR EMBL: U73484; AAB50139.1; -;  
 DR EMBL: U73485; AAB50140.1; -;  
 DR EMBL: U73483; AAB50138.1; -;  
 DR EMBL: U73486; AAB50141.1; -;

DR EMBL: U73487; AAB50142.1; -;  
 DR MGI: 88295; Cacna2d1.  
 DR InterPro: IPR004010; Cache.  
 DR InterPro: IPR002035; VWF\_A.  
 DR Pfam: PF02743; Cache; 1.  
 DR Pfam: PF00092; Vwf; 1.  
 DR SMART: SM00327; Vwf; 1.  
 DR PROSITE: PS00234; VWF; 1.  
 KW Ion channel; Transmembrane; Ion transport; Voltage-gated channel;  
 KW Calcium channel; Glycoprotein; Phosphorylation; Signal;  
 KW Alternative splicing.  
 FT SIGNAL 1 24  
 FT CHAIN 25 957  
 FT TRANSMEM 958 1103  
 FT TRANSMEM 446 469  
 FT TRANSMEM 918 942  
 FT TRANSMEM 1079 1098  
 FT MOD\_RES 501 501  
 FT MOD\_RES 845 845  
 FT CARBOHYD 92 92  
 FT CARBOHYD 136 136  
 FT CARBOHYD 184 184  
 FT CARBOHYD 324 324  
 FT CARBOHYD 348 348  
 FT CARBOHYD 475 475  
 FT CARBOHYD 604 604  
 FT CARBOHYD 613 613  
 FT CARBOHYD 675 675  
 FT CARBOHYD 781 781  
 FT CARBOHYD 824 824  
 FT CARBOHYD 888 888  
 FT CARBOHYD 895 895  
 FT CARBOHYD 985 985  
 FT CARBOHYD 998 998  
 FT VARSPLIC 531 549  
 FT VARSPLIC 531 554  
 FT VARSPLIC 644 644  
 SQ SEQUENCE 1103 AA: 124629 MW: 10377384735120D4 CRC64:  
 Query Match 96.5%; Score 5253; DB 11; Length 1103;  
 Best Local Similarity 94.5%; Pred. No. 2,9e-312;  
 Matches 997; Conservative 23; Mismatches 9; Indels 26; Gaps 2;  
 QY 1 MAAGCLALITLTFQSLIGSSQEPSPSAVTIKSWDKMOEDLVTLAKTAGVQGLVDI 60  
 Db 1 MAAGCLALITLTFQSLIGSSQEPSPSAVTIKSWDKMOEDLVTLAKTAGVQGLADI 60  
 QY 61 YEKYODLVTVBPNNAKROLVETIARDIEKLINRSKALVRLALBAKVOAAHOMREDPASN 120  
 Db 61 YEKYODLVTVBPNNAKROLVETIARDIEKLINRSKALVRLALBAKVOAAHOMREDPASN 120  
 QY 121 EYVYVNAKDDDDPEKNDESPGSORIKPFVIDANFGROIYQHAHVHPIDYIGSGTIVL 180  
 Db 121 EYVYVNAKDDDDPEKNDESPGSORIKPFVIDANFGROIYQHAHVHPIDYIGSGTIVL 180  
 QY 121 EYVYVNAKDDDDPEKNDESPGSORIKPFVIDANFGROIYQHAHVHPIDYIGSGTIVL 180  
 Db 121 EYVYVNAKDDDDPEKNDESPGSORIKPFVIDANFGROIYQHAHVHPIDYIGSGTIVL 180  
 QY 181 NEIMNTSALDEYFKKRNREDPSLLMOYFGSATGLARYPASPWYDNRTPNKIDLYDVR 240  
 Db 181 NEIMNTSALDEYFKKRNREDPSLLMOYFGSATGLARYPASPWYDNRTPNKIDLYDVR 240  
 QY 181 NEIMNTSALDEYFKKRNREDPSLLMOYFGSATGLARYPASPWYDNRTPNKIDLYDVR 240  
 Db 181 NEIMNTSALDEYFKKRNREDPSLLMOYFGSATGLARYPASPWYDNRTPNKIDLYDVR 240  
 QY 241 RPWYIOGASPKMDILYDVSGVSGLTIKLIRSVSEMELETSDDDFVAVASFNNAOD 300  
 Db 241 RPWYIOGASPKMDILYDVSGVSGLTIKLIRSVSEMELETSDDDFVAVASFNNAOD 300  
 QY 301 VSCFOHLVQAVNRKKYKLVKAANNITAKGJTDYKKGSPFAEQLNRYNRAKCNKIML 360  
 Db 301 VSCFOHLVQAVNRKKYKLVKAANNITAKGJTDYKKGSPFAEQLNRYNRAKCNKIML 360  
 QY 361 FTDGEERAQEIFAKYKDKKVRVFTSVQGHNYDRGPIDGMACENKGYEELPSIGAIR 420  
 Db 361 FTDGEERAQEIFAKYKDKKVRVFTSVQGHNYDRGPIDGMACENKGYEELPSIGAIR 420  
 QY 421 INTQEVLDVIGRPVWVLADGAKAQVQWTVNYLDALDELGLVITGTLVPVNTIGNENKTNLK 480

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|||||
Db 421 INTQEYLDVIGRPVYLAGDKAKOVQMTNYLDLDELGLVITGLTPVFNVTGQSEKNTNLK 480
Qy 481 NOLIGVGVVSVLEDIKRLTPRFTLCPNGYFAIDPNGYVLLHPNLQPK----- 530
Db 481 NOLIGVGVVSVLEDIKRLTPRFTLCPNGYFAIDPNGYVLLHPNLQPKGVIGIPTIN 540
Qy 531 -----NPKSQEPTLDFLDELLENDIKVEIRNKMIDGEGSEKTEFTLVKSODERYI 581
Db 541 LKRRBPVQNPKEQEPVYLDLDELLENDIKVEIRNKMIDGEGSEKTEFTLVKSODERYI 600
Qy 582 DKGNTTYTWTVPNGTDSLALVLPYSPFYIKAKIEETIQARSKKGMDSKMDSETLKPDNF 641
Db 601 DKGNTTYTWTVPNGTDSLALVLPYSPFYIKAKIEETIQAR-----SETLKPDNF 653
Qy 642 EESGYTFIAPRDYCNLDKISDNTEFLLNPNFIDRKTPNNPSCNTDLINRVLLDAFTN 701
Db 654 EESGYTFIAPRDYCNLDKISDNTEFLLNPNFIDRKTPNNPSCNTDLINRVLLDAFTN 713
Qy 702 ELVQNTWSKOKNIKGVKARFVYTDGITRVYPKKAGEMWQENPETYEDSEFKRSIDNDNY 761
Db 714 ELVQNTWSKOKNIKGVKARFVYTDGITRVYPKKAGEMWQENPETYEDSEFKRSIDNDNY 773
Qy 762 VFTAPFNKSGPAGVSGIWSKAVEITYQGLKLPVAVGKIDVNSMIENFTKTSIRD 821
Db 774 VFTAPFNKSGPAGVSGIWSKAVEITYQGLKLPVAVGKIDVNSMIENFTKTSIRD 833
Qy 822 CAGPVCCKRNSDVMDCVILDDGFLLMANHDYTNQIGRFGELIDPSLMRLVNSIYA 881
Db 834 CAGPVCCKRNSDVMDCVILDDGFLLMANHDYTNQIGRFGELIDPSLMRLVNSIYA 893
Qy 882 FNKSYDYQSCVCEGAPKQAGARSAVPSIADILQIGMATAAAMSILOQLLSITFPR 941
Db 894 FNKSYDYQSCVCEGAPKQAGARSAVPSIADILQIGMATAAAMSILOQLLSITFPR 953
Qy 942 LLEAVEMEDDFTASLSKOCITEQTYEFDNDKSFSGVLDGNCSTRIFHVEKLMNTNL 1001
Db 954 LLEAVEMEDDFTASLSKOCITEQTYEFDNDKSFSGVLDGNCSTRIFHVEKLMNTNL 1013
Qy 1002 IFIMVESKGTCPCDTRLILQAEOTSQDGPDCDVK 1036
Db 1014 VFIMVESKGTCPCDTRLILQAEOTSQDGPDCDVK 1048

RESULT 5
OBVHS9 PRELIMINARY; PRT: 1079 AA.
AC 08VHS9:
Db 01-MAR-2002 (TREMUREL. 20, Created)
Db 01-MAR-2002 (TREMUREL. 20, Last sequence update)
Db 01-JUN-2002 (TREMUREL. 21, Last annotation update)
Db L-type calcium channel alpha2/delta subunit.
Db Rattus norvegicus (Rat).
Db Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Db Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
Db NCBI_Taxid=10116;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=HEART;
RX MEDLINE=21601730; PubMed=11604404;
RA Yamada Y., Nagashima M., Tetsuura M., Kobayashi T., Seki S.,
RA Makita N., Horio Y., Tohse N.;
RT "Cloning of a functional splice variant of L-type calcium channel
RT beta2 subunit from rat heart."
RL J. Biol. Chem. 276:47163-47170(2001).
DR EMBL: AF400662; AAL47093.1;
DR InterPro: IPR004010; Cache.
DR InterPro: IPR002035; VME_A.
DR Pfam: PF02743; Cache: 1.
DR Pfam: PF00092; Vwa_1.
DR SMART: SM00327; VWA; 1.
DR PROSITE: PS50234; VWA; 1.
SQ SEQUENCE 1079 AA: 122172 MW: DC4A3641195B546C CRC64:

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Query Match 96.0%; Score 5229; DB 11; Length 1079;
Best Local Similarity 95.88; Pred. No. 8, 3e-111;
Matches 992; Conservative 21; Mismatches 11; Indels 12; Gaps 2;

Qy 1 MAAGCLLALTLTLFQSLIGSSQEPSPASVITKSWDKQOEDLVTLAKTASGVNDLVI 60
Db 1 MAAGCLLALTLTLFQSLIGSSQEPSPASVITKSWDKQOEDLVTLAKTASGVNDLVI 60
Qy 61 YEKYODLYTVEBNNAQOLVEIAADIEKLSNRSKALVRLALEKQVQAQHQREDPASN 120
Db 61 YEKYODLYTVEBNNAQOLVEIAADIEKLSNRSKALVRLAMEKQVQAQHQREDPASN 120
Qy 121 EYVYNAKDOLDPEKNDSEPSGSRIRKPVFIDANFGROIYSQAAVNIPTDIYEGSTIVL 180
Db 121 EYVYNAKDOLDPEKNDSEPSGSRIRKPVFIDANFGROIYSQAAVNIPTDIYEGSTIVL 180
Qy 181 NELNMTSALDEYFKKREDEPSLWQVGSATGLARYYPASPVWDSRTFPRKIDLYVRR 240
Db 181 NELNMTSALDEYFKKREDEPSLWQVGSATGLARYYPASPVWDSRTFPRKIDLYVRR 240
Qy 241 RPYITOGAASPKDMLILVDYSGSVGLTKLIRTSVSEMLTSLDDDFVNAFSNAOD 300
Db 241 RPYITOGAASPKDMLILVDYSGSVGLTKLIRTSVSEMLTSLDDDFVNAFSNAOD 300
Qy 301 VSCFOHLVQANVNRKVKVLDVANNITAKGIDYKKGFSFAEOLINLVNSRANCKIIML 360
Db 301 VSCFOHLVQANVNRKVKVLDVANNITAKGIDYKKGFSFAEOLINLVNSRANCKIIML 360
Qy 361 FTDGEEERAOEIFAKYKNDKRVFTFSVQHNVDGRPIQMAKCNKGYEIPISIGAIR 420
Db 361 FTDGEEERAOEIFAKYKNDKRVFTFSVQHNVDGRPIQMAKCNKGYEIPISIGAIR 420
Qy 421 INTQEYLDVIGRPVYLAGDKAKOVQMTNYLDLDELGLVITGLTPVFNVTGQSEKNTNLK 480
Db 421 INTQEYLDVIGRPVYLAGDKAKOVQMTNYLDLDELGLVITGLTPVFNVTGQSEKNTNLK 480
Qy 481 NOLIGVGVVSVLEDIKRLTPRFTLCPNGYFAIDPNGYVLLHPNLQPKRNSQEPVTL 540
Db 481 NOLIGVGVVSVLEDIKRLTPRFTLCPNGYFAIDPNGYVLLHPNLQPK-----EPVTL 535
Qy 541 DFLDELLENDIKVEIRNKMIDGEGSEKTEFTLVKSODERYIDGNTTYTWTVPNGTDSL 600
Db 541 DFLDELLENDIKVEIRNKMIDGEGSEKTEFTLVKSODERYIDGNTTYTWTVPNGTDSL 600
Qy 595 DFLDELLENDIKVEIRNKMIDGEGSEKTEFTLVKSODERYIDGNTTYTWTVPNGTDSL 595
Db 595 DFLDELLENDIKVEIRNKMIDGEGSEKTEFTLVKSODERYIDGNTTYTWTVPNGTDSL 595
Qy 601 ALVLPYSPFYIKAKIEETIQARSKKGMDSFTLKPDNFESGYTFIAPRDYCNLDK 660
Db 601 ALVLPYSPFYIKAKIEETIQARSKKGMDSFTLKPDNFESGYTFIAPRDYCNLDK 660
Qy 648 ALVLPYSPFYIKAKIEETIQAR-----SETLKPDNFESGYTFIAPRDYCNLDK 648
Db 648 ALVLPYSPFYIKAKIEETIQAR-----SETLKPDNFESGYTFIAPRDYCNLDK 648
Qy 661 SNNTEFLNPNFIDRKTPNNPSCNTDLINRVLLDAFTNELVQNTWSKOKNIKGVKAR 720
Db 661 SNNTEFLNPNFIDRKTPNNPSCNTDLINRVLLDAFTNELVQNTWSKOKNIKGVKAR 720
Qy 708 SNNTEFLNPNFIDRKTPNNPSCNTDLINRVLLDAFTNELVQNTWSKOKNIKGVKAR 708
Db 708 SNNTEFLNPNFIDRKTPNNPSCNTDLINRVLLDAFTNELVQNTWSKOKNIKGVKAR 708
Qy 721 FYVTGGLTRVYPKKAGEMWQENPETYEDSEFKRSIDNDNYVFTAPFNKSGPAGVSGI 760
Db 721 FYVTGGLTRVYPKKAGEMWQENPETYEDSEFKRSIDNDNYVFTAPFNKSGPAGVSGI 768
Qy 768 FYVTGGLTRVYPKKAGEMWQENPETYEDSEFKRSIDNDNYVFTAPFNKSGPAGVSGI 768
Db 768 FYVTGGLTRVYPKKAGEMWQENPETYEDSEFKRSIDNDNYVFTAPFNKSGPAGVSGI 768
Qy 781 MYSKAVEITYQGLKLPVAVGKIDVNSMIENFTKTSIRDPCAGPVCCKRNSDVMDCVI 840
Db 781 MYSKAVEITYQGLKLPVAVGKIDVNSMIENFTKTSIRDPCAGPVCCKRNSDVMDCVI 840
Qy 841 LDDGGFLMANHDYTNQIGRFGELIDPSLMRLVNSIYAFNKSVDYQSCVCEGAPKQ 900
Db 841 LDDGGFLMANHDYTNQIGRFGELIDPSLMRLVNSIYAFNKSVDYQSCVCEGAPKQ 888
Qy 901 GAGHRSAVPSIADILQIGMATAAAMSILOQLLSITFPRLLEAVEMEDDFTASLSKQ 960
Db 901 GAGHRSAVPSIADILQIGMATAAAMSILOQLLSITFPRLLEAVEMEDDFTASLSKQ 948
Qy 961 SCITEQOYFPPNDKSFSGVLDGNCSTRIFHVEKLMNTNLIFIMVESKGTCPCDTRLIL 1020
Db 961 SCITEQOYFPPNDKSFSGVLDGNCSTRIFHVEKLMNTNLIFIMVESKGTCPCDTRLIL 1008
Qy 949 SCITEQOYFPPNDKSFSGVLDGNCSTRIFHVEKLMNTNLIFIMVESKGTCPCDTRLIL 1008
Db 949 SCITEQOYFPPNDKSFSGVLDGNCSTRIFHVEKLMNTNLIFIMVESKGTCPCDTRLIL 1008

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QY 1021 QABQTSDBGPPCDMVK 1036  
DB 1009 QABQTSDBGPPCDMVK 1024

## RESULT 6

Q9UD03 PRELIMINARY; PRT; 745 AA.

AC Q9UD03: 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)  
DE WUGSC:H.DJ0560014.1 protein (fragment)  
GN WUGSC:H.DJ0560014.1  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9063792; PubMed=9847074;  
RA Sulston J.E., Waterston R.;  
RT "toward a complete human genome sequence.";  
RL Genome Res. 8:1097-1108(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Mead K., Bauer C.;  
RT "The sequence of Homo sapiens PAC clone RP4-560014.";  
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
RP SEQUENCE FROM N.A.  
RA Waterston R.;  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AC006145; AAD20938.1;  
DR InterPro: IPR004010; Cache.  
DR InterPro: IPR002035; VWF\_A.  
DR Pfam: PF02743; Cache; 1.  
DR PROSITE: PS50234; VWF\_A; 1.  
FT NON\_TER  
SQ SEQUENCE 745 AA; 84396 MW; BC07B53484B71E4A CRC64;

Query Match 66.7%; Score 3634; DB 4; Length 745;  
Best Local Similarity 98.8%; Pred. No. 1.3e-213;  
Matches 682; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 347 YNVSANCKIIMLTDTGGEERAEIFAKYKDKRVFTEFSVGOHNDREGIOMACEN 406  
DB 1 YNVSANCKIIMLTDTGGEERAEIFAKYKDKRVFTEFSVGOHNDREGIOMACEN 60  
QY 407 KGYEIPISGAIRINTQEVLDVGRPVNLADGAKOVQWNTNYLDALDELGLVITGTLPV 466  
DB 61 KGYEIPISGAIRINTQEVLDVGRPVNLADGAKOVQWNTNYLDALDELGLVITGTLPV 120  
QY 467 FNITGQNFKNKLNKQNLILGVAGVDSLEDIKRLTPRETCOPNGYAYADPNQVILHPN 526  
DB 121 FNITGQNFKNKLNKQNLILGVAGVDSLEDIKRLTPRETCOPNGYAYADPNQVILHPN 180  
QY 527 LQPKPKQOEAVTLDLDALENDIKVEIRKMDIGSEGEKTERILVKSODEYIDKGRN 586  
DB 181 LQPKPKQOEAVTLDLDALENDIKVEIRKMDIGSEGEKTERILVKSODEYIDKGRN 240  
QY 587 TYTWPVNGTDYSLALVPTYSFYIKAEETITQARSKKGMKSEITLKDNEESGY 646  
DB 241 TYTWPVNGTDYSLALVPTYSFYIKAEETITQARSKKGMKSEITLKDNEESGY 300  
QY 647 TFLAPRYCNDLKSNDNTEFLINNEFDIKRTPNNPSCNTDILINVLIDAGFTNELVN 706  
DB 301 TFLAPRYCNDLKSNDNTEFLINNEFDIKRTPNNPSCNTDILINVLIDAGFTNELVN 360  
QY 707 YMSKQNIKGVKARFVYTGIGIRVYKRAKEMQENPTTYSYKSLDNDNYVTAP 766  
DB 361 YMSKQNIKGVKARFVYTGIGIRVYKRAKEMQENPTTYSYKSLDNDNYVTAP 420

QY 767 YFNKSGPAGVESGIMVSKAVEIYIOGKLIKPAVGIKIDVNSWTEENFTKSIRPCAGPV 826  
DB 421 YFNKSGPAGVESGIMVSKAVEIYIOGKLIKPAVGIKIDVNSWTEENFTKSIRPCAGPV 480  
QY 827 CDCKRNSDVMDCVILDDGFLMANHDDYTNQIGFEEIDPSTMLRLVNI SYAENKSY 886  
DB 481 CDCKRNSDVMDCVILDDGFLMANHDDYTNQIGFEEIDPSTMLRLVNI SYAENKSY 540  
QY 887 DYQSCGEGAPKQAGRSAYVPSIADILHIGMATAAWSIIQOFLSLTFPRILEAV 946  
DB 541 DYQSCGEGAPKQAGRSAYVPSIADILHIGMATAAWSIIQOFLSLTFPRILEAV 600  
QY 947 EMEDDFTASLSKSCITQYQYFFNDKSFSGVLDGCGCSRIFPVEKMTNLPFIW 1006  
DB 601 EMEDDFTASLSKSCITQYQYFFNDKSFSGVLDGCGCSRIFPVEKMTNLPFIW 660  
QY 1007 ESKGTCPDTRLLQABQTSDBGPPCDMVK 1036  
DB 661 ESKGTCPDTRLLQABQTSDBGPPCDMVK 690

## RESULT 7

Q9NY47 PRELIMINARY; PRT; 1150 AA.

AC Q9NY47: 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)  
DE 01-MAR-2002 (Tremblrel. 20, last annotation update)  
GN Calcium channel, alpha 2/delta subunit 2.  
OS CACNA2D2.  
OC Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA TISSUE=THYROID;  
RA Kluopauer N.;  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA TISSUE=THYROID;  
RC Hobom M., Dai S., Marras E., Iacinoia L.;  
RT "Neuronal distribution and functional characterization of the calcium channel alpha2delta-2 subunit.";  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ251368; CACB6193.1;  
DR InterPro: IPR004010; Cache.  
DR Pfam: PF02743; Cache; 1.  
DR SMART: SM00327; VWA; 1.  
DR PROSITE: PS50234; VWF\_A; 1.  
SQ SEQUENCE 1150 AA; 129876 MW; 37B75F687AE573C CRC64;

Query Match 54.4%; Score 2965; DB 4; Length 1150;  
Best Local Similarity 54.6%; Pred. No. 1.9e-172;  
Matches 575; Conservative 171; Mismatches 274; Indels 34; Gaps 14;

QY 7 LATLTFOSLILGSSQEPFPAVITKSVMDQDLYTLAKTASGVNQLVDIYEKYD 66  
DB 44 LMILLPLPLLPALAPGASVSPFOOHTMOHWARLDEYGVGVRIFGVQOLAEIYKDRN 103  
QY 67 LYIYEPNNAQVEIARDEKLSNRSKALVRLALEAKYQAAHOMEDFASNEVYTN 126  
DB 104 LFEVQENEPQKLEKVAAGIESLDRKVALKRIDAAENFQKAHMODNKEEDIIYD 163  
QY 127 AKDDL--DPEKNSRPGQ--RIKVFIDANFGRQISYQAAVHIPTDIYEGSTIYN 181  
DB 164 AKDADELDPESDEVERGSKASTLRDLFEDPNFKNKYNYSYAAVQPTDIYKSTIYN 223  
QY 182 ELNWTALDENVEKKNREBPSSILMOVFGSAGTATYASAWVNSRPNKIDLYVRR 241  
DB 224 ELNWTALDENVEKKNREBPSSILMOVFGSAGTATYASAWVNSRPNKIDLYVRR 279





RA Minna J.D.;  
 RT "Gene 26, a new candidate human tumor suppressor gene located in the  
 RT 3p21.3 small cell lung cancer homozygous deletion region homologous to  
 RT a voltage gated calcium channel alpha 2/ delta subunit.";  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Wei M.-H., Latif F., Duh F.-M., Adreazoli-Angeloni D., Kashuba V.,  
 RA Zabarovsky E., Johnson B., Lerman M.I.;  
 RT "A new alpha 2 delta subunit of the L-type voltage gated calcium  
 RT channel resides in the lung cancer critical region on 3p21.3.";  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RX MEDLINE-98290545; PubMed-9628581;  
 RA Nagase T., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.,  
 RA Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. IX.  
 RT The complete sequences of 100 new cDNA clones from brain which can  
 RT code for large proteins in vitro.";  
 RL DNA Res. 5:31-39(1998).  
 DR EMBL: AF040709; AAC70914.1; -  
 DR EMBL: AF042792; AAB96913.1; -  
 DR EMBL: AB011130; BAA25484.1; -  
 DR InterPro: IPR004010; Cache.  
 DR InterPro: IPR002035; VWF\_A.  
 DR Pfam: PF02743; Cache; 1.  
 DR SMART: SM00327; VWA; 1.  
 DR PROSITE: PS50234; VWF\_A; 1.  
 SQ SEQUENCE 1145 AA; 129268 MW; 9ADA4807FC70971B CRC64;  
 Query Match 53.7%; Score 2924.5; DB 4; Length 1145;  
 Best Local Similarity 54.2%; Pred. No. 56-170;  
 Matches 572; Conservative 170; Mismatches 271; Indels 43; Gaps 16;

QY 7 LALTLTLPQSLILGSSQSEPPSAVITKSWVDKMQEDLVTLATASVNOVDIYEYOD 66  
 DB 44 LMLLPLPLLAAPGASVSPQOHTWQHARRLEDDVDMKIFGVQOLREITYDNRN 103  
 QY 67 LYTEPPNNAQOLVEIARADIEKLISNRKALVRLALEAEKQAQAHQWREDFASNEVYVN 126  
 DB 104 LFEVQENEPKIVKAGDIESLLDRKQVQLKRLADAENFQAHKQNDIKEDIIYVD 163  
 QY 127 AKDDL--DEKNDSEPGSQ--RIKPVFIDANFGROIYQHAHVHPTDIYEGSTIVLN 181  
 DB 164 AKADAELDESEDEVERGSKASTLRLEDFIEDPNEKNKNVSYAYQIPTDIYKSTVILN 223  
 QY 182 ELNMTSALDVEPKNREDEPSILMOVGSAATGLARYYPASPDWNSRTPKIDLYDVR 241  
 DB 224 ELNMTSALDVEPKNREDEPSILMOVGSAATGLARYYPASPDWNSRTPKIDLYDVR 279  
 QY 242 PMYIOGASPRMDLILVDVSGSVGLTKLIRTSVSEMLETLSDDDPVNVSFNSADY 301  
 DB 280 PMYIOGASPRMDVILVDVSGSVGLTKLIMKTSVCEMLDLSDDVYVNASFNEKQPV 339  
 QY 302 SCFOHLVQANRNKKTVDKAVNNITANGITDYKGFSEFAEOLINVSANCKITMLF 361  
 DB 340 SCFHLVQANRNKKTVDKAVNNITANGITDYKGFSEFAEOLINVSANCKITMLF 399  
 QY 362 TDGGEERAEAFAYN-KDKKRVFTEFSGVGOHNDRIPIOMMACENGYEETPSICAIR 420  
 DB 400 TDGGEERAEAFAYN-KDKKRVFTEFSGVGOHNDRIPIOMMACENGYEETPSICAIR 459  
 QY 421 INTQEDLVIGRPVAVLAGRAKQVQWNTNVLDAELGLVITGLPVENIT--GQENKTN 478  
 DB 460 INTQEDLVIGRPVAVLAGRAKQVQWNTNVLDAELGLVITGLPVENIT--GQENKTN 516  
 QY 479 LKNQILIGWGVYSLDIKRLTPRTFLCPNGYFAIDPKGYVLIHNLDPKPKSKSEPV 538  
 DB 517 -KNQILIGWGVYSLDIKRLTPRTFLCPNGYFAIDPKGYVLIHNLDPKPKSKSEPV 575  
 QY 539 TLDFLDAELNDIKVEIRNKMIDEGSEKTFRTLVKSGDERYIDKGRYTWTPVNCYD 598

DB 576 TLDFLDAELNDIKVEIRNKMIDEGSEKTFRTLVKSGDERYIDKGRYTWTPVNCYD 635  
 QY 599 SLATLVPTSEFYIYAKIEETITTOARSKKGMKQSEETLPDNEESGYTAPRDYCDL 658  
 DB 636 SIGILVLPSTFYLOANLSDILO-----VKYREFLLPSSFESEGVFLAPREYCDL 688  
 QY 659 KISDNTEFLNFPNEDIKRTPNPNDSCTDLINRVLLDAGFTNELVQWYSKQK-NIKGV 717  
 DB 689 NASDNTEFLNFPNEDIKRTPNPNDSCTDLINRVLLDAGFTNELVQWYSKQK-NIKGV 748  
 QY 718 KARFVVTGQITRVYPKKEGEMWQENPEYDESEFKRSGLDNDNYFTAPYNNK-SGPAY 776  
 DB 749 LAVFAATDGLTRVFPNKAEDMTENPEFNASEFRSLDNHGVFKRPHDALLRPLEL 808  
 QY 777 ES---GIMSKAVEITYIOGKLKPAVVGIKIDVNSMINE-----TKSIRDP--CAGP- 825  
 DB 809 ENDYTGILVSTAVELSLGRTLRPAVVGKIDLEMAKFKVYASNRHNOQPKC-GPN 867  
 QY 826 ---VCDCKRNSDVMDCVILDDGFFLLMANHDDYTNOIGRFEGLDPSLMRLVNTSYAF 882  
 DB 868 SHCEMDCEVNNEDLLCYLLDDGFFLVLSNQNHQMOVGREFSEVDANLMLALYNNSEFYTR 927  
 QY 883 NKSVDQSVCEGGAAPKQAGHRSAYVPSIADILHGMWATPAAMSILQOFLSLTFEPL 942  
 DB 928 KESTYDQACACAPQPGNGLAAPRGVFPVADPLMLAMWTSAAASLTFQOLYLITHSW 987  
 QY 943 LEAVEMEDDFTASLSKOSCTEOTYFENDSKSFSGVLDGNCRSRIPEHEKLTNLI 1002  
 DB 988 PQADPAEAGC-SPEIRRESSCVMKQYVGSVNASYNAIMIDGNCRLPFAHQRLNTNLL 1046  
 QY 1003 FIMVESKGTCPDCTRLILDAEO--TSDEPDPDMMK 1036  
 DB 1047 FYVAEKPLCSOCEAGRLLOKETHCPADGPEOCELVQ 1082

RESULT 11  
 ID 0920H6 PRELIMINARY; PRT; 1084 AA.  
 AC 0920H6;  
 DT 01-DEC-2001 (TREMblrel, 19, Created)  
 DT 01-DEC-2001 (TREMblrel, 19, Last sequence update)  
 DT 01-JUN-2002 (TREMblrel, 21, Last annotation update)  
 DE Voltage-dependent calcium channel alpha-2-delta-2 mutant subunit  
 DE 2.  
 GN CACNA2D2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-TKDU;  
 RX MEDLINE-21380284; PubMed-11487633;  
 RA Barclay J., Balazquez N., Mione M., Ackerman S.L., Letts V.A.,  
 RA Brobeck J., Cantl C., Meir A., Page K.M., Kusumi K., Perez-Reyes E.,  
 RA Lander E.S., Frankel W.N., Gardiner R.M., Dolphin A.C., Rees M.;  
 RT "Ducky mouse phenotype of epilepsy and ataxia is associated with  
 RT mutations in the Cacna2d2 gene and decreased calcium channel current  
 RT in cerebellar Purkinje cells.";  
 RL J. Neurosci. 21:6095-6104(2001).  
 DR EMBL: AF247141; AL01650.1; -  
 DR MGI:1929813; Caena2d2.  
 DR InterPro: IPR004010; Cache.  
 DR InterPro: IPR002035; VWF\_A.  
 DR Pfam: PF02743; Cache; 1.  
 DR PROSITE: PS50234; VWF\_A; 1.  
 SQ SEQUENCE 1084 AA; 123104 MW; 197D6B5B37EB9893 CRC64;  
 Query Match 53.5%; Score 2912; DB 11; Length 1084;  
 Best Local Similarity 54.5%; Pred. No. 36-169;  
 Matches 561; Conservative 173; Mismatches 260; Indels 36; Gaps 15;



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33 IKSMDKMOEDLVLTAKTASGVNOLVDIYKDYKDYVPEPNNAQOLVEIARDEKLSLN 92
Db 1 MOHARRLEOEIDGVNRIGVQOLREIKDRNLFEVOENEPOLKIVEKVAADIESLDR 60
Qy 93 RSKALVRLAEKVOAAHOMREDFASNEVYYNAKDDL---DPEKNSEPSQ--RIKP 147
Db 61 KYQALKRLDAEENFOKAHRMOKNIKEEDIMYDKAADAELDDPESEMERSEKSTALRL 120
Qy 148 VFIDANFGROISYOAAVHIPTDIYEGSTIYLNELNMTSALDEYFKKREDEPSLMOY 207
Db 121 DEIEDNPNFKKNVSYTAQVLPDIYKGSYVILNLMNTFALENVFNIRKQDPILLMOY 180
Qy 208 FGSATGLARYPASPWVNDNSTPKNIDLYVRRRPWYOGAASPMDLILVDSGSVGL 267
Db 181 FGSATGVTRYPATPW---RAPKKIDLYVRRRPWYOGAASSPMDVITVDSGSVGL 236
Qy 268 TLKLI RTSVSEMLFETLSDDDPVNVA SFNSNADVSCFOHLYOANVRNKKVLDKAVNNTA 327
Db 237 TLKMKTSVCEMLDITLSDDDVYNVASFNEKAOPVSCFTHLYOANVRNKKVLEKAVOGMYA 296
Qy 328 KGITDYKKGFSPAFBOLLNYSNRANCKIIMLFTDGEERAOEIFAAYN-KDKVRYFT 386
Db 297 KGITDYKAGFEYAFDQOLNSNTRANCNMIMFTDGEDVADVDFEYKYNMNPRTVRYFT 356
Qy 387 FSVGQHNDRGPIOWMACENKGYEIPISGAIRINTOEYLDVLRPVYLAGDKAKOVOM 446
Db 357 FSVGQHNDRGPIOWMACENKGYEIPISGAIRINTOEYLDVLRPVYLAGDKAKOVOM 416
Qy 447 TNYVDALGLVITGTLPVENIT--GONENKTNLKNOLLIGVGVYSLDIEKRLPRF 504
Db 417 TNYVDALGLVITGTLPVENITDODGEEK---KNOLLIGVGVYSLDIEKRLPRF 472
Qy 505 TILCPNGYFAIDPNGVYLLHPNLOPKNPKSOEPTLDFLDAELDENDEKVEIRNKMIDGES 564
Db 473 TLGANGYFAIDLNGVYLLHPNLOPKNKTNPFPYTLDFLDAELDENDEKVEIRNKMIDGES 532
Qy 565 GEKTFRTIYKSDERYIDKGNRTYTPVNGTYSIALVLTPTSYFYIKAKIEETITQAR 624
Db 533 GHKQIRTLVKSIDERYIDEVTRNTYWPVIRSTNYSGLVLPYSTYVYLOANLSQIIOYK 592
Qy 625 SKKGAKMDETLKPDNFEESGTYFLAPRDYCNLKSIDNTEFLNNEFLNNEFLDRTPNNPS 684
Db 593 LPISTLKNFEPFLPSSFESEGHVITAPREYKCDLNASDNSTEFKDTLEMEKVTDPDSQ 652
Qy 685 CNTDLINRVLLDAGFTNELVONVYSKOK-NIKGVKARFVYDGGITRYVPEKAGENNMOEN 743
Db 653 CNMFLNHLIITDGTITQOLVERVWRDOLNNTYSLAVFAADTGGITRVFPMKAEDMTEN 712
Qy 744 PETEDSFYKRSKLDNDNVFTAFYFNK-SGPAGAYES---GIMVSKAVEIYIQLKLPAY 799
Db 713 PEPRNASTYKRSKLDNHGTFIKPRHODSLARPLELENDYVGLVSTAVELSGRRTLRPAV 772
Qy 800 VGKIDVNSMIENF---TKTSIRDP--CAGP---VCDCRNSDVMDCVITLDDGFL 848
Db 773 VGVKLDELEAMEKFKVYLASNRTDODQOKC-GPSSHCEMCEVANNEDLVCYLDDGGFLV 831
Qy 849 MANDDYTNQIGRFFGELIDSLMRHLVNISSVAFNKSVDYOSVCEPAGABKOGAGHSAY 908
Db 832 LSNONHOMDQVGRFSEVDANMLALNNSFYTRKESYDYQACAPQPCNLGAAPRGVF 891
Qy 909 VPSIADILHIGWMTAAASIILOQFLSLTFEPRLLEAVEHEDDFTYSLSKOSTITQOTQ 968
Db 892 VPTIADILNLAAMWTSAAMSLFOOLLGLYHSWFOADPAEAB-SERTRESSCYMKTQ 950
Qy 969 YFPNDKSFSGVLDGNCGRIFHEKIMNTNLIIFIVESKGTCPDTRILLIOAQE--TS 1026
Db 951 YFSGSVANNAIITDGCNCRIFHAQRLTNMLFFVAEKPFLCSQCEAGNLLQKETHCPA 1010
Qy 1027 DGPPPCMVK 1036
Db 1011 DGPPCEIYQ 1020

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RESULT 12
ID Q9UEMO PRELIMINARY; PRT: 1076 AA.
AC Q9UEMO;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-MAR-2002 (Tremblrel. 20, Last annotation update)
OS Alpha 2 delta calcium channel subunit isoform II.
OC Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wei M.-H., Latif F., Duh F.-M., Adreazoli-Angeloni D., Kashuba V.,
RA Zbarovsky E., Johnson B., Lerman M.I.;
RT "A new alpha 2 delta subunit of the L-type voltage gated calcium
RT channel resides in the lung cancer critical region on 3p21.3."
RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF042793; AAB96914.1;
DR InterPro: IPR004010; Cache.
DR InterPro: IPR002035; VWF_A.
DR Pfam: PF02743; Cache; 1.
DR SMART: SM00327; VWA; 1.
DR PROSITE: PS50234; Cache; 1.
DR PROSITE: PS50234; VWA; 1.
SQ SEQUENCE 1076 AA; 122116 MW; EEC474836B7EDA85 CRC64;

Query Match 53.3%; Score 2903.5; DB 4; Length 1076;
Best Local Similarity 54.7%; Pred. No. 9.7e-169;
Matches 563; Conservative 169; Mismatches 255; Indels 43; Gaps 16;

Qy 33 IKSMDKMOEDLVLTAKTASGVNOLVDIYKDYKDYVPEPNNAQOLVEIARDEKLSLN 92
Db 1 MOHARRLEOEIDGVNRIGVQOLREIKDRNLFEVOENEPOLKIVEKVAADIESLDR 60
Qy 93 RSKALVRLAEKVOAAHOMREDFASNEVYYNAKDDL---DPEKNSEPSQ--RIKP 147
Db 61 KYQALKRLDAEENFOKAHRMOKNIKEEDIMYDKAADAELDDPESEMERSEKSTALRL 120
Qy 148 VFIDANFGROISYOAAVHIPTDIYEGSTIYLNELNMTSALDEYFKKREDEPSLMOY 207
Db 121 DEIEDNPNFKKNVSYTAQVLPDIYKGSYVILNLMNTFALENVFNIRKQDPILLMOY 180
Qy 208 FGSATGLARYPASPWVNDNSTPKNIDLYVRRRPWYOGAASPMDLILVDSGSVGL 267
Db 181 FGSATGVTRYPATPW---RAPKKIDLYVRRRPWYOGAASSPMDVITVDSGSVGL 236
Qy 268 TLKLI RTSVSEMLFETLSDDDPVNVA SFNSNADVSCFOHLYOANVRNKKVLDKAVNNTA 327
Db 237 TLKMKTSVCEMLDITLSDDDVYNVASFNEKAOPVSCFTHLYOANVRNKKVLEKAVOGMYA 296
Qy 328 KGITDYKKGFSPAFBOLLNYSNRANCKIIMLFTDGEERAOEIFAAYN-KDKVRYFT 386
Db 297 KGITDYKAGFEYAFDQOLNSNTRANCNMIMFTDGEDVADVDFEYKYNMNPRTVRYFT 356
Qy 387 FSVGQHNDRGPIOWMACENKGYEIPISGAIRINTOEYLDVLRPVYLAGDKAKOVOM 446
Db 357 FSVGQHNDRGPIOWMACENKGYEIPISGAIRINTOEYLDVLRPVYLAGDKAKOVOM 416
Qy 447 TNYVDALGLVITGTLPVENIT--GONENKTNLKNOLLIGVGVYSLDIEKRLPRF 504
Db 417 TNYVDALGLVITGTLPVENITDODGEEK---KNOLLIGVGVYSLDIEKRLPRF 472
Qy 505 TILCPNGYFAIDPNGVYLLHPNLOPKNPKSOEPTLDFLDAELDENDEKVEIRNKMIDGES 564
Db 473 TLGANGYFAIDLNGVYLLHPNLOPKNKTNPFPYTLDFLDAELDENDEKVEIRNKMIDGES 532
Qy 565 GEKTFRTIYKSDERYIDKGNRTYTPVNGTYSIALVLTPTSYFYIKAKIEETITQAR 624
Db 533 GHKQIRTLVKSIDERYIDEVTRNTYWPVIRSTNYSGLVLPYSTYVYLOANLSQIIOYK 590
Qy 625 SKKGAKMDETLKPDNFEESGTYFLAPRDYCNLKSIDNTEFLNNEFLNNEFLDRTPNNPS 684

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Db 591 -----VKYFEFLPSSFSSESGHVFIAPREXCKDLNASDNNTEFLKMFIELMEKVTDSKO 645
QY 685 CMTDLINRVLADAGFTNELVQNTWSKOK-NIKGVKARFVYTDGKITRVYPRKENGMOEN 743
Db 646 CNNFLLHNLIDTIGITQOULVERVWRQDQDNTYSLAVFAATDGTITRPPNKAAEDMTEN 705
QY 744 PENYEDSEFYRSIDNNYVETAFYFNK-SGPGAYES---GIMSKAVEIYIOCKILKRAY 799
Db 706 PEFFNASEFTRSDNHGYEFKPPHODALLRPLELNDVTGILVSTVLESLGRTLRPAV 765
QY 800 VGKIDVNSWIENF-----TKTSIRDP--CAGP---VCDCKRNSDVMCDVILDDGFFLL 848
Db 766 VGKLDLEMAEAEKFKVLASRTHQDPOKC-GPNSHCENDCEVNNNDLCLVILDDGFFLV 824
QY 849 MANHDDITNOIGRFEIDPSLRHLVNTSVAFNKSSTYQSYGCEGAPKQAGHRSAY 908
Db 825 LSNQNHQMDQVGRFESEVANMLALYNSFYRKESYDYQAACAPQPGNIGABRGVF 884
QY 909 VPSIADILHGMWATAAMSIIQOFLSLTFPRLLAEVEMEDDFTASLSKOSCTIEQO 968
Db 885 VPTVAOFLNLAAMWTSAAASLFFQQLYGLYHSWFOADPAEAG-SPTRESSCVMKQTO 943
QY 969 YFENDNSKSGVLDGNGSRIFHVEKLMNTNLIETIMVESKGTCPDTRLLIOAQO--TS 1026
Db 944 YRGSVNASYNATIIDGNCGRPLFHAQRLNTNLLFYVAEKPLCSQCEAGRLLQKETHCPA 1003
QY 1027 DGPDCDMVK 1036
Db 1004 DGEQCELVQ 1013

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RESULT 13  
Q9NSA6 PRELIMINARY: PRT: 975 AA.

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AC Q9NSA6:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE LUAC11.1 (Calcium channel, voltage-dependent, L type, alpha 2D subunit
DE (K1A0558) (Fragment).
GN LUAC11.1.
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Barlow K.;
RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; Z84492; CAB41767.2;
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50234; VWFA; 1.
FT NON_TER
SQ SEQUENCE 975 AA: 110192 MM: C7874D46B88242BF CRC64:

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Query Match 50.1%; Score 2728; DB 4; Length 975;  
Best local similarity 56.8%; Pred. No. 4.4e-158;  
Matches 527; Conservative 142; Mismatches 219; Indels 40; Gaps 15;

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QY 132 DPEKNDSEPGSQ--RIKPVFIDANFGROIYQHAHVHTPTDIYEGSTIVLNELMTSL 189
Db 2 DPESEDEVERGSKASTLRLEFIEDPNFKKNVSYAAVOJPTDIYKSTYILNELMTEAL 61
QY 190 DEYFKNRREDPSLLMQVGSATGLARYPASVWVNDSTPNKIDLYVRRRPWTIOGAA 249
Db 62 ENYFMENRRQDPTLLMQVGSAGVRYYPATPW---RAPKKIDYVRRRPWTIOGAS 117
QY 250 SPKDMILLVDSGVSGLTKLIRTSVEMLETLSDDDVNVNVSFNSNADQVSCFOHLQ 309
Db 118 SPDMVYIYDVSGVSGTLTKLTKTSYCEMLDITLSDDDVNVNVSFNEKAQVSCFTHLVQ 177

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QY 310 ANVRNKKVYLKDAVNNITAKGITDYRKGSFAFEQOLLNVNSRANCKIIMLFTDGEERA 369
Db 178 ANVRNKKVFEKAVQGMVAKGTTGYKAGFEYAFDQLONSNITRANCKIIMLFTDGEDRV 237
QY 370 ORIFAKYN-KDKKVVVFVFSVGQHHYDGRPIOMNACEKGYTELPISGALRINTOEILD 428
Db 238 QVFEKRYMNPNTVAVFVFSVGQHHYDVTPIOMNACAKGYTELPISGALRINTOEILD 297
QY 429 VLGRRPVLADGAKAOVMTNVTYLDALLEGVYTGLPENFT--GQNKNTLNKQILG 486
Db 298 VLGRRPVLADGAKAOVMTNVTYLDALLEGVYTGLPENFT--GQNKNTLNKQILG 353
QY 487 VNGVDVSLEDIKRLTPRETLCPNGYFALIDPNGVYLHPNLOPKNKSQSEPTLIDFLDAE 546
Db 354 VNGIDVALNDIKRLTPNTLTGANGYFALIDNGVYLHPNLOPKNKSQSEPTLIDFLDAE 413
QY 547 LENDIKVELIRNMIDEGEGERTFLVSOBERYIDKRNRYTTPVNGTYSLALVPT 606
Db 414 LEDENKEELIRSMIDGNNGHQIRLVKSLDERYIDEVTRNVTWPIRSTNYSGLVLP 473
QY 607 YSFYIRAKIETITQARSKKGMKDETLKPDNFEESGYFIAPROVCNDLKSNDNTE 666
Db 474 YSTFYLOANLSDQIIQ-----VKYFEFLPSSFSSESGHVFIAPREXCKDLNASDNNTE 526
QY 667 FLNLFNEFIDRKTTPNPNPCNTDLINRVLADAGFTNELVQNTWSKOK-NIKGVKARFVYTD 725
Db 527 FLNLFNEFIDRKTTPNPNPCNTDLINRVLADAGFTNELVQNTWSKOK-NIKGVKARFVYTD 586
QY 726 GGITRVYPRKENGMOENPEYTESFYKRSIDNDNYVETAFYFNK-SGPGAYES---GIM 781
Db 587 GGITRVYPRKENGMOENPEYTESFYKRSIDNDNYVETAFYFNK-SGPGAYES---GIM 746
QY 782 VSKAVEIYIOCKILKRAYGKIDVNSWIENF-----TKTSIRDP--CAGP---VCDCK 830
Db 647 VSTAEVLSIGRTLPAYAVGKLDLEMAEAEKFKVLASRTHQDPOKC-GPNSHCENDCE 705
QY 831 RNSDVMCDVILDDGFFLLMANHDDITNOIGRFEIDPSLRHLVNTSVAFNKSSTYQSY 890
Db 706 VNNEDLCLVILDDGFFLVLSNQHMDQVGRFESEVANMLALYNSFYRKESYDYQA 765
QY 891 VCEPGAARKQGGHSAVPSIADILHGMWATAAMSIIQOFLSLTFPRLLAEVEMED 950
Db 766 ACAPQPGNIGABRGVFPVADFLNLAAMWTSAAASLFFQQLYGLYHSWFOADPAE 825
QY 951 DFTASLSKOSCTIEQOYFENDNSKSGVLDGNGSRIFHVEKLMNTNLIETIMVESKG 1010
Db 826 EG-SPTRESSCVMKQTOYIRFESVNASYNATIIDGNCGRPLFHAQRLNTNLLFYVAEKPL 884
QY 1011 TPCDTRLLIOAQO--TSDGPDPCDMVK 1036
Db 885 CSQCEAGRLLQKETHCPADGPEQCELVQ 912

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RESULT 14  
Q9ZIL5 PRELIMINARY: PRT: 1091 AA.

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AC Q9ZIL5:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Calcium channel alpha-2-delta-C subunit.
GN CACNA2D3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Klugbauer N.; Lachova L.; Marais E.; Hobom M.; Hofmann F.;
RT "Molecular diversity of the calcium channel alpha2delta subunit.";
RL J. Neurosci. 19:648-691(1999).

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Qy	1	MAAGLIALTLTLFOSLITIGPSSPEEPESA	VTIKSWYDKMDEDLVTLAKTASGVNOLVDI	60
Db	1	MAAGLIALTLTLTLFOSLITIGPSSPEEPESA	VTIKSWYDKMDEDLVTLAKTASGVNOLVDI	60
Qy	61	YKKYODIATVPENNMAROLVETIAR	IEKLTLSNRKALVSTALTEAKYQAAHOMEDFASN	120
Db	61	YKKYODLTVPENNMAROLVETIAR	IEKLTLSNRKALVSTALTEAKYQAAHOMEDFASN	120
Qy	121	EYVYVYNAKDDLDPEKNDSEPGSQR	IKPFVIEDANFGROI	180
Db	121	EYVYVYNAKDDLDPEKNDSEPGSQR	IKPFVIEDANFGROI	180
Qy	181	NELNMTSALDEVYKKNRREDEPS	LIMQVGSATGLARYPASPVWYDNRSTPNKIDLYDVR	240
Db	181	NELNMTSALDEVYKKNRREDEPS	LIMQVGSATGLARYPASPVWYDNRSTPNKIDLYDVR	240
Qy	241	RRMYTIGGAASPRMDLITVDVSGSVGLTK	LIRTSVSMELTSLDDDPVYVNAFSPNSAOD	300

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Db 241 RPYIQAASPKDMLILVDVSGVSLTLKILRTSVSEMLETTISDDDFVAVAFNSAOD 300
Oy 301 VSCFOHVOANVRKATLKAANNITAKGTTDYKKGFSFAFEOLNYSRANCKIIML 360
Db 301 VSCFOHVOANVRKATLKAANNITAKGTTDYKKGFSFAFEOLNYSRANCKIIML 360
Oy 361 FTDSGEERAEIENKYNKDKKVVFRSVGONHYERGPLOMACENKGYIETPSIGAIR 420
Db 361 FTDSGEERAEIENKYNKDKKVVFRSVGONHYERGPLOMACENKGYIETPSIGAIR 420
Oy 421 INNOEYIDVGRPMVLADGAKOVQWNTYLDALDELGLVITGTLPEFNITGOPENKTNK 480
Db 421 INNOEYIDVGRPMVLADGAKOVQWNTYLDALDELGLVITGTLPEFNITGOPENKTNK 480
Oy 481 NOILIGMVDVSLIEDIKRLTPEFTCPNGYFAIDPNCGYVLHPLQPKNSQEPVTL 540
Db 481 NOILIGMVDVSLIEDIKRLTPEFTCPNGYFAIDPNCGYVLHPLQPKNSQEPVTL 540
Oy 541 DFLDAELNDIKVELNKKMIDSGEERTLVKSODEYITDKGNTYTWTVNGTIDSL 600
Db 541 DFLDAELNDIKVELNKKMIDSGEERTLVKSODEYITDKGNTYTWTVNGTIDSL 600
Oy 601 ALVLPYSSYITKALEETITQARSKKGMKDETLKPNFESGYTFIAPRDYCNDLKI 660
Db 601 ALVLPYSSYITKALEETITQARSKKGMKDETLKPNFESGYTFIAPRDYCNDLKI 660
Oy 661 SDNTEFLTNFNEEDRKTNNPSCNADLINVLDAEFTNLTNYSKOKNIKVKAR 720
Db 661 SDNTEFLTNFNEEDRKTNNPSCNADLINVLDAEFTNLTNYSKOKNIKVKAR 720
Oy 721 FVYTGCTIRVYPRKAGENWQENPEYEDSFYKRSILDNDNYFTAPYFNKSGPAYESGI 780
Db 721 FVYTGCTIRVYPRKAGENWQENPEYEDSFYKRSILDNDNYFTAPYFNKSGPAYESGI 780
Oy 781 MYSKAVEIYIOGKLKPAVVGKIDVNSWIEFTTSTIRDOACGYCDCKKNSDVMDVI 840
Db 781 MYSKAVEIYIOGKLKPAVVGKIDVNSWIEFTTSTIRDOACGYCDCKKNSDVMDVI 840
Oy 841 LDDGGFLLMANHDYTNIGRFFGIDPSLRHLVNI SVYAFNKS SYDQSCFEGAPKQ 900
Db 841 LDDGGFLLMANHDYTNIGRFFGIDPSLRHLVNI SVYAFNKS SYDQSCFEGAPKQ 900
Oy 901 GAGHSASVPSVADILQIGWATAAASIIQOFLSTLTPRLLBAVEMEDDFTASLSKQ 960
Db 901 GAGHSASVPSVADILQIGWATAAASIIQOFLSTLTPRLLBAVEMEDDFTASLSKQ 960
Oy 961 SCITEQOYFFDNDKSKSFSGVLDCGNSRIFHGEKIMNTNLIETMVSCKGTCPCDTPLI 1020
Db 961 SCITEQOYFFDNDKSKSFSGVLDCGNSRIFHGEKIMNTNLIETMVSCKGTCPCDTPLI 1020
Oy 1021 QAEOTSDGPNPCDMVK 1036
Db 1021 QAEOTSDGPNPCDMVK 1036

```

## RESULT 2

```

US-09-875-423-5
; Sequence 5, Application US/09875423
; Patent No. US20020081657A1
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Roy A. J.
; TITLE OF INVENTION: 21784, A NOVEL HUMAN CALCIUM CHANNEL
; FILE REFERENCE: 10448-059001
; CURRENT APPLICATION NUMBER: US/09/875,423
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,257
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1091

```

```

; TYPE: PRT
; ORGANISM: Mus musculus
US-09-875-423-5
Query Match 19.9%, Score 1085; DB 10; Length 1091;
Best Local Similarity 28.7%; Pred. No. 3,56-70;
Matches 309; Conservative 222; Mismatches 416; Indels 128; Gaps 40;

Oy 3 AGCLLALLTLTFOSSLIPSSSEPPPSAVITKSWDKQOEDLVTLAKTASGNOVDIYE 62
Db 14 ASALLA-TALLIYALGDVREDOOIPLSV-VKLASAFGGKIKSIKAAVSGSLQKKYK 71
Oy 63 KYODLYVEPNNAQVLAARDIEKLNSKSLVSLAEAEVQAHOHREBPASNEV 122
Db 72 EYKQVLAIEIDIGLVYKLLAKIMEEPMHKKSEVRLVLAEEAAHLKHEFDAL--OY 128
Oy 123 VYIYNAK--DDIDPEKNDSEPSQRIKVPFIEDANFGR-QISYQHAHIFPTDIESTY 179
Db 129 EYFNAVILINERDKGNLELGEKEFI--LAPNDFHNLVPNISLSQVPTNMYNKDPAT 185
Oy 180 LNELNMTSALDEVEFKKREEDPSLLMOVFGSATGLAARYTASFPWDSRTPNKIDLYDR 239
Db 186 VNGVYSESLKAVYVNDPDRDPSLIMQVFGSAGKFFRQYGIKMEPDE--NGVIAFDCR 242
Oy 240 RRPYIQAASPKDMLILVDVSGVSGTLKILRTSVSEMLETTISDDDFVAVAFNSAOD 299
Db 243 NRKMYIQAATSPPKDVILVDVSGSMKGLRLTIKQYVSSILDTLGDDEFFNITTYNEELH 302
Oy 300 DVS-CFO-HLYQANVRKATLKAANNITAKGTTDYKKGFSFAFEOLNYSRAN--CN 355
Db 303 YVECLNGTLVQADRINKREHREHDLKLFAGKGMIDALNEAFNILLSPFNHTGQSICS 362
Oy 356 KIIMLFDTGGEERAEIENKYN-KDKKVVFRSVGONHYERGPLOMACENKGYIETP 414
Db 363 QAIMLITDGAVDYDITFAIYNNPDKKVRITLTLIGREAFADNLKMWMAKACNKGFTQIS 422
Oy 415 SIGAIRINNOEYIDVGRPMVLADGAKOVQWNTYLD--ALEGLVI--TGT 463
Db 423 TLDAVOENVEYIHLVSRKVI--DOEHVYVMEYAVIYDSTLTPQAOGLADQGLVIMTVA 480
Oy 464 LPVENITGQFENKTNKNOILIGMVDVSLIEDIKRLTPEFTCPNGYFAIDPNCGYVL 523
Db 481 MPVFS-----KQNETRSGK--ILGVSTGDPVKEKLTIPKYLGIHGAFAITNGYILT 535
Oy 524 HPLQAP--KNRKSQEP--VTIDFLDAELNDIKVELNKKMIDSGEERTLVKSODE 578
Db 536 HPELRPLYEGRKRRKRPNSYVDLSEVEMEDDQV-LRANAMNRRTGK--FSMEYK---- 588
Oy 579 RYIDKGNFT-----YTWTPVNGTIDYSLALVLP--YSEFYIYKALEETITQARSKKGMK 631
Db 589 KTYDKKRVLMNTNDYYTIDIGTFPSLGVALSRGHGKYYF-----RGMYT 634
Oy 632 DSETLKPDNEESGYTFIAPRDYCN-DKISDNNTPEFLTNFNEEDRKTNNPSCNADLI 690
Db 635 IREGU--HDLHPDVSLADEMSYCWTDLHPEHRHLSQLEAIKLYKGEK--LLOCDKELI 691
Oy 691 NRVLDAEFTNLTNYS-----KQKNIKGVKARFVTDGILTRVP----- 733
Db 692 QEVLEDA-VVSAPIEAYTSLALNKSEMSDKGEVAFIGTGTSLRILFLFGARQLNOD 750
Oy 734 -KEAGENQENPEYEDSFYKRSIDN--DNYFTAPY-----FNKSGPAYSGIMSVKAV 786
Db 751 FLKADDKENIRNADHPFLMYRRAAEQIAGSFYVSLPSTGTVNS-----NVYASTASI 804
Oy 787 EYIYQGLKLPKPAVVGKIDVNSWIEFTTSTIRDOACGAPVCDCKRNSDVMDCVIILDDGF 846
Db 805 QILDRKSPVVAAGVIOGKLEFPQKFTASRQASLDKSKSISCDDEYVNCYILDNGF 864
Oy 847 LLMANHDYTNIGRFFGIDPSLRHLVNI SVYAFNKS SYDQSCFEGAPKAGAGHS 906
Db 865 ILVS--EYIT-QTDFGEVEGAVNMKLLTWGSKFRITLYDQAMCR--ANNSSSSAH 918
Oy 907 AYVPSVADILQIGWATAAASIIQOFLSTLTPRLLBAVEMEDDFTASLSK-----QS 961

```

Db 919 GLIDPYKAF-----SAKIMTELEVLVEF-----NICSMWHSMTAKAOKLTQLEP 968  
 QY 962 CITEQOYFFDNDKSSSVLDGNCRIFFHEKLMNTNIFIMESKGCPCDT 1016  
 Db 969 CDEYPAFVSERIKETGTGNACEDCSKSFVIOIPSSMLFVAVDS--SCLES 1021

# RESULT 3 US-09-875-423-2

Sequence 2, Application US/09875423  
 Patent No. US20020081637A1  
 GENERAL INFORMATION:  
 APPLICANT: Curtis, Rory A.J.  
 TITLE OF INVENTION: 21784, A NOVEL HUMAN CALCIUM CHANNEL  
 TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF  
 FILE REFERENCE: 10448-059001  
 CURRENT APPLICATION NUMBER: US/09/875, 423  
 CURRENT FILING DATE: 2001-06-05  
 PRIOR APPLICATION NUMBER: US 60/209,257  
 PRIOR FILING DATE: 2000-06-05  
 NUMBER OF SEQ ID NOS: 6  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 2  
 LENGTH: 1091  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-875-423-2

Query Match 19.9%; Score 1084; DB 10; Length 1091;  
 Best Local Similarity 28.5%; Pred. No. 4.1e-70;  
 Matches 306; Conservative 222; Mismatches 422; Indels 122; Gaps 39;

QY 3 AGCLLATLTFLFOSLLIGPSSSEPPSAVTIKSWDKMOEDLVTLAKTASGNOLVDIYE 62  
 Db 14 ASALIAAAL-LYALGDVVRSEQDPLISV-VKLMSAFSGIKSIKAKYSSQLQKKYK 71  
 QY 63 KYODLYVEPNNAQOLVIAARDIEKLISNSKALVSLAEKVOAAHQMRDPASNEV 122  
 Db 72 EYKQVAIEEIDQLVYKAKNMEMFHKSEAVRLVEAEAHKHEFDADL--QY 128  
 QY 123 VYNAK--DLDPEKNDSEPSORIKPFTIDANPCR-QISYQAAVHIPIDEGSTIV 179  
 Db 129 EYFNAVLINERDKGNFLELKEFL--LADNDHNNLPVVISISDVQVPTNMKNKDAI 185  
 QY 180 INELNMTSALDEVEFKKNEEDPSILMQYFSATGLARYPASPVWDSRTPNKKIDLYDVR 239  
 Db 186 VNGVWSSLSKLVFVNDNRDPSILMQYFSATGLARYPASPVWDSRTPNKKIDLYDVR 242  
 QY 240 RRPWTIGGAASPKMLLVVDSGVSGLTKLIRTSVSEMLETISDDDFVAVASFNNAQ 299  
 Db 243 NRKVIQATSPKDVYILVDSGSMKGLRTIAKOTVSSIIDTIGDDDFNIIAYNEELH 302  
 QY 300 DYS-CFO-HLVQANVRNKKVLKDAVNNITAKGITDYKKGFSPAPOLLNVAVSRAN--CN 355  
 Db 303 IVEPLNGLTVOADRTNKEHREHLDKLPKAGICMLDIALNEAFNILLSDPHHTGOGSICS 362  
 QY 356 KIIMFTDGEERAOEIFNKYN-KDKRVVRFVSGQHNTERGPIQWACENKGYEIP 414  
 Db 363 QAIMLITGADVDTYTIKAKYVMPDKRYRIFTYLLGREAAFDANLKKMAACANKGFFQIS 422  
 QY 415 STGAIRINTOEYLDVIGRPVYLAGDKAKOVONTNYDAL-----ELG--LVITGT 463  
 Db 423 TLADVOENMEYLVLSRPKVI--DOEHVYVTEAYIDSTLPQAKLTDDOGPVYLMTTVA 480  
 QY 464 LVEFNTGQFENKTLKNOILIGVGVDSVLEDIRLTPREFLCPNGYFAIDPFGVYL 523  
 Db 481 MEVFS---KQNETSKG-TILGCVGTDPYKELLKTIPTKYLGIHGAFALTNNIGILT 535  
 QY 524 HENLQ---PKNRQSEP-VTLDFLDALENDIKVEIRKMKIDGSGEKTFEFLVKSDE 578  
 Db 536 HPELRILYEGEKKRRKPNVSSVLDSEVEMEDBDV-LRNAVNRRTGK--FSMEVK----- 588

QY 579 RIYDKGNRT-----YTWPVNGTDYSLALVPT-YSPYIIKAKLEETITQARSKKGMK 631  
 Db 589 KTVDKGRVLTWNTDYIDYIDIGTPESLGVALSRGHGRFF-----RGVNT 634  
 QY 632 DSEITLKPDNFEESGYTFIAPRDYCN-DKISDNNEFLINEFEIDRTKTPNPNPCNADLI 690  
 Db 635 IERGL--HDEHPDVSLADEWSTCYTDLHPRHRLSOLKAIKLYIKGKEP-LIQCDKRLI 691  
 QY 691 NRYLDAGFTNLYQWYS-----KQNIKGVKARFVYVTDGITRYP----- 733  
 Db 692 OEVLFDFA-VVASPIEAYWTSIALNKSENSDKGEVAFLTGTGLSRINILFVGAELTND 750  
 QY 734 -KEAGENQENETYEYSYKRSIDN--DNYVETAPYFNKSGPGAYESGIMSKAVEYI 790  
 Db 751 FLKAGDENIFNADHPELWYRRRAEQIPGSFYSLPE-STGPVKSNTVYATISITOLD 808  
 QY 791 OGKLRPAVVGIRIDVNSWIEFNTKTSIRDPGAGVPCDCRSYDMDCYIIDDGFFLMA 850  
 Db 809 ERKSPVAAVAGIOMKLEFQORFMTASROCASLDKCSISCODETVNCLIDNNGFILVS 868  
 QY 851 NHDDYTNQIGRFFGELIDPSLMRLVNI SYAFNKSTYQSVCEPGAAPKQGA-GHRSAYV 909  
 Db 869 --EDYT-QTGDFEGIEGAVNMKLLTMGSFKRTIYDYQAMCRANKESSDGAHGLDPY- 924  
 QY 910 PSVADLIQGMWATAAANSILOFLLSLTFPRILAEVEMEDDFTASLSP-----QSCIT 964  
 Db 925 -----NAFLSAVKWIMTELEVLVEF-----NICSMWHSMTAKAOKLTQLEP 971  
 QY 965 EOTQYFFDNDKSSSVLDGNCRIFFHEKLMNTNIFIMESKGCPCDT 1016  
 Db 972 EYPAFVSERIKETGTGNACEDCSKSFVIOIPSSMLFVAVDS--SCLES 1021

# RESULT 4 US-10-005-168-2

Sequence 2, Application US/10005168  
 Patent No. US20020133840A1  
 GENERAL INFORMATION:  
 APPLICANT: Brennan, Thomas J.  
 TITLE OF INVENTION: TRANSGENIC MICE CONTAINING DISRUPTIONS  
 TITLE OF INVENTION: IN GENES ENCODING A2D2 CALCIUM ION CHANNEL SUBUNIT PROTEINS  
 FILE REFERENCE: R-10  
 CURRENT APPLICATION NUMBER: US/10/005,168  
 CURRENT FILING DATE: 2001-12-04  
 PRIOR APPLICATION NUMBER: US 60/299,668  
 PRIOR FILING DATE: 2001-06-19  
 PRIOR APPLICATION NUMBER: US 60/282,685  
 PRIOR FILING DATE: 2001-04-09  
 PRIOR APPLICATION NUMBER: US 60/254,802  
 PRIOR FILING DATE: 2000-12-11  
 NUMBER OF SEQ ID NOS: 4  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 2  
 LENGTH: 223  
 TYPE: PRT  
 ORGANISM: Mus musculus  
 US-10-005-168-2

Query Match 6.7%; Score 365.5; DB 12; Length 223;  
 Best Local Similarity 40.3%; Pred. No. 3.2e-19;  
 Matches 64; Conservative 33; Mismatches 61; Indels 1; Gaps 1;

QY 878 SVYAFNKSSTYQSVCEPGAAPKQGAHRSAYVPSVADIIQGMWATAAANSILOFLLSL 937  
 Db 2 SFYTRKESYTDQACAPQPGNLGAARGVFVPTIADFLNIAWMTSAAWSLFOQLLYGL 61  
 QY 938 TEPRLLEAVEMEDDFTASLSKQSCITEQOYFFDNDKSSSVLDGNCRIFFHEKLM 997  
 Db 62 IYHSMPQADPAEAG-SPEITRESSCVAKQOYIYGSVNAYNAILDGCNCSRLFHQRLT 120  
 QY 998 NTNILFIMESKGTGCPDTRILLQAEQTSDEGPNPCDWK 1036  
 Db 121 NTNILFVVAEKPLCSQCEAGRLLQKETHSDGPEQCELVQ 159

```
Query Match      5.0%; Score 272; DB 10; length 51;
Best Local Similarity 100.0%; Pred. No. 2e-13;
Matches      51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 6  
US-09-864-761-38267

Query Match	5.0%;	Score 272;	DB 10;	Length 53;
Best Local Similarity	100.0%;	Pred. No. 2.1e-13;		
Matches	53;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;



QY 294 FNSNADVSCFOHLVQANVRNKKVLDAVNNITAKGTTDYKKGFSPAFQJLLN 346  
DB 1 FNSNAQDVSCFOHLVQANVRNKKVLDAVNNITAKGTTDYKKGFSPAFQJLLN 53

## RESULT 7

US-09-864-761-38318  
; Sequence 38318, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aecm1ca-X-1  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 38318  
; LENGTH: 35  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AC008283.2  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.84  
; OTHER INFORMATION: EST HUMAN HIT: AW051755.1, EVALUATE 1.00e-14  
; OTHER INFORMATION: SWISSPROT HIT: P54289, EVALUATE 2.00e-15  
US-09-864-761-38318

Query Match 3.5%; Score 190; DB 10; Length 35;  
Best Local Similarity 100.0%; Pred. No. 9.7e-08;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 WTSALDEVFKKREDDPSLLMQVFGSATGLARYP 219  
DB 1 WTSALDEVFKKREDDPSLLMQVFGSATGLARYP 35

## RESULT 8

US-09-864-761-36461  
; Sequence 36461, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aecm1ca-X-1  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 36461  
; LENGTH: 35  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AC008283.2  
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.5  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.67  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.7  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.8  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.6  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3  
; OTHER INFORMATION: EST HUMAN HIT: AW051755.1, EVALUATE 3.00e-04  
; OTHER INFORMATION: SWISSPROT HIT: P54290, EVALUATE 6.00e-15  
US-09-864-761-36461

Query Match 3.4%; Score 185; DB 10; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-07;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 GSGRIKPVIEDANFGROIISYQAAVHIPTDIYEG 175  
 DB 1 GSGRIKPVIEDANFGROIISYQAAVHIPTDIYEG 35

RESULT 9  
 US-09-828-423-5  
 Sequence 5, Application US/09828423  
 Patent No. US20020099178A1  
 GENERAL INFORMATION:  
 APPLICANT: Hillman, Jennifer L.  
 Guegler, Karl J.  
 Patterson, Chandra  
 TITLE OF INVENTION: GROWTH-ASSOCIATED TRYPSIN-TYPE  
 INHIBITOR HEAVY CHAIN PRECURSOR  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Incyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Drive  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 OPERATING SYSTEM: DOS  
 SOFTWARE: Word Perfect 6.1/MS-DOS 6.2  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/828,423  
 FILING DATE: 05-Apr-2001  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/388,774  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Cerrone, Michael C  
 REGISTRATION NUMBER: 39,132  
 REFERENCE/DOCKET NUMBER: PF-0505 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-855-0555  
 TELEFAX: 650-845-4166  
 TELEX: <Unknown>  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 885 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: GENBANK  
 CLONE: g1288563  
 SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
 US-09-828-423-5

Query Match 3.3%; Score 182; DB 10; Length 885;  
 Best Local Similarity 20.2%; Pred. No. 4.5e-05;  
 Matches 132; Conservative 107; Mismatches 243; Indels 170; Gaps 33;

QY 27 PPSAVTIKSWDKMQLVLTAKTASVNGQIVDIYERKDYDLYVEPNNAQIVETIARDI 86  
 DB 97 YPGNVKKEVAKKQYEKAVSGKTAG-----LYKASGRKL 131

QY 87 EKLLSNKSL---VSALAEAKYQAAHOMREDFASNEVYIYNAKDDLDPEKNDSEFGSQ 143  
 DB 132 EKFTVSVVAVAGSKVTELELYEELKRHKGR-----YEMYLKVGPK-----Q 173

QY 144 RIKPVIEDANFGROIISYQAAVHIPTDIYEGTIIVLNLWISALDEVRKKRREDDPSL 203

DB 174 LVKHFETI-----VDIPEQGISMLDAEASFINDLL-----GSA 208  
 QY 204 LMQVFGSATGATGARYYPASPVWDSRT-PNKID-----LVDVRRP-----WT 244  
 DB 209 LTKSFSGKKGHVSPKPS---LDOVRSCPCTDLSLNGDPFITDYVNRKESPGNOIYNGF 265  
 QY 245 I-----OG-AASPKMDILVDVSGVSGTLTKLRTSVSMLEPLSDDDPVVAVASNSNA 298  
 DB 266 VHEFAPGLPVYPRNNAFVIDISGSMAGKLEOTKEALLRLLEDKEDYLNIFLFG-- 323  
 QY 299 QDVSCF-OHLVQAVNRKKVLKDAVNNITAKGTTDYRKGFSAFEDLLVNVSR----- 351  
 DB 324 -DVSTWKEHLVQATPENLIQARTFVKSMEDKGMTNINDGLRISML--NKAKEHRJLP 379  
 QY 352 ANCKIIMLTG---GERRAEIIFNKYK--DKAYVRFREVGQHNTERGPIOMACE 405  
 DB 380 ERSTIVIMLTGDGANYESRPERKIQENVNAIGKRPPLYNLGFG--NNLNYFLNMALE 438  
 QY 406 NKGYVEIPISGIRINTQEVLDVLRPNVLADGKAKOVMTNVYLDLE-----L 456  
 DB 439 NHGFARIVEDSDADLOLGFEEVANPL-LTGVEMEYEP--NAIIDLQNTYQHFDGS 495  
 QY 457 GLVITGTLVPENTTGOFEKNTNLK-----NQLILGVMGVDSLEDIKRLTPRETLCPNGY 511  
 DB 496 EIVVAGRL-VDEDMNSF--KADYKGHATNDL--TFTEEDMKEMK-----ALQERYD 544  
 QY 512 YFALDPR-----GYVLHNLQPK---NPKSQEPTLDFLAELENDIKVEIRKMDIG 562  
 DB 545 IFG---NYIERIMAYLTLEOLEKRRNNAHGEKENITARALDSLKYHHPVTPLTSVYVK 601  
 QY 563 ESSEKTFRTLKVSQDERYI-DKGNRTYTWPVYV-GDYSIALVLPYSPYII 612  
 DB 602 PE-----DNEDERAIADKRGEDAEATPVSPASISYLSQPPQNPYYV 644

RESULT 10  
 US-09-828-423-3  
 Sequence 3, Application US/09828423  
 Patent No. US20020099178A1  
 GENERAL INFORMATION:  
 APPLICANT: Hillman, Jennifer L.  
 Guegler, Karl J.  
 Patterson, Chandra  
 TITLE OF INVENTION: GROWTH-ASSOCIATED TRYPSIN-TYPE  
 INHIBITOR HEAVY CHAIN PRECURSOR  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Incyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Drive  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 OPERATING SYSTEM: IBM Compatible  
 SOFTWARE: Word Perfect 6.1/MS-DOS 6.2  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/828,423  
 FILING DATE: 05-Apr-2001  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/388,774  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Cerrone, Michael C  
 REGISTRATION NUMBER: 39,132  
 REFERENCE/DOCKET NUMBER: PF-0505 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-855-0555  
 TELEFAX: 650-845-4166

```

;
; TELEEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 946 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; IMMEDIATE SOURCE:
;   LIBRARY: GENEBANK
;   CLONE: g133985
; SEQUENCE DESCRIPTION: SEQ ID NO: 3 :
US-09-828-423-3

Query Match
Best Local Similarity 19.9%; Score 159.5; DB 10; Length 946;
Pred. No. 0.0021;
Matches 133; Conservative 107; Mismatches 258; Indels 171; Gaps 29;

QY 33 IKSWDKMQLDVLTKTAGSVNOLVDYERKQDLYTVEPNNAQVLEIARDIEKLISN 92
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 26 LSEFVD--YEDLVEL--APGKFOILAENRRYORSLEPSEEMMEFVDQVTLVSYKVOST 80
QY 93 RSKALVSLALEAKVQAQAAHQRE-----DFASN-----EV 122
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 81 ITRMATTMIQSKVYNNSPQONVFEVDQIPKAFISMSKTVGKTFRSSIKETVGRA 140
QY 123 VYNNAK-----DDLPEKNDSE-----PSQRIKPYFIEDANEGROISYOH--- 163
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 141 LYAQAARAGKTAGLVRSSALDMENRFEVNLPGAKVQFELHYQEVKMRKLGSEYHRILYL 200
QY 164 ---AAVHIPDIEGSTITVLELNTWTSALD-----EYFKKNEE-----DPSILMVF 208
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 201 QPGRILAKHLEVDVWVIEPQGRFLHPDTEFGHEDGVVISKGOQKALHVSFKPTVAQO-- 258
QY 209 GSATGLAYYPASPVDNSTRPNKIDLYDVRRP-----WYIGGAS-----PK 252
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 239 -----RIGBSGR--ETAVDDELVLVDYKREKAGELVFNGLFYFPPADNDIPRK 309
QY 253 DMLILVDVSGVSGITLKLIRTSVSEMLETISDDDFVNVASFNNAQDVSCFQHLVQANV 312
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 310 NLFVYIDVSGSMWGMVKMOTVEAMKTIIDDLAKEDHFSVIDPNQIR--TWANDLFLQOK 367
QY 313 RKKKVLKDAVNNITAKGTTDYKGF---SFAEQLLNNTVNSAANKIMLETFOS-----G 365
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 368 HRLQIAKRYIEKIQPSGGTININEALLRAIFILNEANNGLDLPNSVSLIILVSDDPVVG 427
QY 366 EBRADQIFNKYDKKVRFRFSPVGO-----HNYERKGIOWM-----ACENK 407
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 428 ELKSLKIQKNVENIQDNISLFSLMGPRVDYDLKRLSNENHGIQAQRIYGMQDTSQLOK 487
QY 408 GYYEEL--PSIGAIRIN--TOEYLDVL-----GRPMVLAG--DKAKOVQMTNYYLD 452
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 488 KFYNGVSTPLKNOVFNPHTSVTDVQNNFHFYFGSGEIVAAKFKPDAK-----LD 539
QY 453 ALEELGVITGTIPVNTITQFENKTNLKNOLLISYMGVDSLEDI---KRLTPEFTLCP 508
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 540 QLE--SVTIA-----TSANTQVLETLQADDDLDQDLKSKDAADPPTFR-K 582
QY 509 NGYFPAIDNGVYLLHPNLQPKNPKSQEPVTLDFLDAELENDIKKEIRKMKIDGESGEXT 568
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 583 LNAVLTIN---QLIAERSLAP--TAAAKRRTITSIIQMSLDHITVPLISLVLENAGDGR 638
QY 569 FRTLVKSD 577
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 639 MLADAPPD 647

RESULT 11
US-09-815-242-5898
; Sequence 5898, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.

```

```

; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5898
; LENGTH: 1349
; TYPE: PRF
; ORGANISM: Staphylococcus aureus
US-09-815-242-5898

Query Match
Best Local Similarity 19.4%; Score 151; DB 10; Length 1349;
Pred. No. 0.015;
Matches 199; Conservative 121; Mismatches 339; Indels 366; Gaps 48;

QY 16 SLIGPSEPPFSAVITKSWDKMQLDVLTKTAGSVNOLVDYERKQDLYTVEPNNAQVLEIARDIEKLISN 72
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 40 TLIRGLTNOEKAESTNKE-----LNEATTSASDQSSDKVDMOOLNEDNTKND 90
QY 73 NNAQVLEIARDIEKLISNRSKALVSLALEAKVQAQAAHQREDFASNEVYNNAKDLD 132
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 91 NQK-----EAMVSQNETTSNGK-----LIEKESVOST-----IGNKYEVSATSD-- 132
QY 133 PEKNDSEPSQRIKPYFIEDANEGROISYQAAVHIPDIEGSTITV----- 179
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 180 -----LN-----ELNMTSALDDEVKKNREEDPSLLM-----QYFGSATGLARYYRA 220
QY 181 AKTESTILNVKSDAIKSDETLVYDNNNSNNENNADITLPEKSTAPKRLNTRMRIAAYQPS 240
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 221 SPWVDN-----SRPNKIDLYDVRRPWYIYGASPRKMLILVDVSGVSGITLIRT 274
QY 241 STEAKNVVDLTSTNTLTVADAKNNKIVPAQDYLISLSQITVDDKKKSGDYFIK--- 297
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 275 SVSEMLETLISDDDFVNVASFN--SNAQDVSCFQHLVQANVNNKVKLDAVNNITAKGITT 332
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 298 SDTVQVYVLEPEDIKNIDIKDPNNGETIATAKH-----DTANNLTITYFTD 344
QY 333 YKGFSAFEDQLNANV-----SRANC-----NK 356
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 345 YVDRFN--SVQMGINSIYMDADTIPVSKNDVEFNVNTIGNTTKTANIQPDIYVNNKNS 403
QY 357 IIMLETD-----GGEER-----AOEIF-----NKYNDKRVFRFS-----VGOHNYERG 397
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 404 IGSATFETVSHVKNKENGYYKQTIYVPSNSLNAKLKQVQAAHSSVPNNIGQINDVY 463
QY 398 PIQWACE-----NKGYEELPSIGAIRINQOEYLDVGRPM--VLAGDKAKOV----- 444
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 464 DIKIYQVPEKGYLANKGY-----DVNTKELTDVYNOYLQKRTIYGDNNNAVIDEGNA 513

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OY 445 -----QWTV----- 448
Db 514 DSAIVVMVNTKQYTNSESPILVOMATLSTGNKSVSTGNALGFTNNOSGAGQGEVYKIG 573
OY 449 --VYLDALGLVITGTLVFNIT--GQENKTNLKNOLILGVMGVDSLEIDIKRLTPRT 505
Db 574 NYVWETNKNNGVQELGEKGVAVTVTFEDNNTNK-----VGEAVYKEDGSYLIPNL- 625
OY 506 LCPNGY--FAIDPNGVYLHPNLOPKNPK-----SOEPTVLDLDELNDIKVEIRN 557
Db 626 --PNGDYRVEFNLPRGYEVT--PSKOGNNEELDSGLSVITVKNKD--NLADGLIYKPK 681
OY 558 KNIDESEGEKTRTLVKSODERYIDKGNRTYTWPNVGTDSLALVLPYSFYIKALE 617
Db 682 YNLCYVWEDTNKNGIQODEKGI--SGVTVLKDENG-----DVL 720
OY 618 ETTQARSKKGMKSEILKPDNEESGYTFIAPRDYCNLDKISDNTEFLNNEFIDR 677
Db 721 KVTITDADGKYFTD--LHNGNYK--VEFTTPEGYPTVTVTSGSDIE----- 763
OY 678 KTPNPNSCNADLIN--RYLDDAGFTN--ELVQNVY-----SKOKNIKV-- 717
Db 764 -KDSNGLTTGTVNGADMWTLDSGYKTPKYNLGNVWEDTNKDKODSTEGISGYVT 822
OY 718 -----KARFVYTDGSTRV-----YPKRGENWQF----- 742
Db 823 LKNENGEVLQTTKDKDKQYQFTGLENGTYVVEFTTPEGYPTVQVSGTDEGIDSNGST 882
OY 743 -----NPEYEDSFYKRSIDNDNYVFTAPYFNKSGGAYE-----SGIMSKAVEIYQ 791
Db 883 TGVIKDNNDTIDSGFYKPTYNLGDYVWEDT--NKNQVQODEKGISGYVTTLADE--N 937
OY 792 GKILK 796
Db 938 DKVLK 942

```

RESULT 12  
US-09-815-242-13137

Sequence 13137, Application US/09815242

Patent No. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 13137

LENGTH: 1349

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; TYPE: PR1
; ORGANISM: Staphylococcus aureus
; US-09-815-242-13137

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Query Match  
Best Local Similarity 19.4%; Score 151; DB 10; Length 1349;  
Matches 199; Conservative 121; Mismatches 339; Indels 366; Gaps 48;

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OY 16 SLILGSPSEFPFSAVITIKSVMDKQEDLVTLAKTAGVNO--LVDIYERQDLYTVEP 72
Db 40 TLLFGLNGQAKAESTNKE-----LNFAITTSASDOSSDKYMOQLNEDMTKND 90
OY 73 NNAOLVEIARDEKLLRSKALVSLAEAKYQAHQWRDFASNEVYVYVNAADD 132
Db 91 NQK-----EMVSSQENETTSNGK-----LIEKSVOST-----TGNVEVSTAKSD-- 132
OY 133 PEKNDSEPGSORIKPVYIEDANFGROIISYQAAVHIPTDIYEGSTIV----- 179
Db 133 --EQASPSTN-----EDLNTKOTISNQE--LQPDQENKSVYVYVQPTNEKKYD 180
OY 180 -----LN-----ELNWTSADEVPKRRREDPSLW-----OVFSATGLARYPA 220
Db 181 AKTESITLANKSDALISNDETLVDNNSNSNENNADIIIPKSTAPKRLNTRMIAVOPS 240
OY 221 SPWVDN-----SRTENKIDLYVRRRPYIQAASPKMLILVDSGSGLITLIR 274
Db 241 STEAKVNDLITNTLITVVDADKNNKIYPAOYIISLKSQIIVYDDKVGSGDYFTIKY 297
OY 275 SVSEMLETSDDFVAVASFN--SNAQVSCQOHLVQAVNRKKYLKDAVNNITAKITD 332
Db 298 SDTVQVYAGLNPEIDIKINGIDIKDPNGETIATAKH-----DTANLLIYTFPD 344
OY 333 YKKGSFAFEOLINTVY-----SRANC-----NK 356
Db 345 YVDRFN--SVQMGINTYIYADDTIYVSKNDVEBNVTITGTTKRTANIQPYDVYENKNS 403
OY 357 IMLETD-----GGEER-----AQEIR-----NKYNKDKKVVFRFS-----VGQHNTERG 397
Db 404 ICSAFETVSHVGNKENPGYKOTIYVNSSENSLNAAKAKYQAHSSYTNNGIINKDVT 463
OY 398 PIQWMAE-----NKGYIEISIGAIRINIOEYLDVLCRPV--VLADKRAQV----- 444
Db 464 DIKIYVPRGYLTKGY-----DVNTKELDVYMOYLQKITGYGDNNSAVIDFGNA 513
OY 445 -----QWTV----- 448
Db 514 DSAIVVMVNTKQYTNSESPILVOMATLSTGNKSVSTGNALGFTNNOSGAGQGEVYKIG 573
OY 449 --VYLDALGLVITGTLVFNIT--GQENKTNLKNOLILGVMGVDSLEIDIKRLTPRT 505
Db 574 NYVWETNKNNGVQELGEKGVAVTVTFEDNNTNK-----VGEAVYKEDGSYLIPNL- 625
OY 506 LCPNGY--FAIDPNGVYLHPNLOPKNPK-----SOEPTVLDLDELNDIKVEIRN 557
Db 626 --PNGDYRVEFNLPRGYEVT--PSKOGNNEELDSGLSVITVKNKD--NLADGLIYKPK 681
OY 558 KNIDESEGEKTRTLVKSODERYIDKGNRTYTWPNVGTDSLALVLPYSFYIKALE 617
Db 682 YNLCYVWEDTNKNGIQODEKGI--SGVTVLKDENG-----DVL 720
OY 618 ETTQARSKKGMKSEILKPDNEESGYTFIAPRDYCNLDKISDNTEFLNNEFIDR 677
Db 721 KVTITDADGKYFTD--LHNGNYK--VEFTTPEGYPTVTVTSGSDIE----- 763
OY 678 KTPNPNSCNADLIN--RYLDDAGFTN--ELVQNVY-----SKOKNIKV-- 717
Db 764 -KDSNGLTTGTVNGADMWTLDSGYKTPKYNLGNVWEDTNKDKODSTEGISGYVT 822
OY 718 -----KARFVYTDGSTRV-----YPKRGENWQF----- 742
Db 823 LKNENGEVLQTTKDKDKQYQFTGLENGTYVVEFTTPEGYPTVQVSGTDEGIDSNGST 882
OY 743 -----NPEYEDSFYKRSIDNDNYVFTAPYFNKSGGAYE-----SGIMSKAVEIYQ 791

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Db 883 TGVIKDKNDFTIDSGFKPYNLGDIYEDT--NKNGVDKDEKIGISVTYVLKDE---N 937

Oy 792 GKLLK 796  
Db 938 DKVLK 942

RESULT 13  
US-09-850-351A-6  
Sequence 6, Application US/09850351A  
Patent No. US2002010080A1  
GENERAL INFORMATION:  
APPLICANT: Feltelson, Jerald S.  
Schnepf, H. Ernest  
Narva, Kenneth E.  
Stockhoff, Brian A.  
Schmelts, James  
Loewer, David  
Dullum, Charles Joseph  
Muller-Cohn, Judy  
Stamp, Lisa

TITLE OF INVENTION: No. US2002010080A1el Pesticidal Toxins and Nucleotide  
Sequences Which Encode These Toxins

NUMBER OF SEQUENCES: 144

CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville

STATE: FL

COUNTRY: US

ZIP: 32606-6669

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/850,351A

FILING DATE: 07-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/073,898

FILING DATE: 06-May-1998

APPLICATION NUMBER: US 08/960,780

FILING DATE: 30-Oct-1997

APPLICATION NUMBER: US 60/029,848

FILING DATE: 30-Oct-1996

ATTORNEY/AGENT INFORMATION:

NAME: Sanders, Jay M.

REGISTRATION NUMBER: 39,355

REFERENCE/DOCKET NUMBER: MA-708CD1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 352-375-8100

TELEFAX: 352-372-5800

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 789 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: 81F

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-850-351A-6  
Query Match 2.8%; Score 150.5; DB 10; Length 789;  
Best Local Similarity 20.1%; Pred. No. 0.0072;  
Matches 138; Conservative 100; Mismatches 235; Indels 213; Gaps 34;  
Oy 231 NKIDLYVRRRPWYIGQASPKMDLLVYSSVSGILTKLIRTSVSEMLFTLSD-DFV 289

Db 105 NKIDALNTMLRYVL-----PKITSMLSQVMKONVALSLQI--EYLSKOLDEISDKLII 156

Oy 290 NV-ASFNMAQDS-----CFQHLVQANVANKKVLKDA-----VNNIT-----A 327

Db 157 NVNVLINSTLTLETPAYORIKIYNEKFEELTRFETSSKVKKDGSPADIDBLTLELA 216

Oy 328 KGIDYKKGFSFAFEQLLN--YVNSRANCKIIMLFTDGEERAOIEFNKYNKKKRYVF 385

Db 217 KSVT---KNVDGEFEFLNTHFDMVGN-----NLGRSALKTASELTIKEN-----VITS 264

Oy 386 RFSVGQNNTERCPQIMACENKGYEIEPSIGAIRINTQEDYLDVGRPVNLAGDKAKOYO 445

Db 265 GSEVG--NYYNELVITLALQAKAFLLTTCRKLGLADIDYISIMNEHL-----NKEKEF 318

Oy 446 WTNVYLDALDELGVITGTLPFNITGQFENKTMKN-----QLIL-----GVMGVDSL 494

Db 319 RVNL-----LPLNSTFSPNRYAKVKGSDDEAKMIVAKKGHALVGEFISN 364

Oy 495 EDI-----KRLPRP-----TLCPNG-----YF--ALDPNGVLLH 524

Db 365 DSITVLKYEAKLKQNTQVVDKSLSEVIYGDMDKLLCPDQSEQIYTTNNIVPENEVYIK 424

Oy 525 PNLQPKNKSGEPYTLDFLALENDIKVEIRNKMIDGSEGEFTPTLVKSODERYIDRG 584

Db 425 IDFTKKMKTLYEVYANFYDSSTG---EIDLNKKV--ESSEAEYRTLSANDQGVNPIG 479

Oy 585 NRTYTW-TPVNG---IDYSLALVLPYSPFYIKAKLEETITQARSKKGKMDSEFLKP- 638

Db 480 VISEFELPPIPGFQADENSRLITLCKSYLRLLATLSN-----KETKLIYVP 531

Oy 639 ---DNFEESGYTTPAPDYCNLDKIDNTE--FLNPFEDIRKTPNPNSCNADLINR 692

Db 532 SGFIKNIVENG-----SIEDNLEPKANKNNEYVDH----- 563

Oy 693 VLDAGFTNELVQYWSKOKNIKGVKAFVYTDGCT-----RVYRK----- 734

Db 564 -----TGCVNGTKALYHKDGIQFIDKRLKPTREVIQYVWGP 605

Oy 735 -----ENQENPEYEDSFYKRSLNDNVYTFAPYFNKSGGATGSMVS 783

Db 606 SYHLKDEMGTYIHYEDTNNLNLEDYQTIYKRTGTDLKGYVLLILKSONGDEAMQDNFI- 664

Oy 784 KAVEYIQQKLLKPAVVGKIKIDVNSM 809

Db 665 --LEISPSSEKLLSPEL---INTNMW 684

RESULT 14  
US-09-850-351A-4

Sequence 4, Application US/09850351A

Patent No. US2002010080A1

GENERAL INFORMATION:

APPLICANT: Feltelson, Jerald S.

Schnepf, H. Ernest

Narva, Kenneth E.

Stockhoff, Brian A.

Schmelts, James

Loewer, David

Dullum, Charles Joseph

Muller-Cohn, Judy

Stamp, Lisa

Morrill, George

TITLE OF INVENTION: No. US2002010080A1el Pesticidal Toxins and Nucleotide

Sequences Which Encode These Toxins

NUMBER OF SEQUENCES: 144

CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: FL

COUNTRY: US

ZIP: 32606-6669

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/850,351A  
FILING DATE: 07-MAY-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/073,898  
FILING DATE: 06-MAY-1998  
APPLICATION NUMBER: US 08/960,780  
FILING DATE: 30-OCT-1997  
APPLICATION NUMBER: US 60/029,848  
FILING DATE: 30-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Sanders, Jay M.  
REGISTRATION NUMBER: 39,355  
REFERENCE/DOCKET NUMBER: MA-708CD1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 352-375-8100  
TELEFAX: 352-372-5800  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 790 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: 36a  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-850-351A-4

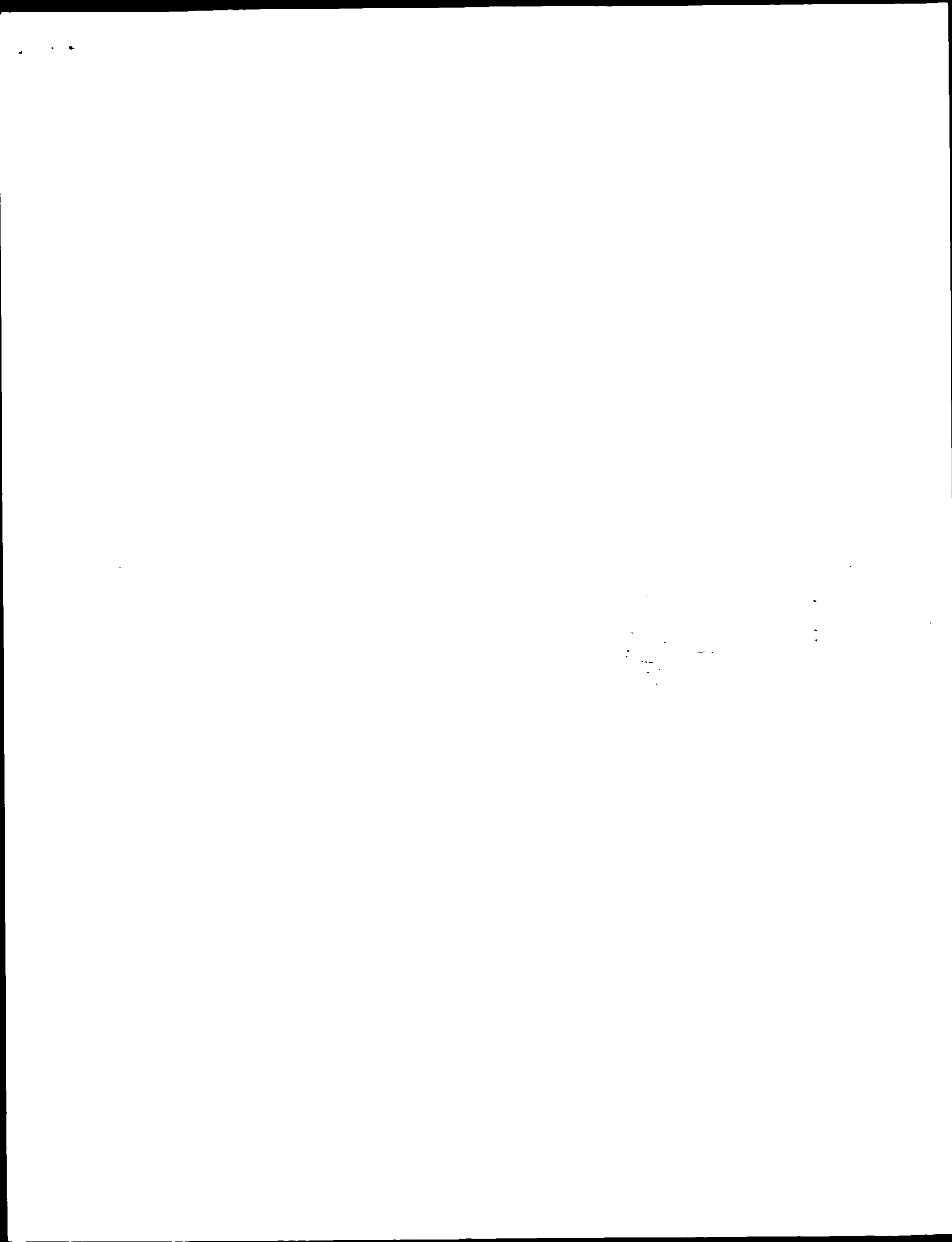
Query Match 2.7%; Score 148.5; DB 10; Length 790;  
Best Local Similarity 19.9%; Pred. 0.01;  
Matches 137; Conservative 100; Mismatches 232; Indels 221; Gaps 34;

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105 NKIDALITMLRVYL-----PKITSMISDMKONVALSLDI--EYLSKQLQETISDKLDII 156  
290 NV-ASFNNAQDVS-----CFQHLVQANVANKVYLKDA-----VNNIT-----A 327  
157 NVNVLINSLTETTPAVORIKYNEFEELTETESSVKKDGSPANLIDELTLELA 216  
328 KGITDKKGGSPAFKQDLN--YVSAKCNKIMLFTDGEERRAOEIFNKYKKDKKRVVF 385  
217 KSVT---KNDVDFEFLYLMFHDVWGN-----NLFGRSALKTASELITKEN---VKT 264  
386 RFSVGHNTERGPIOMMAGCNKGYEIPSGAIRINQEVLDVGRPMVLAGKAKQVQ 445  
265 GSEVG--NVYNFLIVLTAQAKAFLLTTCRLGLGLADIDYTSINNEHL---NKEKEEF 318  
446 WTVNVDALDELGLVTTGTLPEFNITGQFENKTNLKN-----QLIL-----GVAGVDVSL 494  
319 RVNI-----PRLSNTEFSNPYAKVKGSDAKMIYEAKGHALIGFEISN 364  
495 EDI-----KRLTPF-----TLCNG-----YF--AIDPNCVYLH 524  
365 DSTIVAKYEALIKONTQVDKDISSEVYIGDMKLLCPDQSEQIYNNIYFPMEVYITK 424  
525 PNIQPKRKSQBPVTLDELDAELNDIKVEIRNKMIIDSEGEKTFRLVKSODERYIDKG 584  
425 IDFTKKMKTLRYEVANFYDSSTG--FLIDNKKV--ESSEAEYKILSADDDGVYPLG 479  
585 NRTYTM-TPVNG-----TYSIALVLPYTSYYIAKLEETITQARSKKGKKQSEITLKP- 638  
480 VISEFTFLPPINGFLQADENSRLTITLTKSYLRELLATDLSN-----KETKLVLP 531  
639 ----DNFEESGYTFIAPDYCNDLKISDNTE--FLNFNFTDRKTPNPNNSCADILNR 692

532 SGFISNIYENG-----SIEDNLEPKANKNKAAYVDH----- 563  
693 VLDAGFTNELVQNYWYSKQNIKGVKARFVYTDGITRYVPKKEGEMWQENPTY----- 747  
564 -----TGGVNGTKALYVHKDGGISQF-----IGDNLKPKTEVIYQYTV 601  
748 -----EDSFYKSLDNDNYFTAPYFNK-----SGPGAYESG 779  
602 KKKPSIHLIDENTGYIHEDYNNMLIEDYQTLNKRFTGTDLKGVYLKSGNDDEAMGN 661  
780 IMVSKAVEIYIOGKLLKPAVVGIRKIDVNSW 809  
662 FII---LEISPEKILSPEL-----INTNNW 684

RESULT 15  
US-09-850-351A-8  
Sequence 8, Application US/09850351A  
Patent No. US2002010080A1  
GENERAL INFORMATION:  
APPLICANT: Feltelson, Jerald S.  
Schnepl, H. Ernest  
Naeva, Kenneth E.  
Stoekhoff, Brian A.  
Schmeits, James  
Loewer, David  
Dulum, Charles Joseph  
Muller-Conn, Judy  
Stamp, Lisa  
Morrill, George  
TITLE OF INVENTION: No. US2002010080A1el Pesticidal Toxins and Nucleotide  
Sequences Which Encode These Toxins  
NUMBER OF SEQUENCES: 144  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanichik, Lloyd & Saliwanichik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: US  
ZIP: 32606-6669  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/850,351A  
FILING DATE: 07-MAY-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/073,898  
FILING DATE: 06-MAY-1998  
APPLICATION NUMBER: US 08/960,780  
FILING DATE: 30-OCT-1997  
APPLICATION NUMBER: US 60/029,848  
FILING DATE: 30-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Sanders, Jay M.  
REGISTRATION NUMBER: 39,355  
REFERENCE/DOCKET NUMBER: MA-708CD1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 352-375-8100  
TELEFAX: 352-372-5800  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 790 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: Jay90  
SEQUENCE DESCRIPTION: SEQ ID NO: 8:







GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 10, 2003, 14:22:34 : Search time 7.8606 Seconds  
(Without alignments)  
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Gapop 10.0 , Gapext 0.5

Searched: 129505 seqs, 22169297 residues  
Total number of hits satisfying chosen parameters: 129505

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5599	100.0	1091	10	US-09-875-423-4
2	1119.5	20.0	1091	10	US-09-875-423-5
3	1114.5	19.9	1091	10	US-09-875-423-2
4	462.5	8.3	223	12	US-10-005-168-2
5	272	4.9	51	10	US-09-864-761-44281
6	272	4.9	51	10	US-09-864-761-38267
7	190	3.4	35	10	US-09-864-761-38318
8	185	3.3	35	10	US-09-864-761-36461
9	182	3.3	35	10	US-09-828-423-5
10	159.5	2.8	946	10	US-09-828-423-3
11	151	2.7	1349	10	US-09-815-242-5898
12	151	2.7	1349	10	US-09-815-242-13137
13	150.5	2.7	789	10	US-09-850-351A-6
14	148.5	2.7	790	10	US-09-850-351A-4
15	145.5	2.6	790	10	US-09-850-351A-8
16	143.5	2.6	1781	9	US-09-995-749A-2
17	136.5	2.4	956	9	US-10-121-032-63
18	136.5	2.4	3169	9	US-10-114-170-257
19	133.5	2.4	764	9	US-10-105-695-4

20	133.5	2.4	764	9	US-10-105-694-4	Sequence 4, Appl1
21	133.5	2.4	764	10	US-09-747-521-4	Sequence 4, Appl1
22	133.5	2.4	764	12	US-10-106-014-4	Sequence 4, Appl1
23	133	2.4	1323	10	US-09-801-368-34	Sequence 34, Appl1
24	132.5	2.4	876	10	US-09-815-242-12623	Sequence 12623, A
25	127.5	2.3	3712	9	US-10-108-605-103	Sequence 103, App
26	123	2.2	2285	10	US-09-932-183A-2	Sequence 2, Appl1
27	121.5	2.2	2125	10	US-09-919-172-29	Sequence 29, Appl1
28	120	2.1	698	9	US-09-820-440-10	Sequence 10, Appl1
29	118.5	2.1	151	9	US-10-050-786-9	Sequence 9, Appl1
30	118	2.1	103	9	US-10-050-786-9	Sequence 29, Appl1
31	117	2.1	811	9	US-10-011-588-29	Sequence 4949, Ap
32	116.5	2.1	764	10	US-09-815-242-4949	Sequence 10593, A
33	116.5	2.1	764	10	US-09-815-242-10593	Sequence 4, Appl1
34	116	2.1	911	10	US-09-828-423-4	Sequence 8, Appl1
35	114.5	2.0	773	12	US-10-067-385-8	Sequence 45, Appl1
36	114.5	2.0	1183	9	US-09-870-759-45	Sequence 12, Appl1
37	114	2.0	673	12	US-10-032-717-12	Sequence 30, Appl1
38	113	2.0	620	12	US-10-032-717-30	Sequence 2, Appl1
39	113	2.0	26926	9	US-09-759-508B-2	Sequence 32, Appl1
40	112.5	2.0	881	10	US-09-850-351A-32	Sequence 10, Appl1
41	111.5	2.0	836	9	US-09-858-525A-10	Sequence 2, Appl1
42	111.5	2.0	871	9	US-09-858-525A-2	Sequence 2, Appl1
43	111.5	2.0	1016	12	US-10-044-303-2	Sequence 8, Appl1
44	111	2.0	711	8	US-08-834-666A-8	Sequence 4, Appl1
45	110	2.0	2835	10	US-09-885-535-4	Sequence 4, Appl1

## ALIGNMENTS

RESULT 1  
US-09-875-423-4  
Sequence 4, Application US/09875423  
Patent No. US20020081657A1  
GENERAL INFORMATION:  
APPLICANT: CURTIS, ROY A. J.  
TITLE OF INVENTION: 21784, A NOVEL HUMAN CALCIUM CHANNEL  
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF  
FILE REFERENCE: 10448-059001  
CURRENT APPLICATION NUMBER: US/09/875,423  
CURRENT FILING DATE: 2001-06-05  
PRIOR APPLICATION NUMBER: US 60/209,257  
PRIOR FILING DATE: 2000-06-05  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 1091  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-875-423-4

Query Match 100.0%, Score 5599, DB 10, Length 1091;  
Best local Similarity 100.0%; Pred. No. 0;  
Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 MAAGCLLALTLTFLQSLILGSPSEPPFAVITKSWDKMOEDVTLAKTAGSVNDYDI 60  
QY 61 YEKYODLYTEPPNNAQOLVIAARDIEKLISNSKALVSLAEAEVQAHOHREDFASN 120  
DB 61 YEKYODLYTEPPNNAQOLVIAARDIEKLISNSKALVSLAEAEVQAHOHREDFASN 120  
QY 121 EYVYNAKDDLPDEKNDSEPGSORIKPVFIEDANFGRQISYQAAVHIFTDIYEGSTIYL 180  
DB 121 EYVYNAKDDLPDEKNDSEPGSORIKPVFIEDANFGRQISYQAAVHIFTDIYEGSTIYL 180  
QY 181 NELNWTALDEVRKKNKEDEPSILMKOVFGSATGLARYYPASPVNDKSRTPNKIDLDVDR 240  
DB 181 NELNWTALDEVRKKNKEDEPSILMKOVFGSATGLARYYPASPVNDKSRTPNKIDLDVDR 240  
QY 241 RPWTIQGAAPSKMILLVDVSGVSGILTKLIRTSVSEMLETLDDDFVNVASFNSMAOD 300



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 Db 1027 MAPLEIRYNESLKCERLKAOKIRRPESCHGFHEENARECGAS 1071

## RESULT 3

US-09-875-423-2  
 ; Sequence 2, Application US/09875423  
 ; Patent No. US20020081657A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Curtiss, Roy A. J.  
 ; TITLE OF INVENTION: 21784, A NOVEL HUMAN CALCIUM CHANNEL  
 ; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF  
 ; FILE REFERENCE: 10448-059001  
 ; CURRENT APPLICATION NUMBER: US/09/875,423  
 ; PRIOR FILING DATE: 2001-06-05  
 ; PRIOR APPLICATION NUMBER: US 60/209,257  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 1091  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-875-423-2

Query Match 19.9%; Score 114.5; DB 10; Length 1091;  
 Best Local Similarity 28.3%; Pred. No. 1.5e-72;  
 Matches 317; Conservative 230; Mismatches 448; Indels 125; Gaps 40;

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 QY 63 KYODLYVEPPNNAQYETIARIDIEKLNSKALVSLALAEKVOAHOHREPASNEV 122  
 Db 72 EYKQVVALEEIDGLVYKLLAKNMEEMHKSEAVRRLVEAAEAHLKHEFDAL--QY 128  
 QY 123 VYNAK--DDIDPEKNDESPGSRKPYFIDANFGR-OISYQAAVHIIPDIESTIV 179  
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 QY 180 LNELMTSALDEVFKKNEEDPSILMOYFGSATGLIARYYPASPVVNSRTNPKIDLYDVR 239  
 Db 186 VNGVWSSSLNKVFYDNDPRLIWOYFGSAKGFGRQYPIKWPEDP--NGVIAFDCR 242  
 QY 240 RRPWTYQGAAPKMLILVDVSGSGLTILKIRSVSEMETLSDDDFVAVASNAQ 299  
 Db 243 NKKWTYQATSPKDVILVDVSGSMKGLTLTAKQTVSSILDTGDDDFENILAVNEHL 302  
 QY 300 DVS-CFO-HLYOANRNKKVLLKDAVANNITAKGITDYKKGFSFAEQLLNYVSRAN--CN 355  
 Db 303 YVEPRLNGVLQADRTNKEHEFHDKLFKACIGMLDALNANAFILSDPNTGGSGICS 362  
 QY 356 KIIMLETDGGERAOEINENKYN-KKKYVRFERSVGOHNYERGPLOMACENKGYIETP 414  
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 QY 415 STGAIKRNQYEDLVLRNVLGAKAQOYQWNTNYLAL-----ELG--LVITGT 463  
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 QY 464 LPEFNTTGFENKTNLKNOLLIGVGVSDLEDIKRLPRTFLCPNGYFAIDPNGYVL 523  
 Db 481 MPVFS-----KONETRSKG-ILGCVGTDPVAVKELLKTIKRYKLGIGVAFATNNNGYILT 535

QY 524 HBNIO--PKNPKSQEP--VTLDFLDAELENDIKVEIRNNKIDGSGEKTRPTLYKCODE 578  
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 QY 579 RTIDGNRI-----YTWTPVNGTQYSLALVLP--YSHYYIKAKLEETITQARSKKGMK 631  
 Db 589 KTVADKGRVLYMTNDYTYDTIKGTPTSLGVALSRCHGKTFP-----KGNVT 634  
 QY 632 DSETLKPONFEESGYTFIAPRDYCN-DKISDNNTFFLNEFIDRKTTPNPNPCNADLI 690  
 Db 635 IEGL--HLEHPDVSIADEMSTCYMTDLAHEHRHLSQLEAIKLYLKGEP--LQCDKRELI 691  
 QY 691 NRYLLDAGFTNLYONVMS-----KQKNKGVKARVYVTOGTRVY----- 733  
 Db 692 QEVLFDA-VYSAPIEAYWTSIALNKSSENSDKGEVAFLGTIRGLSRINLFGVAGELTQND 750  
 QY 734 -KAGENMOENETEDSDYKRSIDN--DNVYFTAPYFNKSGPAGYESGIMVSKAVEIYI 790  
 Db 751 FLKAGKENIFNADHPPLMYRRAEQIPGSEVYSTIP--STGPVKNVNTASTSIQLLD 808  
 QY 791 QGRLKPAVAVGIRIDVNSWIEFTKTSIRDPCAGPYCDCKRNSDVMCVIIDDGFFLMA 850  
 Db 809 ERKSPVAAVAVGIOMKLEFORKFWTASRQCASIDKCSISCDDETVNICYLIIDNGFIIVS 868  
 QY 851 NHDDYTNQIGRPFGEIDPSLMRLVNIYVARNKSDYOSVEPQAPKQGA-GHRSAYV 909  
 Db 869 --EDYT-QTGDFPGEIEGVAMNKLTMGSFKRTITDYQAMCRANKESSDGAHGLDPF- 924  
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 QY 965 EOTQYFFDNDKSGFVLDGNCSTRIFHEKLMNTNLIIFMWSKGTCPDITLLIQAEQ 1024  
 Db 972 EYPAFVSERTIKETGTINACEDSKSFVIOIPSSNLFMVVYDS--SCLESVAPITMAP 1029  
 QY 1025 TSDGPN--PCDMWKOPRYKRGPDVCDNNVLDYTDCCG 1061  
 Db 1030 IEIRYNESLKCERLKAOKIRRPESCHGFHEENARECGG 1069

## RESULT 4

US-10-005-168-2  
 ; Sequence 2, Application US/10005168  
 ; Patent No. US20020133840A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brennan, Thomas J.  
 ; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING DISRUPTIONS  
 ; TITLE OF INVENTION: IN GENES ENCODING A2D2 CALCIUM ION CHANNEL SUBUNIT PROTEINS  
 ; FILE REFERENCE: R-10  
 ; CURRENT APPLICATION NUMBER: US/10/005,168  
 ; CURRENT FILING DATE: 2001-12-04  
 ; PRIOR APPLICATION NUMBER: US 60/299,668  
 ; PRIOR FILING DATE: 2001-06-19  
 ; PRIOR APPLICATION NUMBER: US 60/282,685  
 ; PRIOR FILING DATE: 2001-04-09  
 ; PRIOR APPLICATION NUMBER: US 60/254,802  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 223  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 ; US-10-005-168-2

Query Match 8.3%; Score 462.5; DB 12; Length 223;  
 Best Local Similarity 43.2%; Pred. No. 2.6e-26;  
 Matches 79; Conservative 37; Mismatches 66; Indels 1; Gaps 1;

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US-09-864-761-44281
: Sequence 44281, Application US/09864761
: Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annotmax Sequence Listing Engine vers. 1.1
SEQ ID NO 44281
LENGTH: 51
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC006145.2
OTHER INFORMATION: EXPRESSED IN LONG. SIGNAL = 1.1

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? OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.86
? OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.91
? OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
? OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.93
? OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.81
? OTHER INFORMATION: SWISSPROT HIT: P54289, EVALUE 4.00e-25
US-09-864-761-44281
? OTHER INFORMATION: EST_HUMAN HIT: H86016.1, EVALUE 1.00e-02

Query Match          4.9%: Score 272; DB 10; Length 51;
Best Local Similarity 100.0%; Pred. NO. 1.8e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1      IGRFGEIDPSIMRLVNIISYVAFNKSYDQSVCEGAPAKPGAGHRSAYV 51

RESULT 6
US-09-864-761-38267
? Sequence 38267, Application US/09864761
? Patent No. US20020048763A1
? GENERAL INFORMATION:
? APPLICANT: Penn, Sharon G.
? APPLICANT: Rank, David R.
? APPLICANT: Hanzel, David K.
? TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
? FILE REFERENCE: A60m1ca-x-1
? CURRENT APPLICATION NUMBER: US/09/864,761
? PRIOR APPLICATION NUMBER: US 60/180,312
? PRIOR FILING DATE: 2000-02-04
? PRIOR APPLICATION NUMBER: US 60/207,456
? PRIOR FILING DATE: 2000-05-26
? PRIOR APPLICATION NUMBER: US 09/632,366
? PRIOR FILING DATE: 2000-08-03
? PRIOR APPLICATION NUMBER: GB 24263.6
? PRIOR FILING DATE: 2000-10-04
? PRIOR APPLICATION NUMBER: US 60/236,359
? PRIOR FILING DATE: 2000-09-27
? PRIOR APPLICATION NUMBER: PCT/US01/00666
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00667
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00664
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00669
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00665
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00668
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00663
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00662
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00661
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00670
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: US 60/234,687
? PRIOR FILING DATE: 2000-09-21
? PRIOR APPLICATION NUMBER: US 09/608,408
? PRIOR FILING DATE: 2000-06-30
? PRIOR APPLICATION NUMBER: US 09/774,203
? PRIOR FILING DATE: 2001-01-29
? NUMBER OF SEQ ID NOS: 49117
? SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
? LENGTH: 53
? TYPE: PRT

```

1 LIFE: FNU

TYPE: PRT  
ORGANISM: Homo sapiens

FEATURE:  
OTHER INFORMATION: MAP TO ACC08283.2  
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.5  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.67  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.7  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.8  
OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 0.6  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3  
OTHER INFORMATION: EST\_HUMAN HIT: AM051755.1, EVALUE 3.00e-04  
OTHER INFORMATION: SWISSPROT HIT: P54290, EVALUE 6.00e-15  
US-09-864-761-36461

## Query Match

Best Local Similarity 3.3%; Score 185; DB 10; Length 35;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 GSORIKPVIEDANFGROIYOHAAVHIPTDIYEG 175  
Db 1 GSORIKPVIEDANFGROIYOHAAVHIPTDIYEG 35

## RESULT 9

US-09-828-423-5  
Sequence 5, Application US/09828423  
Patent No. US20020099178A1  
GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

Guegler, Karl J.

Paterson, Chandra

TITLE OF INVENTION: GROWTH-ASSOCIATED TRYPSIN-TYPE

INHIBITOR HEAVY CHAIN PRECURSOR

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESS: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: Word Perfect 6.1/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/828.423

FILING DATE: 05-Apr-2001

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/388,774

FILING DATE: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Cerrone, Michael C

REGISTRATION NUMBER: 39,132

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

TELEX: &lt;Unknown&gt;

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 885 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GENE BANK

CLONE: g1286363

SEQUENCE DESCRIPTION: SEQ ID NO: 5 :

US-09-828-423-5

Query Match

3.3%, Score 182; DB 10; Length 885;

Best Local Similarity 20.2%; Pred. No. 4.3e-05;  
Matches 132; Conservative 107; Mismatches 243; Indels 170; Gaps 33;

QY 27 PPSAVTKSWDKKQEDLVLTAKTASGVNQLVDIYKQDLYTEPPNNAQVLEIAROI 86  
Db 97 YPGVWKEKEVAKKQYERAVSGKTAG-----LVKASGRKI 131

QY 87 EKLISNLSKAL---VSLALEKQVQAHHQREDPASNEVYNAKDDLDPKNDSEPGSQ 143  
Db 132 EKTIVSVNVAAGSKVTELELYEELKRNKKG-----YMYLVQVK 173

QY 144 RIKPFIEDANFGROIYOHAAVHIPTDIYEGSTIYINELNWTSAIDVFKKREDDPSI 203  
Db 174 LVKHFELE-----VDIFEPGISMDEASTINDL-----GSA 208

QY 204 LMVYFGSATGLARYPASPVDNSRT-PNKID-----LYDVRRP-----WY 244  
Db 209 LTKFSFGKKGHVFSKPS---LDQORSCPCTDLSLNGDFTIYDVNRSPGNVQVNGYF 265

QY 245 I-----QG-AASPKDMLIVDVGSGVSGTLKILRTSVSEMLETTSDDPVAVASFNSNA 298  
Db 266 VHFPAQGLPVEPKNVAFYVIDISGMAGRKLEOTKEALRILEDKKEEDYINFIKSG-- 323

QY 299 QDVSCF-OHLVQANVNNKKVLDVANNITAKGTYDKKGFSAFQGLNYSR----- 351  
Db 324 -DVSTWKEHLVQATPENLDGARTFVAKSMEDKGTNINDGLGISKML--NAREHRIP 379

QY 352 ANCKIMLETDG---GERAOEIPNKYNK--DKRVFRFSVQHNTERGPIOMACE 405  
Db 380 ENSTSVIMLTDDANVGSRPEKIDENVRNAIGCFPLYNIGFG-NLNVNFMNMALE 438

QY 406 NKGYVEIPISGIRINTQEVLDVGRPMVLAGDAKQVQWNVYLDAL-----L 456  
Db 439 NHGFARITEDSDADQLQGFYEYVANNPL-LTGVKEIPE--NAILDLQNTYOHFYDGS 495

QY 457 GLVITGTLPEVNTGOFENKTNK-----NOLIGMGVDVSLDIKRLTFRTLCPGY 511  
Db 496 EIVVAGRL-VDEDMNSF--KADVKGHGATNDL--TFTEEDVMKEMK-----ALQEDY 544

QY 512 YFALDPN-----GYVLHPNLPK---NPKSQEVTYLDLDALENDIKYIRNKMDIG 562  
Db 545 IFG---NYIERMAVILITLEOLLEKRNNAHGEKENLTPRALDLSIKYHVPYPLSMVYTK 601

QY 563 ESEKTFPLVKSODERYI-DKGNRTYTWTPVN-GTDSIALVLPYTSFYFI 612  
Db 602 PE-----DNEDERAIADKPGEDATVSPAMSLTSTYQPPQNPYIV 644

## RESULT 10

US-09-828-423-3  
Sequence 3, Application US/09828423  
Patent No. US20020099178A1  
GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

Guegler, Karl J.

Paterson, Chandra

TITLE OF INVENTION: GROWTH-ASSOCIATED TRYPSIN-TYPE

INHIBITOR HEAVY CHAIN PRECURSOR

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESS: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: Word Perfect 6.1/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/828.423

FILING DATE: 05-Apr-2001  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/388,774  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Carrone, Michael C  
 REGISTRATION NUMBER: 39,132  
 REFERENCE/DOCKET NUMBER: PF-0505 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-855-0555  
 TELEFAX: 650-845-4166  
 TELEX: <Unknown>  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 946 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: GENBANK  
 CLONE: g133985  
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
 US-09-828-423-3

Query Match 2.88; Score 159.5; DB 10; Length 946;  
 Best Local Similarity 19.98; Pred. No. 0.0021; Mismatches 258; Indels 171; Gaps 29;  
 Matches 133; Conservative 107;

33 IKSWDKQEDLVTLAKTASGVNQLVDYERKQDLYVEPNNAQOLVEIARDEIKLKN 92  
 26 LSEFED--YEDVEL--APGKFDLVAMENRRYQSLPESEKMEVEVDQVLYSYKVOST 80  
 93 RSKALVSLAEKVAQAAHQRRE-----DFASN-----EV 122  
 81 ITSRAATMIOSKYVNNSPQONVYEDQIPKAFISNFSMTVDGKTFRSSIKETVGRA 140  
 123 VYNNK-----DDLPEKNDSE-----PGSORIKPFIEDANFGROIYOH----- 163  
 141 LTAQRAKAGTAGLVRSSALDMENRTEVNVLPKAKVQFELHYQVKKRKIGSTEHRIYL 200  
 164 ----AAVHIPDIYGSTIVNELNMTSALD-----EVKKKREE-----DPSILMVOYF 208  
 201 QPGRILAKHLEVDVWIEPQGLFELHVPDTEGHEFDGVVISKQOKAHVSEKPTVAQO-- 258  
 209 GSATGLARIYPAWPVNDSSRPENKIDLDVRRRP-----WYIOGAAS-----PK 252  
 259 -----RCPSCR--ETAVDGEVLVLDVKKREKAGELEVNGFVHFEPADNDLPK 309  
 253 DMLIIVDGSVSGTLKILRTSVSEMLETSDDETVNVASFNSNAODVSCFOHLVQANV 312  
 310 NILFVIDVSGSMWGMQVEMAKMTILDRLRAEDHFVIDENQIR--TWENDLFOLOK 367  
 313 RNKKVILKADVANNITAKGIDYKGF--SFAPQOLLNVVSNANCKIIMLTDDG--G 365  
 368 HRQIAKRIETKIQPSGGTINIEALIRALFIIEANNLGLDLPNSVSLIILVSDGDPYVG 427  
 366 EERAOEIFPKYNNKDKVYRFRFSVQO-----HNYERGIQWM-----ACENK 407  
 428 ELKLSIQKNKENIODNISLFSLGMPVDVDFLKLRLNENHNGIAQRIYGNODTSQLOK 487  
 408 GYVEET--PSIGAIRIN--TOEYLDVL-----GRPMVLAG--DKAKQVQWNTVYLD 452  
 488 KFYNQVSTPLLRNVQFNYPHTSVTDTONNFHNYFGSSEIVVAGKDPAPK-----LD 539  
 453 ALBLGVIITGLPVFNITGQFENKTNLKNQILGVAGVVSLEDI-----KRLPREFTLCP 508  
 540 QIE--SVYTA-----TSANQVLETLIAQDDLDQDFLSKOKHAPDPTTR--K 582  
 509 NGYFFALDPNGVYLHPNLIQPKPKSEOPVTLDFDLAELENDIKVEIRKMKIDEGSEK 568  
 583 LMYLFTIN---QLLAERSLAP--TAAAKRRITRSILQMSIDHILVTLPLTSLVIEENAGDER 638

QY 569 FRTLVKSD 577  
 DB 639 MLADAPQD 647

RESULT 11  
 US-09-815-242-5898  
 Sequence 5898, Application US/09815242  
 Patent No. US20020061569A1  
 GENERAL INFORMATION:  
 APPLICANT: Haselbeck, Robert  
 APPLICANT: Ohlsen, Karl L.  
 APPLICANT: Zyskind, Judith W.  
 APPLICANT: Wall, Daniel  
 APPLICANT: Trawick, John D.  
 APPLICANT: Carr, Grant J.  
 APPLICANT: Yamamoto, Robert T.  
 TITLE OF INVENTION: Identification of Essential Genes in  
 FILE REFERENCE: ELITRA.011A  
 CURRENT APPLICATION NUMBER: US/09/815,242  
 CURRENT FILING DATE: 2001-03-21  
 PRIOR APPLICATION NUMBER: 60/191,078  
 PRIOR FILING DATE: 2000-03-21  
 PRIOR APPLICATION NUMBER: 60/206,848  
 PRIOR FILING DATE: 2000-05-23  
 PRIOR APPLICATION NUMBER: 60/207,727  
 PRIOR FILING DATE: 2000-05-26  
 PRIOR APPLICATION NUMBER: 60/242,578  
 PRIOR FILING DATE: 2000-10-23  
 PRIOR APPLICATION NUMBER: 60/253,625  
 PRIOR FILING DATE: 2000-11-27  
 PRIOR APPLICATION NUMBER: 60/257,931  
 PRIOR FILING DATE: 2000-12-22  
 PRIOR APPLICATION NUMBER: 60/269,308  
 PRIOR FILING DATE: 2001-02-16  
 NUMBER OF SEQ ID NOS: 14110  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 5898  
 LENGTH: 1349  
 TYPE: PRT  
 ORGANISM: Staphylococcus aureus  
 US-09-815-242-5898

Query Match 2.78; Score 151; DB 10; Length 1349;  
 Best Local Similarity 19.48; Pred. No. 0.014; Mismatches 339; Indels 366; Gaps 48;  
 Matches 199; Conservative 121;

16 SLIIGPSSSEFPSPAVTIKSNVDMQEDLVTLAKTASGVNQLVDYERKQDLYVEP 72  
 40 TLIFGLGQEKKAESTYKE-----LNEATTSASDNSSDKVDMQOLNEDNTKND 90  
 73 NNAROLVIAARDIEKLSNRSKALVSLAEKVAQAAHQRREDPASNEVYIYAKDDL 132  
 91 NQK-----EMVSSQNETTSNGNK-----LIEKESVOST-----TSNKVEVSTAKSD-- 132  
 133 PEKNDSEPGSORIKPFIEDANFGROIYQAAHAIPTDIYGSTIV----- 179  
 133 ---EQASPKSTN-----EDLNTKOTISNOZ-----LQPDLENKSVYAVQPTNEENKVD 180  
 180 -----LN-----ELNMTSALDEVFKKREEDPSLM-----QVFGSATGLARYPA 220  
 181 AKTESTITLVNSDAIKSNDLTVDNNSNSNNNADNILLPKSTAPKRLNTRMRIAAYQPS 240  
 221 SPWVDN-----SRPKNIDLDVARRRWYIUGAASPRDMLIIVDVSQSVSGTLKILRT 274  
 241 STEARNVNDLITNSNTLTVVDADKRNKKIVPAQDYISLKSQITVDKRYKSGDYFTIKY-- 297  
 275 SVSEMLETISDDPFYVNASFN--SNAODVSCFOHLVQANVRKKVILKDAVNNITAKGITT 332  
 298 SPTVQVYGLNPEDINIGDIKPNNGEFTIATKHH-----DTANMLTYTFTD 344

```

OY 333 YKGFSAFEOILNTNV-----SRANC-----NK 356
| : : : : :
Db 345 YVDRFN-SVQMGINTSIYMDADTIYVSKNDVEFNVTIGNTTKTANIOYDPYVNEKNS 403
OY 357 IIMLEFD-----GGEER-----AOEIF-----NKYNKDKVVRFRFS-----VGOHNERG 397
| : : : : :
Db 404 ISAFTEFVSHVGNKENPGYKOTIYVNPSENSLTNALKVOAHSSIPNNIGQINDVT 463
OY 398 PIGWMAE-----NKGYEIEISIGAIRINTOEYLDVGRPM-----VLADKRAQV-----444
| : : : : :
Db 464 DIKIYQVKGITLANKY-----DVNTKELTDVINOYLOKITGDNNSAVIDFGNA 513
OY 445 -----QMTN-----448
| : : : : :
Db 514 DSAIVVMTNFKFOYTNSPFLVQMATLSTGKNKSVSTGNALGFTNNOSGAGOEYKIG 573
OY 449 --VYIDALEGLVITGILPVFNIT--GOFENKTNIKNOILIGVGVDSLEDIKRLPRFT 505
| : : : : :
Db 574 NYWEDTNKNGVOELGEGVGNVTVTFDNNNTNK-----VGEAVTKEDGSYLIPNL- 625
OY 506 LCPNGY--FAIDPNGYVLLHPNLOPKNK-----SQEPYTLDFDALENDIKYEIRN 557
| : : : : :
Db 626 --PNCQDYVERFSNLPKGYEVT--PSKOGNNEELDSNGISSVITVNGKD--NLSADLGIYKPK 681
OY 558 KMIIDSEGEKTFRLVKSQDERYIDKGNRTYWTVPNGTDYSLALVLPYSSYIIKAKLE 617
| : : : : :
Db 682 YNLCDYVWEDTNKNGIODEKEGI--SGVTYTLKDENG-----DVL 720
OY 618 ETIOARSKKGMKDSITLKPDNFEEGTYFFIAPDYCNDLISDNNTFELNFEIDR 677
| : : : : :
Db 721 KTVTTDADGKKFTPD--LHGNK--VEFTTPEGTYPTVSGSDIE-----763
OY 678 KTPNPSQCNADLIN--RVLLDAGFTN--ELVQNTW-----SKONIKAV--717
| : : : : :
Db 764 --KDSNGLTGTGVINGADNMTLDSGFYKTKPKYKNGVWEDTNKDGKODETEKIGISYVT 822
OY 718 -----KAFYVTDGILTV-----YPRKAGENMOE-----742
| : : : : :
Db 823 LKNGEVLQTTTIDKDGKQFTGLNGTYKVEFTPSGYTPLYOGSSGDEIDENGST 882
OY 743 -----NPEYEDSFYKRLSDNDNVETAPFNKSGPAYE-----SGTMSKAVEIYIO 791
| : : : : :
Db 883 TGVIKDKDNFTIDSGFYKPTYNLGDYVWEDT--NKNGVODKDEKIGSVYTLKDE--N 937
OY 792 GKLLK 796
| : : : : :
Db 938 DKVILK 942

```

## RESULT 12

```

; Sequence 13137, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlssen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: EUTRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26

```

```

; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 13137
; LENGTH: 1349
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-815-242-13137

Query Match      2.7%; Score 151; DB 10; Length 1349;
Best Local Similarity 19.4%; Pred. No. 0.014;
Matches 199; Conservative 121; Mismatches 339; Indels 366; Gaps 48;

OY 16 SLIIGPSSEFPFSAVITKSVWDMQEDVTLAKTAGVNO--LVDIYEKYODLYTVER 72
| : : : : :
Db 40 TLIFGLNGOEKKAESTNKE-----LNFAVTSASDQSSDKYDMQOLNOEDNTKMD 90
OY 73 NNAQIVEIARQDIETKILSNRKALVSLAEAKVQAHOHWRDEPASNVEVYIYNAKDDID 132
| : : : : :
Db 91 NQK-----EMVSSQGNETTSNGK-----LIEKESVOST-----TGKVEVSTAKSD-- 132
OY 133 PEKIDSEPGSORIKPVFIEDANFGROI SYOHAHVHPTDIYEGSTV-----179
| : : : : :
Db 133 --EASPKSTN-----EDLNTKQITSNQEA--LQPDLOENKSVVNOQPINEKNKVD 180
OY 180 -----LN-----ELNMTSALDEYFKKNNREDSPLM-----QVGSATGLARYPA 220
| : : : : :
Db 181 AKTESTITLAKSALIKSNBETLVDDNNSNSENNDIILPKSTAPKRLNTRIRIAVQPS 240
OY 221 SPWVDN-----SRTPNKIDLVRRRPYIQAASPKDMLLVVSSVSGULKILRT 274
| : : : : :
Db 241 STEAKVNDLITNTLTLYVADKNNKIVPADYISLSQIIVDDKYSGGYFTIKY-- 297
OY 275 SVSEMETLSDDFVAVASFN--SNADVSCFOHLVQANVRKKVLDVANNITAKGITD 332
| : : : : :
Db 298 SDIVQVYGLNPEDIKNIGIKDPNNGETIATAKH-----DTANNLTTFYTD 344
OY 333 YKGFSAFEOILNTNV-----SRANC-----NK 356
| : : : : :
Db 345 YVDRFN-SVQMGINTSIYMDADTIYVSKNDVEFNVTIGNTTKTANIOYDPYVNEKNS 403
OY 357 IIMLEFD-----GGEER-----AOEIF-----NKYNKDKVVRFRFS-----VGOHNERG 397
| : : : : :
Db 404 ISAFTEFVSHVGNKENPGYKOTIYVNPSENSLTNALKVOAHSSIPNNIGQINDVT 463
OY 398 PIGWMAE-----NKGYEIEISIGAIRINTOEYLDVGRPM-----VLADKRAQV-----444
| : : : : :
Db 464 DIKIYQVKGITLANKY-----DVNTKELTDVINOYLOKITGDNNSAVIDFGNA 513
OY 445 -----QMTN-----448
| : : : : :
Db 514 DSAIVVMTNFKFOYTNSPFLVQMATLSTGKNKSVSTGNALGFTNNOSGAGOEYKIG 573
OY 449 --VYIDALEGLVITGILPVFNIT--GOFENKTNIKNOILIGVGVDSLEDIKRLPRFT 505
| : : : : :
Db 574 NYWEDTNKNGVOELGEGVGNVTVTFDNNNTNK-----VGEAVTKEDGSYLIPNL- 625
OY 506 LCPNGY--FAIDPNGYVLLHPNLOPKNK-----SQEPYTLDFDALENDIKYEIRN 557
| : : : : :
Db 626 --PNCQDYVERFSNLPKGYEVT--PSKOGNNEELDSNGISSVITVNGKD--NLSADLGIYKPK 681
OY 558 KMIIDSEGEKTFRLVKSQDERYIDKGNRTYWTVPNGTDYSLALVLPYSSYIIKAKLE 617
| : : : : :
Db 682 YNLCDYVWEDTNKNGIODEKEGI--SGVTYTLKDENG-----DVL 720
OY 618 ETIOARSKKGMKDSITLKPDNFEEGTYFFIAPDYCNDLISDNNTFELNFEIDR 677

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Db 721 KVTITADGKTKTD---LINGNYK---VEFTTPEGTTPTVTSQSDIE----- 763
QY 678 KTPNPNPCNADLIN---RVLLDAGFTN---ELVONYW-----SKOKNIKGV--- 717
Db 764 -KDSNGLTITGVANGADNMFLDSGFKTPKYNLGNVWEDTNKDGKODSTENKISGVYTA 822
QY 718 -----KARFVYTDGCTIRV-----YPRKAGEBNMOE----- 742
Db 823 LKMNENGVLOTTTKDQKXQFTGLENGTYKVEFETPSGCTPTQVSGSCUDEGIDSNCTST 882
QY 743 -----NPEYEDSPFKRSLDNDNVFTAPYFNKSGPAGYE-----SGIMVSKAVELIYQ 791
Db 883 TGVTKDKNDNTIDSGFKTPYINLGDVWEDT--NKNGVODKDEKIGISGVYVTLKDE---N 937
QY 792 GKLLK 796
Db 938 DKVLK 942

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```

RESULT 13
US-09-850-351A-6
; Sequence 6, Application US/09850351A
; Patent No. US20020100080A1
GENERAL INFORMATION:
APPLICANT: Feltelson, Gerald S.
Schnepl, H. Ernest
Narva, Kenneth E.
Stockhoff, Brian A.
Schmeltz, James
Loewer, David
Dullum, Charles Joseph
Muller-Cohn, Judy
Stamp, Lisa
Morrill, George
TITLE OF INVENTION: No. US20020100080A1el Pesticidal Toxins and Nucleotide
Sequences Which Encode These Toxins
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSER: Saliwanichik, Lloyd & Saliwanichik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/850,351A
FILING DATE: 07-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/073,898
FILING DATE: 06-May-1998
APPLICATION NUMBER: US 08/960,780
FILING DATE: 30-Oct-1997
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-Oct-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-708CD1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 789 amino acids
TYPE: amino acid
STRANDEDNESS: single

```

```

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: 81F
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-850-351A-6

```

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Query Match 2.7%; Score 150.5; DB 10; Length 789;
Best Local Similarity 20.1%; Pred. No. 0.007;
Matches 138; Conservative 100; Mismatches 235; Indels 213; Gaps 34;

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QY 231 NKIDLVARRRPWYIQGAAPKMLILVDGSGVSGFLTKIRTSVSEMLETSLSD-DFV 289
Db 105 NKLDAINTMLRYVLL-----PKITSMLSDVMKQNALSTQI--EYLSKQLQEISDKLDII 156
QY 290 NV-ASFSNAODVS-----CFQHLVQANVRNKKVLKDA-----VANNIT-----A 327
Db 157 NVNVLINSTLTETIPAYORIKRYNEKEFELTETATTSKRVKDGSPADILDELTELELA 216
QY 328 KGITDYKKGSPFAFQOLN--YVSRANCKIMLFTDGEERAOEIPNKKYKDKVAVF 385
Db 217 KSVT---KNDVDFEYINTFHDVWGN-----NLFGRSALKTASELTITKEN---VKTS 264
QY 386 RRSVGOHNERGPQIMACENKGYIYEIPSGAIRINTQETLDVLRPMVLAKAKAQV 445
Db 265 GSEVG--VYNNELIVLTALQAKAFLLTTCRKLGLADIDYTSIMNEHL---NKEKEEF 318
QY 446 WNNVVLDALEGLVITGTLPVFNINGQFENKTNKN-----QLIL-----CWAGCVYSL 494
Db 319 RKNIT-----LPTLSNTFSNPNYAKVSGSDAKMIVEAKPGHALVGFELSN 364
QY 495 EDI-----KRLTPRF-----TLCPNG-----YFF--AIDPNGYVLLH 524
Db 365 DSITVLKVEAKLKQNYQVQDKSLSEVLYIGMDKILCPDQSEQIYITNNIYFPNHYITK 424
QY 525 PVLQKRNKRSQEPVTLDELDALENDIVEIRKMKIDGSEKTRFRLVKSQDERYIDK 584
Db 425 IDFTKMKTLREYVIANEYDSTG---EIDLNKKKV--ESSEAEVRLISANDCVYVPLG 479
QY 585 NRTYTW-TPVNG---TYSALVLPYTSFYIRAKLEETITQARSKKKKKDSEITLKP- 638
Db 480 VISETFILPINFGLADENSRLLITLTKSYLRELLATDLSN-----KETKLIVPP 531
QY 639 ---DNFEESGYTFIAPRDYCNLDKISDNTE--FLNFEFIDRKTPNPNPCNADLINR 692
Db 532 SGFIKNIVENG-----SIEDNLEPMKANKNEYVDH----- 563
QY 693 VLLDAGFTNELVQYWSOKNIKGVKARFVYTDGKIT-----RYYPK----- 734
Db 564 -----TGGVNGTKALYVHKDGISQFIDGDKLPKTEYVIQYTVKGP 605
QY 735 -----EAG-----ENMQENPEYEDSPFKRSLDNDNVFTAPYFNKSGPAGYSGIMVS 783
Db 606 SIHLDEWNTGYIHEDTNNNLEDYQITTKRFTTGDLKGYVLIILKSQNGDEAWGDNFTLI 664
QY 784 KAVEIYIYGKLLKPAVVGIKIDVNSW 809
Db 665 --LEISPSEKILSPEL-----INTNMW 684

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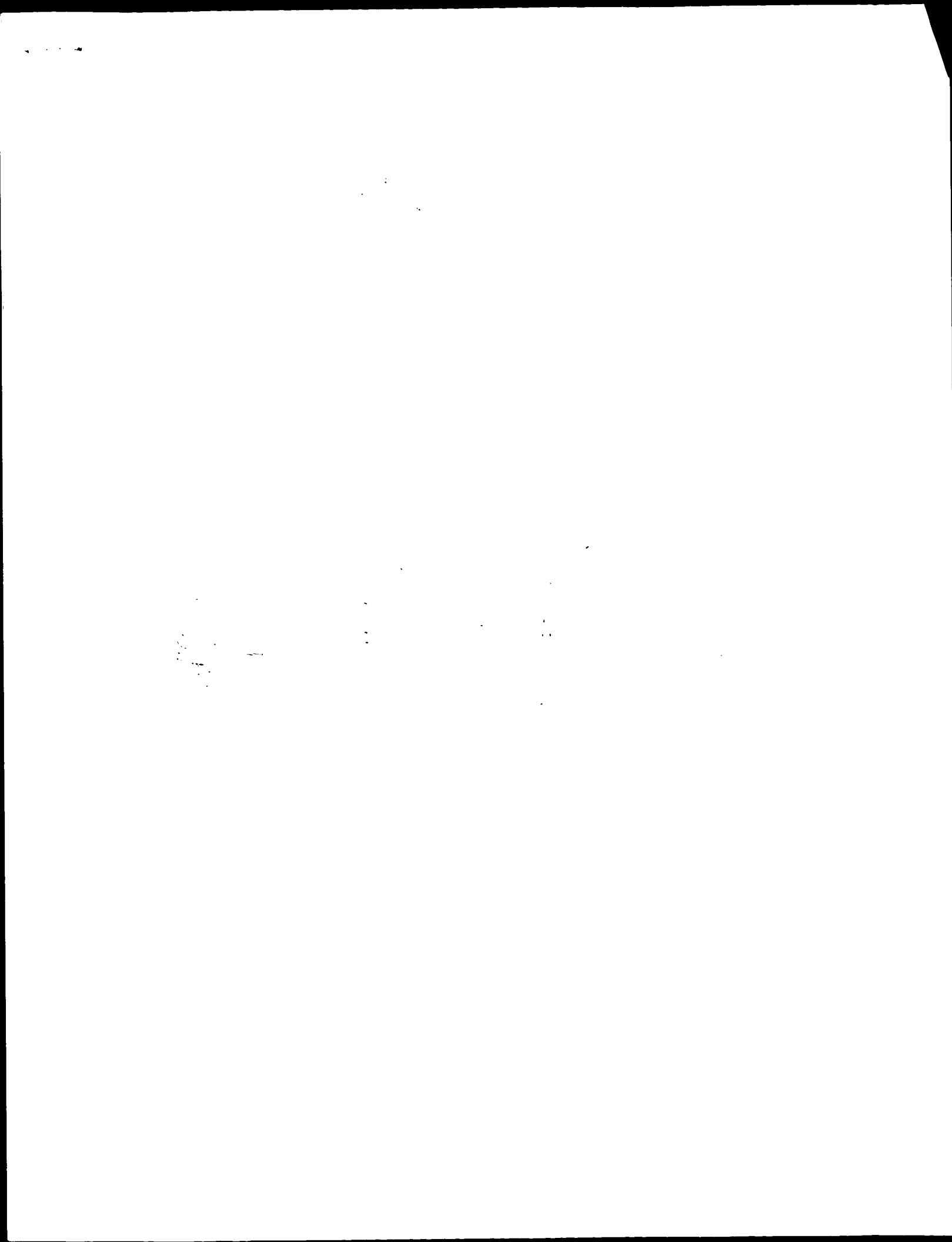
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RESULT 14
US-09-850-351A-4
; Sequence 4, Application US/09850351A
; Patent No. US20020100080A1
GENERAL INFORMATION:
APPLICANT: Feltelson, Gerald S.
Schnepl, H. Ernest
Narva, Kenneth E.
Stockhoff, Brian A.
Schmeltz, James
Loewer, David
Dullum, Charles Joseph
Muller-Cohn, Judy

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OM protein - protein search, using sw model

Run on: February 10, 2003, 14:22:34 ; Search time 7.52732 Seconds

(Without alignments)  
2998.192 Million cell updates/sec

Title: US-10-090-827-13

Perfect score: 5346

Sequence: 1 MAAGCLLALTLTFLFOSLIG.....TNLITFWSKGTCPDTRL 1018

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Search: 129505 seqs, 22169297 residues

Total number of hits satisfying chosen parameters: 129505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published.Applications\_AA.\*  
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14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5346	100.0	1091	10	US-09-875-423-4
2	1085	20.3	1091	10	US-09-875-423-5
3	1084	20.3	1091	10	US-09-875-423-2
4	317.5	5.9	223	12	US-10-003-168-2
5	272	5.1	51	10	US-09-864-761-44281
6	272	5.1	53	10	US-09-864-761-38267
7	190	3.6	35	10	US-09-864-761-38318
8	185	3.5	35	10	US-09-864-761-36461
9	182	3.4	885	10	US-09-828-423-5
10	159.5	3.0	946	10	US-09-828-423-3
11	151	2.8	1349	10	US-09-815-242-5898
12	151	2.8	1349	10	US-09-815-242-13137
13	150.5	2.8	789	10	US-09-850-351A-6
14	148.5	2.8	790	10	US-09-850-351A-4
15	145.5	2.7	790	10	US-09-850-351A-8
16	143.5	2.7	1781	9	US-09-995-749A-2
17	136.5	2.6	956	9	US-10-121-032-63
18	136.5	2.6	3169	9	US-10-114-170-257
19	133.5	2.5	764	9	US-10-105-695-4

20	133.5	2.5	764	9	US-10-105-694-4	Sequence 4, Appli
21	133.5	2.5	764	10	US-09-747-521-4	Sequence 4, Appli
22	133.5	2.5	764	12	US-10-106-014-4	Sequence 4, Appli
23	133	2.5	1323	10	US-09-801-368-34	Sequence 34, Appli
24	132.5	2.5	876	10	US-09-815-242-12623	Sequence 12623, A
25	127.5	2.4	3712	9	US-10-108-605-103	Sequence 103, App
26	123	2.3	2285	10	US-09-932-183A-2	Sequence 2, Appli
27	121.5	2.3	2125	10	US-09-919-172-29	Sequence 29, Appli
28	120	2.2	698	9	US-09-801-220-9	Sequence 4, Appli
29	118	2.2	103	9	US-10-050-786-9	Sequence 9, Appli
30	117	2.2	811	9	US-10-011-588-29	Sequence 29, Appli
31	116.5	2.2	764	10	US-09-815-242-4949	Sequence 4949, Ap
32	116.5	2.2	764	10	US-09-815-242-10593	Sequence 10593, A
33	116	2.2	911	10	US-09-828-423-4	Sequence 4, Appli
34	114.5	2.1	773	12	US-10-067-385-8	Sequence 8, Appli
35	114.5	2.1	1183	9	US-09-870-759-45	Sequence 45, Appli
36	114	2.1	673	12	US-10-032-717-12	Sequence 12, Appli
37	113	2.1	620	12	US-10-032-717-30	Sequence 30, Appli
38	112.5	2.1	861	9	US-09-850-525A-10	Sequence 32, Appli
39	111.5	2.1	871	9	US-09-858-525A-2	Sequence 10, Appli
40	111.5	2.1	871	9	US-10-044-303-2	Sequence 2, Appli
41	111.5	2.1	1016	12	US-08-834-666A-8	Sequence 8, Appli
42	111	2.1	711	8	US-09-885-535-4	Sequence 6, Appli
43	110	2.1	2835	10	US-09-369-735B-6	Sequence 4, Appli
44	109.5	2.0	483	10	US-10-150-821-4	
45	109	2.0	3594	9		

#### ALIGNMENTS

RESULT 1  
US-09-875-423-4  
; Sequence 4, Application US/09875423  
; Patent No. US20020081657A1  
GENERAL INFORMATION:  
; APPLICANT: CURTIS, ROY A.J.  
; TITLE OF INVENTION: 21784, A NOVEL HUMAN CALCIUM CHANNEL  
; FILE REFERENCE: 10448-059001  
; CURRENT APPLICATION NUMBER: US/09/875,423  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US 60/209,257  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; NUMBER OF SEQ ID NOS: 6  
; SEQ ID NO 4  
; LENGTH: 1091  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-875-423-4

Query Match 100.0% Score 5346 DB 10 Length 1091  
Best Local Similarity 100.0% Pred. No. 0;  
Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MAAGCLLALTLTFLFOSLIGPSSEPPPSAVTIKSWVKMOEDLVTAKTASGVNQLYDI	60
DB	1	MAAGCLLALTLTFLFOSLIGPSSEPPPSAVTIKSWVKMOEDLVTAKTASGVNQLYDI	60
QY	61	YKRYDDLYVEENNAKRLVETIARIDIEKLISNRKATVSLAEKRVQAAHQWREDFASN	120
DB	61	YKRYDDLYVEENNAKRLVETIARIDIEKLISNRKATVSLAEKRVQAAHQWREDFASN	120
QY	121	EVVYYNAKDDLDPEKNDSEPSGRILKPFIEIDANRGRIQSHAAVHTPTDIYGSTLYL	180
DB	121	EVVYYNAKDDLDPEKNDSEPSGRILKPFIEIDANRGRIQSHAAVHTPTDIYGSTLYL	180
QY	181	NELNNTSALDEVFKKRNREDSPLLMQVFSATGLARYPASPVVNSRTPKIDLYVRR	240
DB	181	NELNNTSALDEVFKKRNREDSPLLMQVFSATGLARYPASPVVNSRTPKIDLYVRR	240
QY	241	RMWYIGGAASPRDMILYDVSGSVGLTLKLIRTSVSEMLETTSDDDFVNVASFNNSNQD	300

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Db 241 RPYTIGASPKDMLILVDSGSVGLTLKLRTSVEMLETLSDDDPVNVASFNSNQD 300
QY 301 VSCFHLVQANRANKVYKDAVNNITAKGIDYKKGFSFAEQLLNVVSAKCKIIML 360
Db 301 VSCFHLVQANRANKVYKDAVNNITAKGIDYKKGFSFAEQLLNVVSAKCKIIML 360
QY 361 FIDGGEERAEOLFENKYNKDKKRVFRFVGOHNTERGPIOMMACENKGYEISIGAR 420
Db 361 FIDGGEERAEOLFENKYNKDKKRVFRFVGOHNTERGPIOMMACENKGYEISIGAR 420
QY 421 INTGEXLDVIGRPVYLAGKAKOVOMTVNYLDALDELGLVITGTLPEVNIITGOFENKINL 480
Db 421 INTGEXLDVIGRPVYLAGKAKOVOMTVNYLDALDELGLVITGTLPEVNIITGOFENKINL 480
QY 481 NGLIIGVGVVSLIEDIKRTPRFITLCPNGYFFALDPNGVYLLHNPLOPKMPSQEPYTL 540
Db 481 NGLIIGVGVVSLIEDIKRTPRFITLCPNGYFFALDPNGVYLLHNPLOPKMPSQEPYTL 540
QY 541 DFLDAELENDIKVEIRNKKMIDEGSEKTFRLVKSQDERYIDKGNRTYTWTPVNGTDSL 600
Db 541 DFLDAELENDIKVEIRNKKMIDEGSEKTFRLVKSQDERYIDKGNRTYTWTPVNGTDSL 600
QY 601 ALVLPYSFYIYKAKLEETITQARSKKGMKDEFTLKPDPNEESGYTFIAPRDYCNDLKI 660
Db 601 ALVLPYSFYIYKAKLEETITQARSKKGMKDEFTLKPDPNEESGYTFIAPRDYCNDLKI 660
QY 661 SNNTEFLINFEIDRKTNNPNSCNADLINVLDAEFTNELVONYMSKOKNIKGVAR 720
Db 661 SNNTEFLINFEIDRKTNNPNSCNADLINVLDAEFTNELVONYMSKOKNIKGVAR 720
QY 721 FVVTGGITRVYPKEAGENMOENPETYEDSFYKRSILDNDNVFTAPYFNKSGPAGESGI 780
Db 721 FVVTGGITRVYPKEAGENMOENPETYEDSFYKRSILDNDNVFTAPYFNKSGPAGESGI 780
QY 781 MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIEFTKTSIRDPCAGVYCCCKRNSDMCVI 840
Db 781 MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIEFTKTSIRDPCAGVYCCCKRNSDMCVI 840
QY 841 LDDGFLMANHDDYTNOIGRFEGLDPSLMHNLVINSYAFANKSYDYOSVCEPGAAPKO 900
Db 841 LDDGFLMANHDDYTNOIGRFEGLDPSLMHNLVINSYAFANKSYDYOSVCEPGAAPKO 900
QY 901 GAGHSAYVSVADILQIGMWATAAAMSILOQFLSLTFPRLLAEVEMEDDFTASLSKO 960
Db 901 GAGHSAYVSVADILQIGMWATAAAMSILOQFLSLTFPRLLAEVEMEDDFTASLSKO 960
QY 961 SCITGOTOYFFNDNSKSPSGVLDGNCSTRIFHGEKLTMTNLIETVNESKGTCPDCTL 1018
Db 961 SCITGOTOYFFNDNSKSPSGVLDGNCSTRIFHGEKLTMTNLIETVNESKGTCPDCTL 1018

RESULT 2
US-09-875-423-5
; Sequence 5, Application US/09875423
; Patent No. US20020081657A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, ROY A.J.
; TITLE OF INVENTION: 21784, A NOVEL HUMAN CALCIUM CHANNEL
; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-059001
; CURRENT APPLICATION NUMBER: US/09/875,423
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1091
; TYPE: PR
; ORGANISM: Mus musculus
US-09-875-423-5

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Query Match 20.3%; Score 1085; DB 10; length 1091;
Best Local Similarity 28.7%; Pred. No. 3.6e-70;
Matches 309; Conservative 222; Mismatches 416; Indels 128; Gaps 40;

QY 3 ACCLIALTLTFLFOSLIGSPSEPPSAVTKSWVDKMODLVLTAKTAGVNOQVLYE 62
Db 14 ASALLA-TALLYALGADVNSEOQIPLSV-VKLMAAFGEIKSIKAAKSGSOLLQKKY 71
QY 63 KYODLYVEENNAKOLVEIARDEIKLSNRKALVSLMEKVOAQAOMREDFASNV 122
Db 72 EYEDVAIEEDIGLOLKKLAKIMEEFHKSARVLEABAEALHKEFDAL---OY 128
QY 123 VYVNAK---DDIDPEKNDSEPGSQRKPVFLEDAFGR-QISYOAHAHPTDIEGSTIV 179
Db 129 EYFNAVLINERDKDGNLELGKEFI---LAPNHFNNLPVNISLSVQVPTMNYNNDPAI 185
QY 180 LNELNMTSALDEYFKKREDEPSLMOVGSATGLARYTPASWVDNSRTPKIDLYDR 239
Db 186 VNGYVWSESINKYFVDFDPSLIWOYFGSAGFROYGKIMPEDE---NGVIAFDGR 242
QY 240 RRPYIIGASPKDMLILVDSGSVGLTLKLRTSVSEKLETLSDDDPVNVASFNSNQ 299
Db 243 NRKYIOAATSPKDVYLLVYSSGSKGLRTITAKOTYSSILDTLGDDEFFNITTYEEH 302
QY 300 DVS-CFQ-HLVQANRANKVYKDAVNNITAKGIDYKKGFSFAEQLLNVVSAKCKI 355
Db 303 YVEPCLNGTLVQADRTKEHFEHLDELKFAKIGMDIALNEAFNILLSDFNHTGQGSIC 362
QY 356 KIIMLFIDGGEERAEOLFENKYN-KDKKRVFRFVGOHNTERGPIOMMACENKGYEELP 414
Db 363 QALMLITDGAVDYDTLEAFYNNPDRKRVLELYLIGHEAFAADNLKMWACANGFPTQIS 422
QY 415 SIGAIRINTOEYLDVIGRPVYLAGKAKOVOMTVNYLDALDELGLVITGTLPEVNIIT 463
Db 423 TLADVOENWMEYELVLSRPKYI--DOEHVYVWIEATIDSLPQAKLADOGGLVLTYYA 480
QY 464 LPVENITGQENKTNLKNQILIGVGVVSLIEDIKRTPRFITLCPNGYFFALDPNGVYLL 523
Db 481 MPVFS---KONETRSKG-ILLGVGTDVPVKEKLTIPYKKGIGYAFATINNGYIILT 535
QY 524 HPNLP---KNPSQOE--VTLDFLDAELENDIKVEIRNKKMIDEGSEKTFRLVYSQOE 578
Db 536 HPELRPLYEGRKKRKNYSVDLSEVEMEDRDV-LRNAMVNRKTGK--FSNEV---- 588
QY 579 RYIDKGNRT-----YTFPVNGIDYSLALVLT--SYFYIKAKLEETITQARSKGKKK 631
Db 589 KTVDKGKRVLYMTNDYYTIDIKGPSLSGVALSRGKHGYF-----RGNTV 634
QY 632 DSEFLKPDNEESGYTFIAPRDYCN-DLKTSDNNTPELLNFEIDRKTNNPNSCNADLI 690
Db 635 IEEGL--HDLHPDVSLADEMSYCNLDLHPHHLSQLEAIKLYLKKEP-LIQCDBKEI 691
QY 691 NRVLDAEFTNELVONYMS-----KOKNIKGVARVYVTDGITRVY----- 733
Db 692 QEVLFDA-VVSAPLEAVWTSIALNKSNSDKGYEVAFLGTRGLSKINLFLVGAEOULTND 750
QY 734 -KEAGENMOENPETYEDSFYKRSIDN--DNYVFTAPY---FNKSGPAGESGINVSKAV 786
Db 751 FLKAGDKENIFNDHPFLWRRAAEQJAGSFVSIIPSTGTVKS-----NVYTASTSI 804
QY 787 EITIOGKLLKPAVVGIKIDVNSWIEFTKTSIRDPCAGVYCCCKRNSDMCVIIDDGE 846
Db 805 QLDERSKPVAAVAGIOMKLEFQKRKWTASROCASLDGKCSISCDDEYTNCLYINNNG 864
QY 847 LMANHDDYTNOIGRFEGLDPSLMHNLVINSYAFANKSYDYOSVCEPGAAPROGAGHS 906
Db 865 ILVS--EDYT-QTGDFFGEVGAVMNKLITMGSKRTITLYDQAKR---ANKESDSAH 918
QY 907 AYVPSVADILQIGMWATAAAMSILOQFLSLTFPRLLAEVEMEDDFTASLSK-----OS 961
Db 919 GLDLPYKAFI-----SAKWMITELVLFVEF-----NCSWMSHSMITAKAOKLKTQTL 968
QY 962 CITGOTOYFFNDNSKSPSGVLDGNCSTRIFHGEKLTMTNLIETVNESKGTCPDCTL 1016

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Db 969 CDEYPAFVSERTIKETGTGNACEDCSKSFVIOQIPSSNLFMYVDS--SCLCES 1021

## RESULT 3

US-09-875-423-2  
 ; Sequence 2, Application US/09875423  
 ; Patent No. US20020081657A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Curtis, Roy A. J.  
 ; TITLE OF INVENTION: 21784, A NOVEL HUMAN CALCIUM CHANNEL  
 ; FILE REFERENCE: 10448-059001  
 ; CURRENT APPLICATION NUMBER: US/09/875, 423  
 ; CURRENT FILING DATE: 2001-06-05  
 ; PRIOR APPLICATION NUMBER: US 60/209,257  
 ; PRIOR FILING DATE: 2000-06-05  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 1091  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-875-423-2

Query Match 20.3%; Score 1084; DB 10; Length 1091;

Best Local Similarity 28.5%; Pred. No. 4,2e-70;  
 Matches 306; Conservative 222; Mismatches 422; Indels 122; Gaps 39;

QY 3 AGCLIALTLTFLQSLIGPSSSEPPSAVITIKSWDKQEDVLTLATAGSNOLVDIYE 62  
 Db 14 ASALIAAL-LYALGDVVRSEQIPLSV-VKLWASAFGGEIKSIAAKYSGSOLLQKKYK 71  
 QY 63 KYODIYEPNNAQVLAIRADIEKLNSKALVSLAEKVOAHOOREFPASNEV 122  
 Db 72 EYKQVALEEDIGLQVLKLLKMEEMHKSEAVRRLEVAEENHKLHEHDAL--QY 128  
 QY 123 VYNNAK--DDLDPEKNDSEPSORIKPFIEDANFGR-OISYOHAAVHIPIDYEGSTIV 179  
 Db 129 EYFNNAVILNENDKGNFLELKEPL--LAVNDHNNLPVNISLSDVQVPTNMYNKDPAI 185  
 QY 180 LNELMTSALDEYFKKNEEDPSLIMOVFGSATGLARIYPSAPWDSNRTNKIDLYVR 239  
 Db 186 VGVYVMSSESLNKVFVNDPRDPSLIMQVSGKGFROYPGIKWEPD--NGVIAFCR 242  
 QY 240 RBPWTIOGASPKMLIIVDVGSGVSLTLKLRFSVSEMLTSLDDDFVNVASFNSAQ 299  
 Db 243 NKKWTIOATSPKDVYIIVDVSGSKGLRLITAKQTVSSIDTLGDDDFNIAVNEELH 302  
 QY 300 DVS-CFO-HLVQANVRNKKVLLKDAVNNTAKGIDYKKGFSFAEQQLINYNVSRAN--CN 355  
 Db 303 YVEPCINGTLVQADRNKHFREHLDKLFAKIGIMDIALNAEAFNLSDFNHTGCGSICS 362  
 QY 356 KILMLFTDGGERRAOEIFKRYN-KDKYRVFRFSVGOHNHENGPIOWMACEKKGYYEIP 414  
 Db 363 QAIMITDAVDYDTITFEKRYMPKRYKIFTYLLIGREAAFDNLKMAACAKKGFETQS 422  
 QY 415 SIGAIRINTOEYLDVIGRPMVLADGKAKOVNTNYLDAL-----ELG--LVITGT 463  
 Db 423 TLADVOENMEYLIHLRSKYI--DOEHVYVTEAVIISTLQAKLDDOGPVLMTTYA 480  
 QY 464 LPEVNTIGFENKTLNKLNLIGVNGVDVSLIEDIKRLPRFLCPLNGYFAIDPNGYVL 523  
 Db 481 MPVFS-----KONETRSKG--TILGVVQTDVPVKELLTKTPRYKIGHGVAFTTNGCYILT 535  
 QY 524 HPLDQ--PKNPKSOEP--VTLDLDAELENDIKVEIRKMKIDGESGEKTFRLVKSQE 578  
 Db 536 HPELRLLYEGKKRKKPNTSSVDLSEVEDRQD--LRNAAMNRKTKG--FSMEYK----- 588  
 QY 579 RYIDKGNRT-----YTWTPVNGTDVSLALVLP--VSFYIRAKLEETITQARSKKGMK 631  
 Db 589 KTYDKKRVLYVMNDYYIYDIDIKGTSPSLGVALSRGKGKYE-----RGNVT 634

QY 632 DSETLKPDNFEESGYTFLAPRDYCN-DKISDNTEFLNNEFIDRTPNPNSCANDLI 690  
 Db 635 IEQGL--HDLHPDVSLADEMSYCNMHLPEHRHLSQLEATIKLYKKEP--LLOCDKELI 691  
 QY 691 NRVLDACTTNELVQNTYS-----KKNIKGVKARFVVTDOGITRYVP----- 733  
 Db 692 QEVLFEPA-VYSAPIEAIFYWSTALNKSSENSDKGVAEFGTGRISRLILFYGAEDLIQMOD 750  
 QY 734 -KEAGENQENDEYTEDSKYKSLDN--DNVFTAPFNKSGPGAYESGIWASKAVEIYI 790  
 Db 751 FLKAGCKEIKFNADHPLMLYRRAAQIIPGSFYSLPF--SIGPVKSNVYTASTSIQOLD 808  
 QY 791 QGRLLKPAVVGIRIDVNSNIENFTITSRDPACAPVCDCKRNSDYMDCVIILDDGFLMA 850  
 Db 809 ERKSPVAVAVGIQMLKEFPQRFKFWTASROCASLDGCSISCDDEFVNCYLLIDNNGFIIVS 868  
 QY 851 NHDDYTNQGRFPGEIDPRLMRLVNIYAVANKSYDVQSCVECPGAAPRQGA-GHRSAYV 909  
 Db 869 --EDYT-QTGDFEGELEGVAMNKLTMGSFKRTTYIDYQAMCRANKESSDGAHGLDLP- 924  
 QY 910 PSVADILQIGMWTAAWMSILOQFLSLTPEPRLLEAVEMEDDFTASLSK-----QSCIT 964  
 Db 925 -----NAFLSAVKWIMTELVFLVEF--NLCSMWHSDMTAKAKQKLTQLEPCDT 971  
 QY 965 EGTQYFFDNDKSGFSGLVDCGNCRIFFHGEKLMNTYLIFIMESKGTCPCDT 1016  
 Db 972 EYPAFVSERTIKETGTGNACEDCSKSFVIOQIPSSNLFMYVDS--SCLCES 1021

## RESULT 4

US-10-005-168-2  
 ; Sequence 2, Application US/10005168  
 ; Patent No. US20020133840A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brennan, Thomas J.  
 ; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING DISRUPTIONS  
 ; FILE REFERENCE: R-10  
 ; CURRENT APPLICATION NUMBER: US/10/005,168  
 ; CURRENT FILING DATE: 2001-12-04  
 ; PRIOR APPLICATION NUMBER: US 60/299,668  
 ; PRIOR FILING DATE: 2001-06-19  
 ; PRIOR APPLICATION NUMBER: US 60/282,685  
 ; PRIOR FILING DATE: 2001-04-09  
 ; PRIOR APPLICATION NUMBER: US 60/254,802  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 223  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 ; US-10-005-168-2

Query Match 5.9%; Score 317.5; DB 12; Length 223;

Best Local Similarity 39.9%; Pred. No. 9.4e-16;  
 Matches 55; Conservative 29; Mismatches 53; Indels 1; Gaps 1;

QY 878 SVYAFNKSVDYQVCEPQAPKQAGHRSAYVPSVADILQIGMWTAAWMSILOQFLSL 937  
 Db 2 SFYTRKESYDYQACAPQPPGNLGAAPRGVVPITADFLNLAWMTSAAWMSLFOQLLYGL 61  
 QY 938 TFPRLLEAVEMEDDFTASLSKOSCIITEQYQFPDNDKSGFSGLVDCGNCRIFFHGEKLM 997  
 Db 62 TYHSWFQADPAEABG-SPTRESSCVMKQTYDYGVSANASTNAIILDCGNCRLFLAORLT 120  
 QY 998 NTNLIIFIMESKGTCPCD 1015  
 Db 121 NTNLIIFVAEKPLCSQE 138

## RESULT 5

US-09-864-761-44281

```
; Sequence 44281, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmca-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 44281
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006145.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.86
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.91
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.93
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.81
; OTHER INFORMATION: SWISSPROT HIT: P54289, EVALUATE 4.00e-25
; OTHER INFORMATION: EST_HUMAN HIT: H86016.1, EVALUATE 1.00e-02
US-09-864-761-44281

Query Match          5.1%; Score 272; DB 10; Length 51;
Best Local Similarity 100.0%; Pred. No. 2e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
RESULT 6
US-09-864-761-38267
; Sequence 38267, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aecmca-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 38267
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC008283.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.86
; OTHER INFORMATION: EST_HUMAN HIT: AL134437.1, EVALUATE 3.00e-24
; OTHER INFORMATION: SWISSPROT HIT: P54289, EVALUATE 4.00e-25
US-09-864-761-38267

Query Match          5.1%; Score 272; DB 10; Length 53;
Best Local Similarity 100.0%; Pred. No. 2.1e-13;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



```
RESULT 7
US-09-864-761-38318
; Sequence 38318, Application US/09864761
; Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aemica-x-1
CURRENT APPLICATION NUMBER: US/09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 38318
LENGTH: 35
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC008283.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.84
OTHER INFORMATION: EST_HUMAN HIT: AW051755.1, EVALUATE 1.00e-14
OTHER INFORMATION: SWISSPROT HIT: P54289, EVALUATE 2.00e-15
US-09-864-761-38318

Query Match          3.6%; Score 190; DB 10; Length 35;
Best Local Similarity 100.0%; Pred. No. 9.7e-08;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 185 WTSADEVFKKREEDPSILMQVFSATGLARYYP 219
1 WTSADEVFKKREEDPSILMQVFSATGLARYYP 35
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RESULT 8
US-09-864-761-36461
; Sequence 36461, Application US/09864761
; Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
FILE REFERENCE: Aemica-x-1
CURRENT APPLICATION NUMBER: US/09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 36461
LENGTH: 35
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC008283.2
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.67
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.7
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.8
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.6
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
OTHER INFORMATION: EST_HUMAN HIT: AW051755.1, EVALUATE 3.00e-04
OTHER INFORMATION: SWISSPROT HIT: P54290, EVALUATE 6.00e-15
US-09-864-761-36461

Query Match          3.5%; Score 185; DB 10; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 141 GSGRIKPFIEDANFGROISYOHAAVHPTDIYEG 175  
 DB 1 GSGRIKPFIEDANFGROISYOHAAVHPTDIYEG 35

RESULT 9  
 US-09-828-423-5  
 Sequence 5, Application US/09828423  
 Patent No. US20020099178A1  
 GENERAL INFORMATION:  
 APPLICANT: Hillman, Jennifer L.  
 Guejler, Karl J.  
 Patterson, Chandra  
 TITLE OF INVENTION: GROWTH-ASSOCIATED TRYPSIN-TYPE  
 INHIBITOR HEAVY CHAIN PRECURSOR  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Drive  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: Word Perfect 6.1/MS-DOS 6.2  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/828,423  
 FILING DATE: 05-Apr-2001  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/388,774  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Cerrone, Michael C  
 REGISTRATION NUMBER: 39,132  
 REFERENCE/DOCKET NUMBER: PF-0505 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-855-0555  
 TELEFAX: 650-845-4166  
 TELEX: <Unknown>  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 885 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: GENEBANK  
 CLONE: g1288563  
 SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
 US-09-828-423-5

Query Match 3.4%; Score 182; DB 10; Length 885;  
 Best Local Similarity 20.2%; Pred. No. 4.5e-05;  
 Matches 132; Conservative 107; Mismatches 243; Indels 170; Gaps 33;

QY 27 FPSAVITKSVWDMQEDLVLTAAFTAGVNOVDIYKYODLYVEPNNAKOLVEIARPI 86  
 DB 97 YPGNVKEKVAKKQYKAVASQCKTAG-----LVKASGRLL 131

QY 87 EKLISNRSKAL---VSLAEAEKVQAAHOMREDFASNEVYVYNAKDDLPEKNDSFPGSQ 143  
 DB 132 EKTETVSNVAAGSKVTFELTELLRHKGK-----YEMYLKVPK-----Q 173

QY 144 RIKPVELEDANFGROISYOHAAVHPTDIYEGSTIVLNEIWNLSALDEYFKKNNREDPGL 203  
 DB 174 LVKHFEIE-----VDLFEQGISMDAENSFTINDLL-----GSA 208

QY 204 LMQVPSAIGLARIYAFSPWVNSRT-PKKID-----LYVARRP-----WY 244

DB 209 LTKSESGKGGVSVSRPS---LDQGRSCPTCTDLSLNGDFTITYDVNNESPGNQYIVNGYF 265  
 QY 245 I-----QG-AASPKDMLLVDSGVSGLTFLKLRISVSMELEFLTDODDVPVNAFSPNSA 298  
 DB 266 VHFAPQGLPVYKPNVAFVIDISGSMAGRKLEQTKKALLILEDMKEEDYLNILFSG-- 323  
 QY 299 QDVSCF-QHLYQAVNRKKYKLDKAVNNITAKGTDYKKGFSFAFEDLLNYSR----- 351  
 DB 324 -DVSTWKEHLVQAVPENLQEARTEFVKSMEDKGMNINDGLRQISML--NKAREHRIP 379

QY 352 ANCKRIIMLEFDG---GEERAQEIFPKYKN--DKYRVRFRESVQGHNTERGFIQMAQE 405  
 DB 380 ERSISYIMLDGANGESPERKIDENVYNAIGKFPPLNLGFG--NNLNYNLENNMALE 438

QY 406 NKGYVEIPISGIRINTQETLDYLGPRVLAGDKAKQVQWTVYIDALE-----L 456  
 DB 439 NHGFARIVEDSDADLQGFEEVANPL-LTGVENEYPE--NAIIDLQNTYQHIFYDGS 495

QY 457 GLVITGLTPYENITGOPEKNTNK-----NQLLGVMGVDSLEDIKRLTPRETLCPNGY 511  
 DB 496 EIVVAGRL-VDEDMNSF--KADYKGQATNDL--TFTEVDKEMEK-----ALQERDY 544

QY 512 YFAIDPN-----GYVLHPNLQPK---NPKSQEPYTLDFLAELENDIKVEIRKMDIG 562  
 DB 545 IFG---NYIERLWAYLIEQLLEKRNNAHEEKENITARALDSLKYHHVTPPLTSKVVYK 601

QY 563 ESEGEKFRILVKSODERYI-DKGNRTYTWTPVN-GTDSIALVLPTYSYVI 612  
 DB 602 PE-----DNEDERAIADKPGEDAENATPVSPAMSYLTSQPPQNPYYV 644

RESULT 10  
 US-09-828-423-3  
 Sequence 3, Application US/09828423  
 Patent No. US20020099178A1  
 GENERAL INFORMATION:  
 APPLICANT: Hillman, Jennifer L.  
 Guejler, Karl J.  
 Patterson, Chandra  
 TITLE OF INVENTION: GROWTH-ASSOCIATED TRYPSIN-TYPE  
 INHIBITOR HEAVY CHAIN PRECURSOR  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Drive  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: Word Perfect 6.1/MS-DOS 6.2  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/828,423  
 FILING DATE: 05-Apr-2001  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/388,774  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Cerrone, Michael C  
 REGISTRATION NUMBER: 39,132  
 REFERENCE/DOCKET NUMBER: PF-0505 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-855-0555  
 TELEFAX: 650-845-4166  
 TELEX: <Unknown>  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 946 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENEBANK  
CLONE: g133985  
SEQUENCE DESCRIPTION: seq ID NO: 3  
US-09-828-423-3

Query Match 3.0%; Score 159.5; DB 10; Length 946;  
Best Local Similarity 19.9%; Pred. No. 0.0021;  
Matches 133; Conservative 107; Mismatches 258; Indels 171; Gaps 29;

33 IKSVDMKQDILVLAATAGVNOVDYIEKYODLYVEENNRKOLYEIARDIEKLIN 92  
26 LSEFVD--YEDLVEL--APGKPOLVAENRKYORSLPGESEMEAEVDYLYSYKVSQT 80  
93 RSKALVSLAEAEKVQAHOHRE-----DFASN-----EV 122  
81 ITSMATPMIQSKVNNSPQNVVFDVQIPKGAIFISFMTYDGTKFRSSIKEITYGRA 140  
123 VYNAK-----DDLDPEKNDE-----PQSORIKVFIEDANFGQISYOH----- 163  
141 LYAQRARAKGTAGLYRSSALDMENFREVNYLPQAKVQFELHYQEVKWKRLGSTEHRITL 200  
164 ----AAVHIPTDIESTIVLEINMTSALD-----EVEKKNRE-----DPSLMQVF 208  
201 QPGLAKHLEVDVAVITPQGLRFLHVDTEFGHFDGVPVLSKGGQAKHVSFKPTVAQ-- 258  
209 GSATGLARYPASPWVNSRTPNKIDLYVRRP-----WTYGAAS-----PK 252  
259 -----RIPSCSR--ETAVDGEVLVLYDVKREKAGELEVFGVYFHFAPDMIDPIPK 309  
253 DMLIVVSGSVSLTLKILFTSVSEMEETLSDDDFNVASFNADVSQFQHLVQANV 312  
310 NILVVIDVSGSMGVKMKQVYEAAMKTTILDDRADHPSVIDFNQINIR--TWKNDLFOLOK 367  
313 RKKVLDKAVANNITAKGTTDYKGF--SFAPFOLLNLYNSRANCKIIMLTG-----G 365  
368 HRLQAKYIEKIQPSGNTINELALRAIFILNEANNLGLDPPNSVSLIILVSGDPTVG 427  
366 EERAOEITFNKKNKKVAVRFVSQ-----HNERPIQOM-----ACENK 407  
428 ELKLSKIOKNVENIODNISLSLGMGFVDYDFLKLRLSNHNIQARIYENODTSSQOLK 487  
408 GYVEI--PSIGAIRIN--TOEYLDVL-----GRPVYLAG--DKAKOVQWNTNYLD 452  
488 KFYNOVSTPLLRNVQFNPHSTVDYTONNHNHNFSGSEIYVAKFKDPK-----LD 539  
453 ALEGLVITGLPVFNITQFENKTNLKNOLILGVMGVDSLEDI---KRLTFRFTLCP 508  
540 QIE--SVITA-----TSANTQLVLETLAQMDILOPFLSKDKHADDFTR-K 582  
509 NGYTAIDPNNGVLLHPULOQRNRSQSPVYLDLDALENDIKVEIKKKKIDDESSEKXT 568  
583 LMAVYLTIN--QLAERSLAP--TAAAKRRITRSIIQMSLDHHTVPLTSLVIEENAGDER 638  
569 FRTLVSOD 577  
639 MLADAPPOD 647

RESULT 11  
US-09-815-242-5898  
Sequence 5898, Application US/09815242  
Patent No. US20020061569A1  
GENERAL INFORMATION:  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Karl L.  
APPLICANT: Zyskind, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.  
APPLICANT: Xu, H. Howard  
TITLE OF INVENTION: Identification of Essential Genes in  
TITLE OF INVENTION: Prokaryotes  
FILE REFERENCE: ELITRA 011A  
CURRENT APPLICATION NUMBER: US/09/815,242  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
NUMBER OF SEQ ID NOS: 14110  
SOFTWARE: FastSeq for Windows version 4.0  
SEQ ID NO: 5898  
LENGTH: 1349  
TYPE: PR1  
ORGANISM: Staphylococcus aureus  
US-09-815-242-5898

Query Match 2.8%; Score 151; DB 10; Length 1349;  
Best Local Similarity 19.4%; Pred. No. 0.015;  
Matches 199; Conservative 121; Mismatches 339; Indels 366; Gaps 48;

16 SLILGSPSEPPPSAVTIKSWDKMOEDLVYLAATKAGVNO--LVDIYEKYODLYTVEP 72  
40 TLIFGLNQAKKAESTNKE-----LNERTTASDNQSSDKYDMQQLNGEDNKTMD 90  
73 NNAQOLVEIARDIEKILSNRSALVSLAEKVQAHOHREDFASNEVYTNKADLD 132  
91 NOK-----EMVSSQGNFTTSNGK-----LIEKESVOST--GNKVEVSTAKSD-- 132  
133 PEKNDSEPPSQRIKPIVEIEDANFGROISYQHAHVHPTDIESTIV----- 179  
133 ---EQASPSTN-----EDLNTKQITISNOEA--LQPDLOEKSVYNNVQPTNEKKYD 180  
180 -----LN-----ELNMTSALDEVEFKKREDDPSLW-----OVFSATGLARYPA 220  
181 AKTESTTLNKKSAKISNDETLVDNNSNENNADIIIPKSTAPKRLNTRMRIAIVOPS 240  
221 SPWYDN-----SRTPKIDLYVRRRPWYITQGAAPKMLILVYSGVSGLTLLKILFT 274  
241 STEAKVNDLITSTNTLLTVADADKNKRIYPAQDYLISLSQITVDDKVGSGDYFTIKY-- 297  
275 SVSEMLETISDDPVNVASFN--SNAODVSCFOHLVQANRNKVKLDAVNNTAKGTTD 332  
298 SDYQVYGLNPEDKIKNGIDIKDPNNGETIATAH-----DTANNLITTFPD 344  
333 YKKGSPAFBOLLNLYN-----SRANC-----NK 356  
345 YVDRFN--SVQGINYSIYMDADTIPVSKNDVEFNVTIGNTTTRKTANIQYPDVYNEKNS 403  
357 IIMFTD-----GGEER-----AQEIF-----KNYNDKKVYFRRS-----VGOHNYERG 397  
404 IGSAFTETVSHVKNKKNPGYKQITIVNPSNLSLTKLKVQAVHSSYPNNIQQIINDYV 463  
398 PLOWMAGE-----NKGYEIEPSIGAIRINTOEYLDVLAGRPM--VLAGDKAKOV----- 444  
464 DIKITVYPKGYTLNKGY-----DVMTKELTDVTNQYLQKITVYGDNNSAVIDPGNA 513  
445 -----QMTN----- 448  
514 DSAYVVMVNTKFOYTENSESPTYVQMATLSSTGNKSVSTGNALGFTNNQSGAGOEYKIG 573

QY 449 ---VYLDALGLVITGLTFVFNIT--GOFENKTNLKNQILGVMGVADVSLIEDIKRLTPRT 505  
 Db 574 NTWETNTNNGVOELGEGKGVGNVTVTFEDNNTNTR-----VGEAVTKEDGSYLIPNL- 625  
 QY 506 LCPNGY---FAIDPNGVYLLHPNLQPKPK-----SQEPVTLDFLDALENDIKVEIRN 557  
 Db 626 --PNDGYRVEFENLPRKGYEVT--PSKQGNNEELDSGLSVITVNGKD--NLSADLGIYKPK 681  
 QY 558 KVIDEGSEKTFRTLVKSODERYIDKGNRTYTPVNGTDSLALVLPYTFYIKAKLE 617  
 Db 682 YMLCDYVWEDTNKNGIODEDEKGI--SGVTYTLKDENG-----DYL 720  
 QY 618 ETTIQAARSKGKMKDSETLKPDNEESGYTFIAPRDYCNDLKISDNNTEFLINNEFLDR 677  
 Db 721 KVTITDADGKYFTD--LHNGNYK--VEFTTPEGYPTTVTSGSDIE----- 763  
 QY 678 KTPNPNSCNADLIN--RYLDDAGFTN---ELVQNYW-----SKQNIKGY--- 717  
 Db 764 -KDSNGLTTTGVINGADNMVTLDSGFYKTPKYNLGNVWEDTNKDKGKODSTKGISGYTVT 822  
 QY 718 -----KARFVYTDGITRV-----YPKAGENMOE----- 742  
 Db 823 LKNEGEVLQTTKTDKDKQYQFTGLENGTYVEEFTPSGYPTQVSGTDEGIDSNGTST 882  
 QY 743 -----NPEYEDSFYKRSIDNDNYVFTAPYFNKSGGAYE-----SGIMSKAVEIYIQ 791  
 Db 883 TGVIKDKNDNTIDSGFYKPTYNLGDYWEDE--NKNGVQDKDEKGISGVYTLKDE---N 937  
 QY 792 GKLLK 796  
 Db 938 DKVLK 942

## RESULT 12

US-09-815-242-13137  
 Sequence 13137, Application US/09815242  
 Patent NO. US20020061569A1  
 GENERAL INFORMATION:  
 APPLICANT: Haselbeck, Robert  
 APPLICANT: Ohlsen, Karl L.  
 APPLICANT: Zyskind, Judith W.  
 APPLICANT: Wall, Daniel  
 APPLICANT: Trawick, John D.  
 APPLICANT: Carr, Grant J.  
 APPLICANT: Yamamoto, Robert T.  
 APPLICANT: Xu, H. Howard  
 TITLE OF INVENTION: Identification of Essential Genes in  
 TITLE OF INVENTION: Prokaryotes  
 FILE REFERENCE: ELITRA.011A  
 CURRENT APPLICATION NUMBER: US/09/815,242  
 CURRENT FILING DATE: 2001-03-21  
 PRIOR APPLICATION NUMBER: 60/191,078  
 PRIOR FILING DATE: 2000-03-21  
 PRIOR APPLICATION NUMBER: 60/206,848  
 PRIOR FILING DATE: 2000-05-23  
 PRIOR APPLICATION NUMBER: 60/207,727  
 PRIOR FILING DATE: 2000-05-26  
 PRIOR APPLICATION NUMBER: 60/242,578  
 PRIOR FILING DATE: 2000-10-23  
 PRIOR APPLICATION NUMBER: 60/253,625  
 PRIOR FILING DATE: 2000-11-27  
 PRIOR APPLICATION NUMBER: 60/257,931  
 PRIOR FILING DATE: 2000-12-22  
 PRIOR APPLICATION NUMBER: 60/269,308  
 PRIOR FILING DATE: 2001-02-16  
 NUMBER OF SEQ ID NOS: 14110  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 13137  
 LENGTH: 1349  
 TYPE: PRF  
 ORGANISM: Staphylococcus aureus  
 US-09-815-242-13137

Query Match 2.8%; Score 151; DB 10; Length 1349;  
 Best Local Similarity 19.4%; Pred. No. 0.015;  
 Matches 199; Conservative 121; Mismatches 339; Indels 366; Gaps 48;  
 QY 16 SLIGPSSEEPFSAVTKISWVDMQEDLVTLAKTAGSVNQ---LVDIYKRYODLTVE 72  
 Db 40 TLIFGLNQEAKAEKSTNKE-----LNFAVTSASDQSSDKYDMQMLNEDNTKND 90  
 QY 73 NNAQVLEIARDEKLKSRKALVSLAEAEKVOAAGHWRDEFAANEVYVNAKDD 132  
 Db 91 NQK---EMVSSQENETTSNGK---LIEKESVST---IGNKVEYSTAKSD- 132  
 QY 133 PEKNDSEPGSORIKPVIFEDANFGROISYQAAVHLPDIIEGSTYV----- 179  
 Db 133 ---EQASPKSTN---EDLNTKQITISNOEA---LQPDQENKSVYVNOPTNEENKVD 180  
 QY 180 -----LN-----ELNMTSALDEYFKKREDEPSILW-----QVFSGATGLARYPA 220  
 Db 181 AKTESITLANKSDAIKSNDETLVDNNSNSNENNAIDILPKSTAPKRLMTRRIAAVOPS 240  
 QY 221 SPWVDN-----SRTPNKIDLYVRRRPWTIGCAAPSKMLILVDVSGSGITLKIT 274  
 Db 241 STAKVNVNDLITNTLLTVVADAKNKKIVPADYLSLKQITVDKVKSGDYFTIKY--- 297  
 QY 275 SVSEMLETLDSDDFVWVASEN--SNAQVSCFOHLVQAVNRKKVLLKDAVNNITAKG 332  
 Db 298 SDTVQYVGLNPEDIKNGIDKDPNNGETIATAKH-----DTANMLITYTFD 344  
 QY 333 YKGFSAFEQLLNVV-----SRANC-----NK 356  
 Db 345 YDRFN-SVQMGINSIYADADTIPYKNDVFNNTIGNTTKTANIQPDYVNEKNS 403  
 QY 357 IIMFTD-----GGEER-----AOEIP-----NKYKOKKVVAFRES-----VGQINTEBG 397  
 Db 404 IGSAFTETYSHGKNKKNPQYKQITIVNPSSENSLNAAKIKVQVHSSPPNNQINKDYT 463  
 QY 398 PIQWMAE-----NKGYEIPISGAIRINTQYLDVGRPM--VLADGKAKOV----- 444  
 Db 464 DIKITOVPRGYTLNKGY-----DVNTKELDYVNOYQKTTYDDNNSAVIDFGNA 513  
 QY 445 -----OMTN----- 448  
 Db 514 DSAIVYVMTKFOYTNSESPTLVQMATLSSGKNSVSTGMALGFTNNOSGAGQEVYKIG 573  
 QY 449 ---VYLDALGLVITGLTFVFNIT--GOFENKTNLKNQILGVMGVADVSLIEDIKRLTPRT 505  
 Db 574 NTWETNTNNGVOELGEGKGVGNVTVTFEDNNTNTR-----VGEAVTKEDGSYLIPNL- 625  
 QY 506 LCPNGY---FAIDPNGVYLLHPNLQPKPK-----SQEPVTLDFLDALENDIKVEIRN 557  
 Db 626 --PNDGYRVEFENLPRKGYEVT--PSKQGNNEELDSGLSVITVNGKD--NLSADLGIYKPK 681  
 QY 558 KVIDEGSEKTFRTLVKSODERYIDKGNRTYTPVNGTDSLALVLPYTFYIKAKLE 617  
 Db 682 YMLCDYVWEDTNKNGIODEDEKGI--SGVTYTLKDENG-----DYL 720  
 QY 618 ETTIQAARSKGKMKDSETLKPDNEESGYTFIAPRDYCNDLKISDNNTEFLINNEFLDR 677  
 Db 721 KVTITDADGKYFTD--LHNGNYK--VEFTTPEGYPTTVTSGSDIE----- 763  
 QY 678 KTPNPNSCNADLIN--RYLDDAGFTN---ELVQNYW-----SKQNIKGY--- 717  
 Db 764 -KDSNGLTTTGVINGADNMVTLDSGFYKTPKYNLGNVWEDTNKDKGKODSTKGISGYTVT 822  
 QY 718 -----KARFVYTDGITRV-----YPKAGENMOE----- 742  
 Db 823 LKNEGEVLQTTKTDKDKQYQFTGLENGTYVEEFTPSGYPTQVSGTDEGIDSNGTST 882  
 QY 743 -----NPEYEDSFYKRSIDNDNYVFTAPYFNKSGGAYE-----SGIMSKAVEIYIQ 791  
 Db 883 TGVIKDKNDNTIDSGFYKPTYNLGDYWEDE--NKNGVQDKDEKGISGVYTLKDE---N 937  
 QY 792 GKLLK 796

DB 938 DKVLR 942

## RESULT 13

US-09-850-351A-6

Sequence 6, Application US/09850351A

Patent No. US20020100080A1

## GENERAL INFORMATION:

APPLICANT: Feltelson, Jerald S.

Schnepf, H. Ernest

Narva, Kenneth E.

Stockhoff, Brian A.

Schmeits, James

Loewer, David

Dullum, Charles Joseph

Muller-Cohn, Judy

Stamp, Lisa

Morrill, George

TITLE OF INVENTION: No. US20020100080A1el Pesticidal Toxins and Nucleotide

Sequences Which Encode These Toxins

NUMBER OF SEQUENCES: 144

CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik, Lloyd &amp; Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: FL

COUNTRY: US

ZIP: 32606-6669

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/850,351A

FILING DATE: 07-May-2001

CLASSIFICATION: &lt;Unknown&gt;

PRIORITY INFORMATION:

APPLICATION NUMBER: US 09/073,898

FILING DATE: 06-May-1998

APPLICATION NUMBER: US 08/960,780

FILING DATE: 30-Oct-1997

APPLICATION NUMBER: US 60/029,848

FILING DATE: 30-Oct-1996

ATTORNEY/AGENT INFORMATION:

NAME: Sanders, Jay M.

REGISTRATION NUMBER: 39,355

REFERENCE/DOCKET NUMBER: MA-708CD1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 352-375-8100

TELEFAX: 352-372-5800

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 789 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: 81F

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-850-351A-6

Query Match

Best Local Similarity 20.1%; Pred. No. 0.0072;

Matches 138; Conservative 100; Mismatches 235; Indels 213; Gaps 34;

QY 231 NKIDYVRRPWYIOGAASPKMLILYVSGSVGLTKLIRTSVSEMLETSLDD-DFV 289

DB 105 NKIDALNTMLRYVL-----PKITSLMSDVKNOMYALSLQI- EYLSKOLQEIISDKLDIT 156

QY 290 NV-ASFNNAQDVS-----CFQHLVQANVRNKKVYLKDA-----VNNIT-----A 327

DB 157 NVNVLINSLTETTPAYQRIKYVNEKFEELTPATETSSKVKKDSPADIDELTELTELA 216

QY 328 KGITDKKGSFAFEQLN--YNSRANCKIIMFTDGEERAOEIPNKKKKRVF 385

DB 217 KSVT---KNDVDFEFLYLTFFHVMGN-----NIFGSALKTASELTITKN-----VKT 264

QY 386 RFSVGHNYERKPIOMWACENKGYEIPISGIRINTOEYLDVGRPMVLADKANQVO 445

DB 265 GSEVG--NVYNFLIVLALQAKAFILTTCKRLGLADIYTSINHEHL-----NKEKEEF 318

QY 446 WTVNYDALDELGLVITGTLPLVFNITQGFENKTNK-----QLL-----GYMGVDSL 494

DB 319 RVNI-----LPTLSNFTSNPNYAKVGSDEDAKMIYEAAPGHALVGEFELS 364

QY 495 EDI-----KRLTPRF-----TLCPNG-----YTF--AIDPNGVLLH 524

DB 365 DSTIVLKVYFAKLKQNYQVNDKDSLEVIYGDMDKLCPQSQIYITNNIYVPPNYVTK 424

QY 525 PNLOPKNPKSQEYVTLDFLDALENDIKVEIRNKMIDGESGKTRTLVKSQDERYIDKG 584

DB 425 IDFTKKKKTLYEYTAIFYDSSTG---EIDLNKKV--ESSEAEYRTLSANDGVYMLG 479

QY 585 NKRTTW--TPYNG---TDVSLVLPYSPRYIKAKLEETIQOASKKGKMDSEFLKP- 638

DB 480 VISFTPLTPINGGLADENSRLITLCKSYLRELLATDLS-----KETLIYPP 531

QY 639 ---DNFESGYTFIAPRDYCNLKDLSNNT---FLNNEFTIDRKTNPNSCNADLNR 692

DB 532 SGFIKNIVENG-----SIEDNLBPWKANNNEVYD----- 563

QY 693 VLDAGFTNELVONYSKQKINIGVAKARFYVTDGTL---RVYRK----- 734

DB 564 ---TGCVNGTAKLYVHKDGIISQFGLDKLKTETVYIQYVYKGP 605

QY 735 ---EAG---ENMOENPETEYEDSFYKRSIDNNYVYTFAPYFKSPGAYESGIWVS 783

DB 606 SIHLKDENTGYIHEDINNNLEDYQITTKRFTGTDLKGVYLLKQNDDEAMGDVFI- 664

QY 784 KAVEIYIOGKLLKPAVYGIKIDVNSW 809

DB 665 --LEISPEKLLSPEL---INTNNW 684

RESULT 14

US-09-850-351A-4

Sequence 4, Application US/09850351A

Patent No. US20020100080A1

## GENERAL INFORMATION:

APPLICANT: Feltelson, Jerald S.

Schnepf, H. Ernest

Narva, Kenneth E.

Stockhoff, Brian A.

Schmeits, James

Loewer, David

Dullum, Charles Joseph

Muller-Cohn, Judy

Stamp, Lisa

Morrill, George

TITLE OF INVENTION: No. US20020100080A1el Pesticidal Toxins and Nucleotide

Sequences Which Encode These Toxins

NUMBER OF SEQUENCES: 144

CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik, Lloyd &amp; Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: FL

COUNTRY: US

ZIP: 32606-6669

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS



Matches 137; Conservative 99; Mismatches 233; Indels 221; Gaps 34;

```
QY 231 NKIDLYDVRRRPMYIQGAASPKDMLIVDVGSGVLTGLKIRTSVSEMLETSLDD-DEV 289
Db 105 NKLDALNTMLKVL-----PKITSMLSDVAKQNYALSLQI--EYLSKQLOEISDKLDII 156
QY 290 NV-ASFNSNADVS-----CFQHLVQAVRKKVKLKDA-----VNNIT-----A 327
Db 157 NVNVLINSTLLEITPAORIKYVNEKEFELTFATESSKVKKDGSPADILDELTELTA 216
QY 328 KGITDYKKGSEFAEQLIN--YVNSRANCKIIMLFTDGEERAQEIENKYNKDKKRVF 385
Db 217 KSVT---KNDVDGEFFYLNTFHDVMGN-----NLFRSALKTASELITKEN-----VKTIS 264
QY 386 RFSYGQHNTERGP IQMACEKGGYIEIPSIGAIRINTQEIYLDVYLGKRPVYLAGDKAKQV 445
Db 265 GSEVG--NVYNELIVLALQAKAFLLTTCCKRLGLADIDYTSIMNEHL-----NKEKEEF 318
QY 446 WTNVYLDALDELGLVITGLTFPNTGQFENKTNLKN-----OLIT-----GYMGVDVSL 494
Db 319 RVNI-----LPTLSNTEFSPNAYAKVKGSDADAKMIVEAKPGHALIGFEISN 364
QY 495 EDI-----KRLPRF-----TLCPNG-----YYP--AIDPNGVVLH 524
Db 365 DSITVLKVEAKLKQNYQVDSLSSEVIYGDMDKLCPPQSEQIYYTNNIVFPNEVYITK 424
QY 525 PNLQPKPKSOEPTLDFLDAELENDIKVIRNKMIDGESGEKTFRTLVKSQDERYIDKG 584
Db 425 IDFTKKMKTLRYETANFYDSSTG--EIDLNRKV--ESSEAEYRFLSANDGVYMPILG 479
QY 585 NRTYTW--TPVNG---TDYSLAVLPTSFYIYAKLEETITQARSKKGMKDSITLKP- 638
Db 480 VISFTFLTPINGFGLOADENSRLITLCKSYLRELLLATDLSN-----KETKLIVPP 531
QY 639 ---DNFESGYPIAPRDYCNLDKISDNTE--FLINFEPIIDRKTNNPNSCNADLINR 692
Db 532 SGFISNIVENG-----SIEDNLEPMKANNNKNAVYDH-----563
QY 693 VLLDAGFTNELYQNYMSKOKINIGVAKAFVYVTGGITRVPYKRAGENWQENPETY----- 747
Db 564 -----TGGVNGTKALYVHKDGLISQF---IGDKLRKPTXYVIOYTV 601
QY 748 -----EDSFYKRSLDNDNYVFTAPYFNK-----SGPGAYESG 779
Db 602 KGRPSIHLKDENTGYLHYEDTNNNLEDYQTIINKRFTTGIDLKGVYLLLSQNGDEAMGDN 661
QY 780 IAVSKAVEIYIGKLLKPAVVGIIKIDVNSW 809
Db 662 FII--LEISPSEKLSPEL---INTNNW 684
```

Search completed: February 10, 2003, 14:49:08  
Job time : 12.5273 secs





GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 10, 2003, 14:13:50 : Search time 9.80734 Seconds  
(without alignments)  
4520.920 Million cell updates/sec

Title: US-10-090-827-9

Perfect score: 5650  
Sequence: 1 MAGGLLTLTLFQSLILG.....NNALEDYDGGVSHHHHH 1069

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5532	97.9	1091	CIC2_HUMAN	P54289 homo sapien
2	5420	95.9	1091	CIC2_RAT	P54280 rattus norv
3	5405.5	95.7	1106	CIC2_RABIT	P13806 oryctolagus
4	754	13.3	1205	YLJ9_CAEEL	P34372 caenorhabdi
5	611	10.8	734	UN36_CAEEL	P34374 caenorhabdi
6	196.5	3.5	886	ITTH3_MOUSE	061704 mus musculu
7	185	3.3	885	ITTH3_HUMAN	006033 homo sapien
8	183.5	3.2	887	ITTH3_RAT	063416 rattus norv
9	168.5	3.0	575	YFBK_ECOLI	P76481 escherichia
10	166	2.9	886	ITTH3_MESAU	P97280 mesocricetu
11	162	2.9	1829	DPOL_THRST	O33845 thermococcu
12	160.5	2.8	420	Y103_SYNY3	O55874 synechocyst
13	155.5	2.8	946	ITTH2_HUMAN	P19823 homo sapien
14	155	2.7	1956	ATFX_PLAFA	O04956 plasmodium
15	153	2.7	946	ITTH2_MESAU	P97279 mesocricetu
16	149.5	2.6	634	WPCB_BACSU	P54576 bacillus su
17	149.5	2.6	921	ITTH4_PIG	P79283 sus scrofa
18	147	2.6	1087	YXNX_CLODM	P38535 clostridium
19	144.5	2.6	929	CALC_NOVI	O91145 notophthalp
20	144	2.5	930	ITTH4_HUMAN	O14654 h interalp
21	143.5	2.5	935	ITTH2_PIG	O02668 sus scrofa
22	142	2.5	964	DPOL_CBEPU	P20339 choristoneu
23	142	2.5	3063	CALC_HUMAN	O99775 homo sapien
24	141.5	2.5	946	ITTH2_MOUSE	O61703 mus musculu
25	141	2.5	1290	BXCI_CLOBO	P18640 clostridium
26	140.5	2.5	764	PAG_BACAN	P13423 bacillus an
27	140	2.5	1180	CAAA_BACTI	P16480 bacillus th
28	138.5	2.5	382	YLJ0_CAEEL	P34373 caenorhabdi
29	137.5	2.4	862	WOTS_BORBU	O51737 borrelia bu
30	137	2.4	3305	ADLP_MANSE	O25490 manduca sex
31	136	2.4	305	YB9C_SCHPO	O13773 schistosach
32	134	2.4	1251	RB2P_PLAIV	O00799 plasmodium
33	133	2.4	1169	SMC_METUA	O59037 methanococc

34	132	2.3	984	HYSA_STRAG	O53591 streptococc
35	132	2.3	1875	MLP1_YEAST	O02455 saccharomyc
36	131.5	2.3	1487	BLM_DROME	O9vg18 drosophila
37	131.5	2.3	3712	LMA_DROME	O00174 drosophila
38	131	2.3	1513	STUL_YEAST	P38198 saccharomyc
39	131	2.3	2710	TOXA_CLODI	P16154 clostridium
40	131	2.3	3119	CALC_MOUSE	O60847 mus musculu
41	130.5	2.3	1323	ADRI_YEAST	P07248 saccharomyc
42	129.5	2.3	1254	UBPC_YEAST	P39538 saccharomyc
43	128.5	2.3	547	SYM_BUCAL	P57210 buchnera ap
44	128	2.3	1658	YV67_YEAST	O03661 saccharomyc
45	127.5	2.3	1176	SLAP_BACSH	P38537 bacillus sp

## ALIGNMENTS

RESULT 1  
ID CIC2\_HUMAN STANDARD: PRT: 1091 AA.  
AC P54289;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta  
DE subunits precursor.  
GN CACNA2D1 OR CACNA2A OR CCHL2A.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
ON NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92110010; PubMed=1309651;  
RA Williams M.E., Feldman D.H., McCue A.F., Brenner R.,  
RA Velicelahi G., Ellis S.B., Harpold M.M.;  
RT "Structure and functional expression of alpha 1, alpha 2, and beta  
RT subunits of a novel human neuronal calcium channel subtype.";  
RL Neuron 8:71-84(1992).  
CC -1- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN  
CC -1- EXCITATION-CONTRACTION COUPLING.  
CC -1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:  
CC ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS  
CC HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- TISSUE SPECIFICITY: CENTRAL NERVOUS SYSTEM, SKELETAL MUSCLE AND  
CC AORTA TISSUES.  
CC -1- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM  
CC A PRECURSOR FORM (BY SIMILARITY).  
CC -1- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.  
CC -1- SIMILARITY: CONTAINS 1 WMFA DOMAIN.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL: M76559; AAA51903.1; -  
CC GenBank: HGNC:1399; CACNA2D1.  
CC MIM: 114204; -  
CC InterPro: IPR004010; Cache.  
CC InterPro: IPR002035; WMFA\_A.  
CC Pfam: PF00092; vwa; 1.  
CC Pfam: PF02743; Cache; 1.  
CC SMART: SM00327; vwa; 1.  
CC POSITIVE: PS50234; WMFA; 1.  
CC Ionic channel, Transmembrane, Ion transport, Voltage-gated channel;  
CC Calcium channel; Glycoprotein; Phosphorylation; Signal.  
FT SIGNAL 1 24  
FT CHAIN 25 944 L-TYPE CALCIUM CHANNEL ALPHA-2 SUBUNIT

Query Match	Score 5532;	DB 1;	Length 1091;
Best Local Similarity	98.7%;	Pred. NO. 0;	
Matches 1049;	Conservative	6;	Mismatches 8;
			Indels 0;
			Gaps 0;

QY	1	MAAGLALTLTLFOSLILIGSSOEPPPSAVTIKSWMDKMOEDVTLTAKTAGVNOQVLDI	60
Db	1	MAAGLALTLTLFOSLILIGSSOEPPPSAVTIKSWMDKMOEDVTLTAKTAGVNOQVLDI	60
QY	61	YKYODLTVBPNNARQVETIARQIEKLSRSRSLVRLALEAKVOAAHQRDEFPASN	120
Db	61	YKYODLTVBPNNARQVETIARQIEKLSRSRSLVRLALEAKVOAAHQRDEFPASN	120
QY	121	EYVYYNADDDLPKENDSEPGSQRIKPYFIDDANFGROIYQHAANHITPTDIEGSTITVL	180
Db	121	EYVYYNADDDLPKENDSEPGSQRIKPYFIEDANFGROIYQHAANHITPTDIEGSTITVL	180
QY	181	NELMWTSAIDVEFKNNREDEPSLIMQVGSATGLARRYPASWYNQNSTPKNTIDLXYDVR	240
Db	181	NELMWTSAIDVEFKNNREDEPSLIMQVGSATGLARRYPASWYNQNSTPKNTIDLXYDVR	240
QY	241	RPWTIOGAASPKMDLIVDVGSVSGTLTKLIRTSVSEMLETLSDDDVNVNASEFNSNAD	300
Db	241	RPWTIOGAASPKMDLIVDVGSVSGTLTKLIRTSVSEMLETLSDDDVNVNASEFNSNAD	300
QY	301	VSCFOHLYQVAWVRNKKVLKDAVNNITLKGIDYDKGSEFAEQOLLNVNVSANCKITML	360
Db	301	VSCFOHLYQVAWVRNKKVLKDAVNNITLKGIDYDKGSEFAEQOLLNVNVSANCKITML	360
QY	361	FTDGEERAOEIFAKYNNKDKKVRVFESVGOHNYDRGPIQMACENKGYEIEFISIGAIR	420
Db	361	FTDGEERAOEIFAKYNNKDKKVRVFESVGOHNYDRGPIQMACENKGYEIEFISIGAIR	420
QY	421	INNOEYLDVGRPRVYLAGDKAKOQWNNYIDLAELELVITGTLPVENITQONENKTNLK	480
Db	421	INNOEYLDVGRPRVYLAGDKAKOQWNNYIDLAELELVITGTLPVENITQONENKTNLK	480
QY	481	NOLILGAVDVSLDEIKRLTPRETLCPNGYFEAIDENGVIYLHPNLOPKNPKSOEPPVL	540
Db	481	NOLILGAVDVSLDEIKRLTPRETLCPNGYFEAIDENGVIYLHPNLOPKNPKSOEPPVL	540
QY	541	DEIDAELENDIKVEIRKMKMIDGSGEETPRTLYKSODERYIDKCNRTYWTVPVNGTDSL	600
Db	541	DEIDAELENDIKVEIRKMKMIDGSGEETPRTLYKSODERYIDKCNRTYWTVPVNGTDSL	600
QY	601	ALVLPYTSFYIKAEIETITTOARSKKGGKKDSETLKPDNFESGTYFIAPROYCNDLKI	660
Db	601	ALVLPYTSFYIKAEIETITTOARSKKGGKKDSETLKPDNFESGTYFIAPROYCNDLKI	660

QY	1021 QAEQTSDBGPDPCDMVKQPRYRKGPVCFDNNAL	EDYTDGGYS	1063
	:		
Db	1021 QAEQTSDBGPNPCDMVKQPRYRKGPVCFDNNV	LEDYTDGGYS	1063

	CICG_RESULT_2		
	CICG_RAT		
ID	CICG2_RAT	STANDARD:	PRT: 1091 AA.
AC	PS4250;		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta subunits precursor.		
DE	SUBUNIT PRECURSOR.		
GN	CACNA2D1 OR CACNL2A OR CCHL2A.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxId=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=92228762; PubMed=1314383;		
RA	Kim H.L., Kim H., Lee P., King R.G., Chin H.;		
RT	"Rat brain expresses an alternatively spliced form of the		
RT	dihydropyridine-sensitive L-type calcium channel alpha 2 subunit."		
RL	Proc. Natl. Acad. Sci. U.S.A. 89:3251-3255(1992).		
CC	- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN EXCITATION-CONTRACTION COUPLING.		
CC	- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS: ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS HEREKODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).		
CC	- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE SPLICING.		
CC	- 1-PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM A PRECURSOR FORM (BY SIMILARITY).		
CC	- 1-SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.		
CC	- 1-SIMILARITY: CONTAINS 1 WWFA DOMAIN.		
CC	-----		
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CC	EMBL; M86621; AAA41088.1; -		

DR InterPro: IPR004010; Cache-  
 DR InterPro: IPR002035; vwf\_A.  
 DR Pfam: PF00092; vwf: 1.  
 DR Pfam: PF02743; Cache: 1.  
 DR SMART: SM00327; vwf: 1.  
 DR PROSITE: PS00334; vwfA: 1.  
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;  
 KW Calcium channel; Glycoprotein; Phosphorylation; Signal;  
 KW Alternative splicing.  
 FT SIGNAL 1 24  
 FT CHAIN 25 944  
 FT CHAIN 945 1091  
 FT TRANSMEM 445 468  
 FT TRANSMEM 906 930  
 FT TRANSMEM 1067 1086  
 FT DOMAIN 252 429  
 FT CARBOHYD 136 136  
 FT CARBOHYD 184 184  
 FT CARBOHYD 323 323  
 FT CARBOHYD 347 347  
 FT CARBOHYD 474 474  
 FT CARBOHYD 584 584  
 FT CARBOHYD 593 593  
 FT CARBOHYD 663 663  
 FT CARBOHYD 769 769  
 FT CARBOHYD 812 812  
 FT CARBOHYD 876 876  
 FT CARBOHYD 983 983  
 FT CARBOHYD 973 973  
 FT CARBOHYD 986 986  
 FT MOD\_RES 500 500  
 FT MOD\_RES 833 833  
 FT SOURCE 1091 AA; 123822 MW; 705490709D343B34 CMC64;  
 Query Match 95.9%; Score 5420; DB 1; Length 1091;  
 Best Local Similarity 96.2%; Pred. No. 1.3e-315;  
 Matches 1024; Conservative 23; Mismatches 15; Indels 2; Gaps 2;

QY 481 NOLLGVGVDSVLEIDIKRLTPRTLCPPNGYFFAIDPNGVYLLHPNLQPKNPSQSEPVTL 540  
 DB 480 NOLLGVGVDSVLEIDIKRLTPRTLCPPNGYFFAIDPNGVYLLHPNLQPKNPSQSEPVTL 539  
 QY 541 DELAELNDIKVETRNKMDIGESGKTEFTLVSOBERYIDKNGRTYTTPVNGTDS- 539  
 DB 540 DELAELNDIKVETRNKMDIGESGKTEFTLVSOBERYIDKNGRTYTTPVNGTDS- 539  
 QY 600 LALVLPYSFYIRAKIEETITQARSKKKKKKDESEITKPDNEESGYTFIAPRDYCNLDK 659  
 DB 600 LALVLPYSFYIRAKIEETITQARSKKKKKKDESEITKPDNEESGYTFIAPRDYCNLDK 659  
 QY 660 ISDNTEFLNPNETIDKTPNNSCNTDLNRLVLAAGFNNELVONWMSKOKNIKGYKA 719  
 DB 660 PSDNTEFLNPNETIDKTPNNSCNTDLNRLVLAAGFNNELVONWMSKOKNIKGYKA 719  
 QY 720 RRVVTDGCTIRYPRKAEENNOENPEYEDSFYKSLDNDYVETAPYFNKSGAVESG 779  
 DB 720 RRVVTDGCTIRYPRKAEENNOENPEYEDSFYKSLDNDYVETAPYFNKSGAVESG 779  
 QY 780 IMVSRVETIYIGKLLKPAVVGIKIDVNSWLENFTKISRPPCAGPVCDCKRNSDMDCV 839  
 DB 780 IMVSRVETIYIGKLLKPAVVGIKIDVNSWLENFTKISRPPCAGPVCDCKRNSDMDCV 839  
 QY 840 ILDDGFFLMAHDDYTNOIGRFGFIDPSLRHLVNSVYAFNKSXYDQYCEFGAAR 899  
 DB 840 ILDDGFFLMAHDDYTNOIGRFGFIDPSLRHLVNSVYAFNKSXYDQYCEFGAAR 899  
 QY 900 OGAGHSVAVPSIADILHGMWATAAASIILOFLISTFPRLLEAVEMEDDTASISK 959  
 DB 900 OGAGHSVAVPSIADILHGMWATAAASIILOFLISTFPRLLEAVEMEDDTASISK 959  
 QY 960 OSCITQOTQYFPDNDKSSSYLDGCGNCRIFHYKIMNTNLIFFIMVSKGCPDFTLL 1019  
 DB 960 OSCITQOTQYFPDNDKSSSYLDGCGNCRIFHYKIMNTNLIFFIMVSKGCPDFTLL 1019  
 QY 1020 IOAETSDPDDPCDMYKQPRYKGPVPCFNNALIEDYTDGCGVS 1063  
 DB 1020 IOAETSDPDDPCDMYKQPRYKGPVPCFNNALIEDYTDGCGVS 1063

RESULT 3  
 C1C2.RABIT  
 ID C1C2.RABIT STANDARD; PRT; 1106 AA.  
 AC P13806;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Dihydropyridine-sensitive I-type, calcium channel alpha-2/delta  
 DE subunits precursor.  
 GN CACNA2D1 OR CACNA2A OR CCHL2A.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OC NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=8836904; PubMed=2458626;  
 RA Ellis S.B., Williams M.E., Mays N.R., Brenner R., Sharp A.H.,  
 RA Leung A.T., Campbell K.P., McKenna E., Koch W.J., Hui A.,  
 RA Schwartz A., Harpold M.W.;  
 RT "Sequence and expression of mRNAs encoding the alpha 1 and alpha 2  
 RT subunits of a DHP-sensitive calcium channel.";  
 RL Science 241:1661-1664(1988).  
 RN [2]  
 RP SEQUENCE OF 961-973.  
 RX MEDLINE=9131636; PubMed=1847144;  
 RA Jay S.D., Sharp A.H., Kahl S.D., Vedvick T.S., Harpold M.W.,  
 RA Campbell K.P.;  
 RT "Structural characterization of the dihydropyridine-sensitive calcium  
 RT channel alpha 2-subunit and the associated delta peptides.";  
 RL J. Biol. Chem. 266:3287-3293(1991).  
 RN [3]

	Query Match	Best Local Similarity	Score 5405.5	DB 1	Length 1106
	Matches 1035; Conservative 11;	Pred No. 9.6e-315;		Mismatches 10;	Indels 29; Gaps 4
OY	1	MAAGCATTATTTTPOF--LLIGSSDQPPFSANTYIKSWDKMEDIVLTAKTASGVNOVL	58		
QY	1	MAAGRPATAMTLTITMOAILLIGFSSEPPFSATYIKSWDKMEDIVLTAKTASGVNOVL	60		

Qy	59	DREKQDLYTVPBNNAQOLVETAAADIEKLISNSKALVRLAEKVOQAHOWREDEFA	118
Db	61	DIYEKODLTVEBNNAQOLVETAAADIEKLISNSKALVRLAEAEKVOQAHOWREDEFA	120
Qy	119	SNEVYYNANADDDLPKRNDESEPSQRIKRVFIDDDANFGQISYOAHAHIFTDIEBESTI	178
Db	121	SNEVYYNANADDDLPKRNDESEPSQRIKRVFIDDDANFRQVSYOAHAHIFTDIEBESTI	180
Qy	179	VLEMLNMTSLADVEFKKNEEDBSLIQVFGSATGLARYPASPWVDSRTPNKTIDELYD	238
Db	181	VLEMLNMTSLADVEFKKNEEDBSLIQVFGSATGLARYPASPWVDSRTPNKTIDELYD	240
Qy	239	RRRPWYIOGAASPEKDMILIVDYSGSVGLTKLINTSVSEMLFETLSDDDPYNNAFSPNA	298
Db	241	RRRPWYIOGAASPEKDMILIVDYSGSVGLTKLINTSVSEMLFETLSDDDPYNNAFSPNA	300
Qy	299	QDVSCQOHLVQANVRNKKVLKDAVNNITAKGTTDKKCFSAFEPOLLNYNVSRANCKIT	358
Db	301	QDVSCQOHLVQANVRNKKVLKDAVNNITAKGTTDKKCFSAFEPOLLNYNVSRANCKIT	360
Qy	359	MLTDDGEEBAOEIPAKYKDKKVVFFPSGQHNTRYBGPLOMACENKGYEYIEPSIGA	418
Db	361	MLTDDGEEBAOEIPAKYKDKKVVFFPSGQHNTRYBGPLOMACENKGYEYIEPSIGA	420
Qy	419	IRINTQEVLDVGRPMVYLAGDAKAKOVMTNYLDALELGVTGTLVFNITQONEKKN	478
Db	421	IRINTQEVLDVGRPMVYLAGDAKAKOVMTNYLDALELGVTGTLVFNITQONEKKN	480
Qy	479	LKNQOLLGMYGADVSLIEDIKRLTPREFTLCPNGYYFAIDPNGVYLLHPNLOPK	530
Db	481	LKNQOLLGMYGADVSLIEDIKRLTPREFTLCPNGYYFAIDPNGVYLLHPNLOPK	540
Qy	531	-----NPKQEPVTLDFDLDAELENDIKYEINKMIMDESGEKTRTLVKSQDER	579
Db	541	IMLRKRRPVQONPKSQEPVTLDFDLDAELENDIKYEINKMIMDESGEKTRTLVKSQDER	600
Qy	580	YIDKGNRTYTWTPVNGTDY-SLALVLPFTSFYYIKAKIETITQARSKKKMKMDSFTLPR	638
Db	601	YIDKGNRTYTWTPVNGTDYSLALVLPFTSFYYIKAKIETITQARY-----SETLPR	653
Qy	639	DNEESGTFIAPRDYCDNLKISNNTEPILNFPNEFIDRKTPNPNSCNDLIRNYLLDAG	698
Db	654	DNEESGTFIAPRDYCDNLKPSDNNTEPILNFPNEFIDRKTPNPNSCNDLIRNYLLDAG	713
Qy	699	FTNELVONYMSKOKNIKGVKARFVYTGGITTRYYPKEAGENQENBETJEDSFYKRSIDN	758
Db	714	FTNELVONYMSKOKNIKGVKARFVYTGGITTRYYPKEAGENQENBETJEDSFYKRSIDN	773
Qy	759	DNYVTATYFNKSSPGVAESGIMVSKAVEITYOGKLIKPAVVGIKIDVNSWIENTFKTSI	818
Db	774	DNYVTATYFNKSSPGVAESGIMVSKAVEITYOGKLIKPAVVGIKIDVNSWIENTFKTSI	833
Qy	819	RDPGAGPYCDCKRNSDMVDCVILDDGGFLMANHDDYTOIGFPEGEIDPSIMRLVLNIS	878
Db	834	RDPGAGPYCDCKRNSDMVDCVILDDGGFLMANHDDYTOIGFPEGEIDPSIMRLVLNIS	893
Qy	879	VYAANKSTYDIOSVCEBGAAPKOGAGHRSAVYPSIADILHIGMMATPAAMSLIOQFLSLYT	938
Db	894	VYAANKSTYDIOSVCEBGAAPKOGAGHRSAVYPSIADILHIGMMATPAAMSLIOQFLSLYT	953
Qy	939	FPRLLEAVEEMDDFPAUSLISKOCITBEOYFPFNDNSKFSFVULDCGNCSTRIFHEKLMN	998
Db	954	FPRLLEAVEEMDDFPAUSLISKOCITBEOYFPFNDNSKFSFVULDCGNCSTRIFHEKLMN	1013
Qy	999	TNLIIFINVESKGTCPDTRLILQAEOTISGPPCDKVVKOPRRKRGPDVCFPNMNALEOYTD	1058
Db	1014	TNLIIFINVESKGTCPDTRLILQAEOTISGPPCDKVVKOPRRKRGPDVCFPNMNALEOYTD	1073
Qy	1059	CGGVS 1063	
Db	1074	CGGVS 1078	



UN36-CAEEL STANDARD; PRT; 734 AA.

ID UN36-CAEEL

AC P34374;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Protein unc-36.

DE UNC-36 OR C50C3.11.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OC NCBI\_TaxID=6239;

RM (1)

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RX MEDLINE=94150718; PubMed=7906398;

RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,

RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,

RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,

RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,

RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,

RA Lettelle P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,

RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkhen R.,

RA Sims M., Smaldon N., Smith A., Smith K., Sonhammer E., Staden K.,

RA Sulston J., Therry-Mieg J., Thomas K., Vaudin M., Vaughan K.,

RA Watson J., Watson A., Wainstock L., Wilkinson-Sproat J.,

RA Woldman P.;

RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

RT elegans";

RL Nature 368:32-38(1994).

CC -1- SIMILARITY: TO CALCIUM CHANNEL ALPHA-2B SUBUNIT.

CC -1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----

DR EMBL: L14433; AAA27969.1; -

DR PIR: S44617; S44617.

DR WormRep: C50C3.11; CE00117.

DR InterPro: IPR004010; Cache.

DR InterPro: IPR002035; VWF\_A.

DR Pfam: PF00092; vwa; 1.

DR Pfam: PF02743; Cache; 1.

DR SMART: SM00327; VWA; 1.

DR PROSITE: PS50234; VWA; 1.

DR Ionic channel; Ion transport; Voltage-gated channel; Calcium channel;

KW Glycoprotein.

KW DOMAIN 250 435

FT CARBOHYD 100 435

FT CARBOHYD 140 140

FT CARBOHYD 146 146

FT CARBOHYD 302 302

FT CARBOHYD 476 476

FT CARBOHYD 514 514

FT CARBOHYD 734 AA; 85034 MW; CCEB78C8DEE4B71F CRC64;

SEQUENCE

Query Match 10.8%; Score 611; DB 1; Length 734;

Best local Similarity 26.5%; Pred. No. 5,5e-29;

Matches 179; Conservative 127; Mismatches 261; Indels 108; Gaps 19;

QY 47 LAATAGVNOVDYKRYQDLYVEFNARQLEYIARDIEKLRSKAL--VRLALBA 104

DB 36 MKETFSKSHETILKQNYELVEEEDFDRALSKKHIEDLAKRSQPAIKAKISLA 95

QY 105 EKVOAAHQWREDFASNEVVYNAKDLDPK-NDSEPGSORIKP-----VFIDANF-G 156

DB 96 RSVRNDSTVNDPQSKSFIRFMAKQGNDDGTYYESHNLKRLKVNTEKSFNLQNANFT 155

QY 157 ROISYQHAHVHPTDIEGSTIVLANLNTSALDEYFKKRNREDSILMOVFSGATGLAR 216

DB 156 LPTSSVSSAAVHPTPLDYRNEDLLRLKIDW-SDIDAYRTNRETFDLAFLFCSAGYMR 214

QY 217 YYPASPVV-DNSRTPKIDLYVRRRPWYIGQASPKDILLVDVSGSVGLTLILFIS 275

DB 215 YYPASPVV-DNSRTPKIDLYVRRRPWYIGQASPKDILLVDVSGSVGLTLILFIS 275

QY 276 VSEMLETLLSDDDFVNVASFNSNA---QDVSCFQHLVQANVRKKVYLKDVANNITFAKGTID 332

DB 273 TEALITETLSHNYFNIMFESKNTFFLLDCCNGTNGILLQATMRKKALRRKMDTYQSEKAE 332

QY 333 YKKGFSFAFEQOLLNVN-----VSRANCKIIMLFDGGEERQELFATYKNDKATVTF 387

DB 333 YKALPLAFSLVLDLIDNGCGDNNGACENVIMLTIDGAPNAVKKITEDYNAKRVPTF 392

QY 388 SVQGNHYDRGPLOMNAECNKGYYEIPISGATIRITQEVLT-----DVLGRPVYLAGDKAKQ 443

DB 393 LVGDEALIDENEYREMAKCNNGYVAVANADVDEKIHHRMSKRVYGRHKRESGLS-- 450

QY 444 VQNTNYLDALDELGL-VITGTLVPVNTTGQENKTN----- 478

DB 451 -WNTGVYRRLYLPRPELFAEPVPTTNOFAYVNMKASRRKIRLOKSEARSMEVTVSY 509

QY 479 --LKNOLIGVAGVDSLEDIKRLTPRTLCNGYFALDPNGYVLLPNIQPKND----- 532

DB 510 PVIYVETFGVAAVNIPLETVAKQSHPANIGSKSTFFMLDQGFVWTPHQLRPDPTKY 569

QY 533 KQEPVTLDFLD-----AELNDIKVEIRNMDIGE 563

DB 570 HKQNYNMDDLLEVGONONVRSSQKQAVSDLVCSGANVAECVDLRKAVRKIIDCD 629

QY 564 SGKPTFRLYKQSDERY---IDK---GKRITYTPVNGTDSLALVLPYTSFYIAKI 616

DB 630 NSD-----VQDLVLYATELIDRVYPOTNYTAPCINHANFVLGLAVAKDDRYVRK- 682

QY 617 EETITQARSKKGMK 631

DB 683 -----QKRYDFGRVK 692

RESULT 6

ID ITH3\_MOUSE STANDARD; PRT; 886 AA.

AC 061704;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Inter-alpha-trypsin inhibitor heavy chain H3 precursor (ITI heavy

DE chain H3).

GN ITH3.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI\_TaxID=10090;

RM (1)

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6N; Tissue=Liver;

RX MEDLINE=95194326; PubMed=7534067;

RA Chan P., Risler J.-L., Raguenez G., Sallier J.-P.;

RT "The three heavy chain precursors of the inter-alpha-inhibitor

RT family in mouse: new members of the multicopper oxidase protein group

RT with differential transcription in liver and brain";

RL Biochem. J. 306:505-512(1995).

CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A

CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,

CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE

CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE

CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY

CC SIMILARITY).

CC -1- SUBUNIT: I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM

CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,

CC BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-1) IS COMPOSED OF H1, H2

CC AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-II) OF H2 AND  
CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BOTH LIVER AND BRAIN.  
CC -1- PM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN  
CC 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY  
CC SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.  
CC -1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; X70393; CAA49843.1; .  
CC DR MGD; MGI:96620; Tlth3.  
CC DR InterPro: IPR002035; VWF\_A.  
CC DR Pfam: PF00092; vwa; 1.  
CC DR SMART; SM00327; VWF; 1.  
CC DR PROSITE; PS50234; VWFA; 1.  
CC KM Serine protease inhibitor; Repeat; Signal; Multigene family;  
KM Glycoprotein.  
FT SIGNAL 1 18 POTENTIAL.  
FT PROPEP 19 30 BY SIMILARITY.  
FT CHAIN 31 646 INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN  
FT PROPEP 647 886 BY SIMILARITY.  
FT DOMAIN 279 439 VWFA.  
FT CARBOHD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHD 577 577 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT BINDING 646 646 CHONDROITIN 4-SULFATE, CROSS-LINK SITE  
FT (BY SIMILARITY).  
SQ SEQUENCE 886 AA: 98977 MW: 15953087cF5030A CXC64;  
Query Match 3.5%; Score 196.5; DB 1; Length 886;  
Best Local Similarity 20.5%; Pred. No. 0.00039;  
Matches 189; Conservative 142; Mismatches 349; Indels 243; Gaps 46;  
QY 45 VTLAKTASGVNDIYEGYODLYVERPNARQLEIARDLEKILSNRSKALVLALEA 104  
DB 78 VELPKAFITNLTLT-----DGVY-PENYKE-KEVAKQYKEKAVSOGKTAGL----- 124  
QY 105 EKVQAAHQWREDF-----ASNEVYVYNAKDLDEPEKNDSBGSQRKPYETIDANFGR 157  
DB 125 --VKASGRLEKFTYSVNAAGSKVTELTPELLKRNKGYEMYLKQVP-----K 173  
QY 158 QISYQAAVHIPTDIYEGSTIVLNLNMTSALDEYFKKREDDPSILMOYFGSA-----T 212  
DB 174 QL-VRH--FEIDAHIFEPQI-----SMLD-----AASFTINDLGSALTRKSPS 215  
QY 213 GLARYYPASPWVDSNRT--PNKID-----LYDYRRRP-----WYI-----QG- 247  
DB 216 GKKGHVSFKPSLDQORSCTPCTDLSLNGPFTIYDVNRSPPGNOIVNGYVHFHFRPQL 275  
QY 248 AASPKDMLILVDYSGVSGSLTKLIRTSVSEMLETSLDDFVNAVVSFNADVSCFO-H 306  
DB 276 PVPKNIIVFIDVSGSMGRKIQOTREALKILDDVEKEDDYLFILFST---DVTWKDH 332  
QY 307 LVQANRNKKVYLKDAVNNITAKITTYKGFSAFQQLNLYNSRAN-----CNKIIML 360  
DB 333 LVQATPANLKEAKTEPVKNIHDSMTNINDGLKIGIML---NARDHDPVPERKSTIIM 389  
QY 361 FTGG-----GERAQETFAKYNK--DKKVFYTFVSQGHNYDRPIOMACENKGYEYIEP 414  
DB 390 LTQGDANTGSRPEKTOENRNALIGKFPYLYNGFG-NNLNYFETLLENGLARIRY 448  
QY 415 SIGAIRINQEIYLDVIGRPVNLGAKRAKOVQMTNVDLDELGLVITGTIPVNTIGONE 474  
DB 449 EDS DANIQLOGFEYEVANPLL-----TNVEVEPEANA-----LIDLTRNSY 489

QY 475 NKTNLKNOILLGVGVDSLEDIKILTPPTLCSPNGYFAIDPNQGVLLHPNLOKRNKS 534  
DB 490 PHFYDSESEIVAAERLVDKRNNDN-----FKADYKGGALN-----DLTE 527  
QY 535 QEEVITLDFIDAELENIKVEIRNKKMIDGESGK--TFRTLVSOEDERYIDKGNRTYTWP 592  
DB 528 TEEVDMEEMDAALK-----EGYIFGDIERYLMAYLTIEOLLEKRNKAKDEKENT- 579  
QY 593 VNGTDSLA--LVLPYSEFYIYAKITEETITQARSKKMKDSET-----LKPNEESG 645  
DB 580 AEAALDSLAKHAFYPTLSMVVTKPEEDNEDOTSIAONAGAEAFETTMFTLTQOSSQSP 639  
QY 646 YTIAPRDYCNDKLSDNTEFLNNEFLDKTRPNPNSCNDLIRVLLDGFTEIYLO 705  
DB 640 YYYV-----DGDPHFIQI-----PKANDSCFNIDKEPQTVLRILQ 676  
QY 706 NYMSKQKNIKGVAKARFVYTDGITRVYPRKAGENOMENBETYEEDSPYKSLDNDNYVFTA 765  
DB 677 D-----PYT--GIT-VTQGIIG-----KKS--NASSRTGK 702  
QY 766 PYENKSGPAGYEGIMVSKAVEIYIOGKILKPAVVGIKIDVNSWIENTPTKSTRDPCAP 825  
DB 703 TYFGKLGITNAMDMFVEYETTEKILIG-----TGAELSTFEMLDPTVYVTO-----TGL 750  
QY 826 VCDCKRSDVMDCYIIDDG-GFLLMAN-----HDDYTNQIGRFGELDPSLMRLVY 876  
DB 751 SVTINRRKNMV--VSPFGDISFVILIHQVKKHPHODFLG-----FYVDSHRMSAQTH 803  
QY 877 ISVYAFNKSVDYOSV-CEPGAAP 898  
DB 804 GLLGQFQFPDFKYPFGIRPSSDP 826  
RESULT 7  
ID ITIH3 HUMAN STANDARD; PRT; 885 AA.  
AC 006033; 099085;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Inter-alpha-trypsin inhibitor heavy chain H3 precursor (ITI heavy  
DE chain H3) (Serum-derived hyaluronan-associated protein) (SHAP).  
GN ITIH3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=93215656; PubMed=7681778;  
RA Bourguignon J., Diarra-Mehrpour M., Thiberville L., Bost F.,  
RA Seaboue R., Martin J.P.;  
RT "Human pre-alpha-trypsin inhibitor-precursor heavy chain. cDNA and  
RT deduced amino-acid sequence.";  
RL Eur. J. Biochem. 212:771-776(1993).  
RN [2]  
RP SEQUENCE OF 341-885 FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=89137072; PubMed=2465147;  
RA Diarra-Mehrpour M., Bourguignon J.P.,  
RA Passage E., Salier J.P., Martin J.P.;  
RT "Human plasma inter-alpha-trypsin inhibitor is encoded by four genes  
RT on three chromosomes.";  
RL Eur. J. Biochem. 179:147-154(1989).  
RN [3]  
RP SEQUENCE OF 30-49; 463-477 AND 497-515.  
RX MEDLINE=89380192; PubMed=2476436;  
RA Enghild J.J., Thøgersen I.B., Pizzo S.V., Salvesen G.;  
RT "Analysis of inter-alpha-trypsin inhibitor and a novel trypsin  
RT inhibitor, pre-alpha-trypsin inhibitor, from human plasma.";  
RL J. Biol. Chem. 264:15975-15981(1989).  
RN [4]



RP SEQUENCE OF 631-647, AND CROSS-LINKAGE SITE TO BIKUNIN.  
 RX MEDLINE-91093267; PubMed-1898736;  
 RA Enghild J.J., Salvesen G., Hefta S.A., Thøgersen I.B.,  
 RA Rutherford S., Pizzo S.V.;  
 RA Chondroitin 4-sulfate covalently cross-links the chains of the  
 RT human blood protein pre-alpha-inhibitor.";  
 RL J. Biol. Chem. 266:747-751(1991).  
 CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A  
 CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,  
 CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE  
 CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE  
 CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES.  
 CC -1- SUBUNIT: I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM  
 CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,  
 CC BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-1) IS COMPOSED OF H1, H2  
 CC AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND  
 CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-1) OF H3 AND BIKUNIN.  
 CC -1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN  
 CC 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE.  
 CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.  
 CC -----  
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 CC -----  
 DR EMBL: X67055; CAA47439.1; -  
 DR EMBL: X14690; CAA32821.1; -  
 DR Gene: HGNC:6168; ITIH3.  
 DR MIM: 146650;  
 DR InterPro: IPR002035; VWFA-A.  
 DR Pfam: PF00092; vwa; 1.  
 DR SMART: SM00327; VWFA; 1.  
 DR PROSITE: PS50234; VWFA: 1.  
 KW Serine protease inhibitor; Repeat; Signal; Multigene family;  
 KW Glycoprotein.  
 FT SIGNAL 1 17 POTENTIAL.  
 FT PROPEP 18 30  
 FT CHAIN 31 647  
 FT -----  
 FT PROPEP 648 885  
 FT DOMAIN 278 438 VWFA.  
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 576 576 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT BINDING 647 647 CHONDROITIN 4-SULFATE, CROSS-LINK SITE.  
 FT CONFLICT 344 344 R -> K (IN REF. 2).  
 FT CONFLICT 357 357 N -> G (IN REF. 2).  
 FT CONFLICT 846 846 Q -> H (IN REF. 2).  
 SO SEQUENCE 885 AA; 99121 MW; BC63856F8F5E4A1B CRC64;  
 Query Match 3.38; Score 185; DB 1; Length 885;  
 Best Local Similarity 21.38; Pred. No. 0.0019;  
 Matches 137; Conservative 113; Mismatches 243; Indels 150; Gaps 36;  
 QY 45 VTLAKTASGVNQVLDYIEKQDLYTPPNNAKQVLETAANDIEKLSNRSKALVRLALEA 104  
 DB 77 VELKTAFTITNFTLTI-----DGYTY-PGNVKE-KEYAKKQYKAVSQGKTAGL----- 123  
 QY 105 EKVQAAQWQWEDF-----ASNVEVYVYNAKDDLDPEKNSPEGQSQRIRKVFIPDANFGR 157  
 DB 124 --VVASGRKLEKFTVSVNAAGSVTFELTYELLRKHKKQYEMYLKQV-----K 172  
 QY 158 QISYQHAHVHPIDYEGSTIVNELNMTSALDEVEKKNREDDPSLIMQVFGSA-----T 212  
 DB 173 QL-VKHEIEV--DIEPQGI-----SMLD-----AASFTINDLSGALNKSRS 214  
 QY 213 GLARYVASHVWVDSNR-PMKID-----LYDVRRRP-----WTI-----QG- 247  
 DB 215 GKRGHVSFKPSLDQKSCPTDLSLNGDFTITYDVNRSPGNVQIVNGYFVHFAPQGI 274

QY 248 AASPDKMLIVDVGSGVGLTKLIRTSVSEMLETLDSDDEPVNVAFSNSNAQVSCF-QH 306  
 DB 275 PVVPRNVAFVLDISGSMAGKTEQTKKALLRLDEMKEDYLNFLPSC---DSTWKEH 331  
 QY 307 LVQAVNRKRYLKAQVNNITAKGTDYKGFSPFEOGLNANVS-----ANCKTIML 360  
 DB 332 LVQATPEMLQARFVYVSMEDKGTNINDGLRISML---NKAREHRIPERSTIVIM 388  
 QY 361 PTDG---GEERAQEIFAKYK--DKRYVFTFVSQGHNYDRCPIDWACENNGYVEIP 414  
 DB 389 LTDEGANVGESEPRKEIDENVAALIGKFPFLYNLGF--NLNLYNLEMALENHGFARIY 447  
 QY 415 SIGAIRNTQCYLYLVGRPMVLADKAKQYQWNTVYDALE-----LGVITGTLR 465  
 DB 448 EDSADADQLQGFYEYEVANPL-LTGEEMEYDE--NAILDQNTYQHYPYDSEIYVAGRLV 504  
 QY 466 VENITGQENKNTNK-----NQLITGVAGVDSLEDIKRLPFTLCPNGYFAIDPN-- 518  
 DB 505 DEDM---NSFKADYKGAINDL---TFTEVDKKEKEMK-----ALQERDYIFG---NYI 550  
 QY 519 ---GYVLHPNIQPK--NPKSQEPTLDPLDAELENDIKVEIRNKMIDGESGEKTFRT 571  
 DB 551 ERLWAVLTIEQLLEKRRNAGEEKENLTARALDLSTKYHVPFLTGMVYTKPE----- 603  
 QY 572 LVKSQDERYI-DKGNRTYTWTPVN-GTDYSIALVLPYISYTI 612  
 DB 604 --DNEDRALADKRGEDAEATPVSPMSYLTYSQPNPPYVV 644  
 RESULT 8  
 ITIH3-RAT  
 ID ITIH3-RAT STANDARD; PRT; 887 AA.  
 AC 063416;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Inter-alpha-trypsin inhibitor heavy chain H3 precursor (ITI heavy  
 DE chain H3).  
 GN ITIH3.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Sprague-Dawley; TISSUE-Liver;  
 RA Blom A., Files E.;  
 RL Submitted (Dec-1994) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A  
 CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,  
 CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE  
 CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE  
 CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY  
 CC SIMILARITY).  
 CC -1- SUBUNIT: I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM  
 CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,  
 CC BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-1) IS COMPOSED OF H1, H2  
 CC AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND  
 CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-1) OF H3 AND BIKUNIN.  
 CC -1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN  
 CC 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY  
 CC SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.  
 CC -----  
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 CC -----





Db 133 YANVRRLTNOGLPPPPDAVVEEIVNFPSPDMDI--KDKOSIPASKPIPFAMRYELA---187  
 QY 219 PASPVNDSRTPNKIDLYDVRRRPMYIOGASPKMDILVYSGS--VSGILIKLIRTSVS 277  
 Db 188 PA-FW-NBQRTLLKAVDILAKRKESELPAS-----NLVFLIDTSSSMKSIDERLPIQSSLK 241  
 QY 278 EMLETLSDDDVYVNAFSRNSADVSCFOHLVQAVNRKKYLKDAVNNITAKGITYDKGKF 337  
 Db 242 LLLVELRQDNDIAIVYAGSRIA-----LPISGSHKAEINADISDLDAEINGAGL 296  
 QY 338 SFARQLLNVSRANKITIMFTDG-----GEERAQELIFAKYNDKKVRVFTPSVGO 391  
 Db 297 ELAVQAKTK-GEIKGGINR-ILLATDDDFVNGIDDPKSIEMVKKQRESGVLTSTEGVN 354  
 QY 392 HNDVRGPIQWACENKNGYVEIPISGIRINTQEDYDLGRPMVL--AGDKAKOV-----445  
 Db 355 SNVEAMKAVHIVADGNNGSYIDTIS---EAQKVINSEKQMLITAKYKQIEFNPA 410  
 QY 446 WTNYVLDALDELGVITGTLEVFNTQGENEKNLKNOLLGVNGVD-VLEEDI---KRLT 501  
 Db 411 WYTER---RQIGYE-----KRLRVEHFNNDVADIGACKHIT 447  
 QY 502 PRETLCPNGYFAIDPNGVYLLHPNLQPKNPKSOE 536  
 Db 448 LLEFLINGOKASIDKLRYA--PDNKLAKSDKTE 480

RESULT 10  
 ITIH3\_MESAU STANDARD; PRT: 886 AA.  
 AC P97280;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Inter-alpha-trypsin inhibitor heavy chain H3 precursor (ITI heavy chain H3) (H33).  
 GN ITIH3.  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 OX NCBI\_TaxID=10036;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=97420688; PubMed=9276673;  
 RA Nakatani T., Suzuki Y., Yamamoto T., Sinohara H.;  
 RT "Molecular cloning and sequencing of cDNAs encoding three heavy-chain precursors of the inter-alpha-trypsin inhibitor in Syrian hamster: implications for the evolution of the inter-alpha-trypsin inhibitor heavy chain family";  
 RT J. Biochem. 122:71-82(1997).  
 RL [2]  
 RN SEQUENCE OF 31-50; 446-472 AND 504-523, AND SUBUNITS.  
 RP TISSUE=Plasma;  
 RC MEDLINE=97018241; PubMed=8864857;  
 RA Yamamoto T., Yamamoto K., Sinohara H.;  
 RT "Inter-alpha-trypsin inhibitor and its related proteins in Syrian hamster urine and plasma";  
 RL J. Biochem. 120:145-152(1996).  
 CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY SIMILARITY).  
 CC -1- SUBUNIT: I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN, BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-1) IS COMPOSED OF H1, H2 AND BIKUNIN. INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND BIKUNIN. AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.  
 CC -1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN

CC 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.  
 CC -----  
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 CC -----  
 DR EMBL: D89287; BAA13940.1;  
 DR InterPro: IPR002035; VWFA\_A.  
 DR Pfam: PF00092; vwa; 1.  
 DR SMART: SM00327; VWFA; 1.  
 DR PROSITE: PS50234; VWFA; 1.  
 KW Serine protease inhibitor; Repeat; Signal; Multigene family;  
 KW Glycoprotein.  
 FT SIGNAL 1 18  
 FT PROPEP 19 30 POTENTIAL.  
 FT CHAIN 31 646 BY SIMILARITY.  
 FT PROPEP 647 886 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN  
 FT DOMAIN 279 439 H3.  
 FT CARBOHYD 88 88 BY SIMILARITY.  
 FT CARBOHYD 577 577 VWFA.  
 FT BINDING 646 646 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CHONDROITIN 4-SULFATE, CROSS-LINK SITE (BY SIMILARITY).  
 SQ SEQUENCE 886 AA; 99018 MW; AC0594C6852576B8 CRC64;

Query Match 2.9%; Score 166; DB 1; Length 886;  
 Best Local Similarity 23.2%; Pred. No. 0.026;  
 Matches 66; Conservative 57; Mismatches 111; Indels 51; Gaps 11;

QY 202 SLNQVFGSATGLARYYPASPVWNSRT-PNKID-----LYDVR-R-PWYIGA-- 248  
 Db 208 SALNKSFSKRGKGVSPRS---LDQGRSCTPCHDSILNCGFTIYVDRKSPGNVQVNG 264  
 QY 249 -----ASPKMLILVYSGSVSGILTLKLTFSVSEMLETLSDDPVNVASFNS 296  
 Db 265 YVHFEPAPQGLPVVKNIVVIDISGSMAGRKIQOTRVALLKILDDMKQDYINFLTFST 324  
 QY 297 NAQDVSCFOHLVQAVNRKKYLKDAVNNITAKGITYDKGFSFAFDQLN-----YVNSA 352  
 Db 325 GV--TWKDSLVQATPANLEARTFVRSIDQGTNINDELGICRMLTDAREQHTVPER 382  
 QY 353 NCKNITMLFTDG-----GEERAQELIFAKYNDKKVRVFTPSVG--OHNYDRGPIQWACENK 407  
 Db 383 STSITIML-TDGDANGTESRPERKIOENVRKAIIEGRPLVNLGFGNNLNYNLETMALLENH 441  
 QY 408 GYVEELPSIGAIRINTQEDYDLGRPMVLAGDAKQOVMTNYVLD 452  
 Db 442 GVARRIYEDSDANLQQLQGYEVANPUL-----TWEEVE 475  
 RESULT 11  
 DPOL\_THEST STANDARD; PRT: 1829 AA.  
 AC 033845;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE DNA polymerase (EC 2.7.7.7).  
 GN POL.  
 OS Thermococcus sp. (strain TY).  
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
 CC Thermococcus.  
 OX NCBI\_TaxID=110163;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98094267; PubMed=9434178;

RA Niehaus F., Frey B., Antikainen G.;  
 RT Cloning and characterization of a thermostable alpha-DNA polymerase  
 from the hyperthermophilic archaeon Thermococcus sp. TY.";  
 RL Gene 204:153-158(1997).  
 CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate  
 + [DNA](N).  
 CC -1- PM: THIS PROTEIN UNDERGOES A PROTEIN SELF SPLICING THAT INVOLVES  
 A POST-TRANSLATIONAL EXCISION OF THE THREE INTERVENING REGION  
 (INTERIN) FOLLOWED BY PEPTIDE LIGATION.  
 CC -1- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.  
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 or send an email to [license@sdb.ch](mailto:license@sdb.ch)).  
 CC  
 CC EMBL: Y13030; CAJ73475.1; -  
 DR HSP: P56689; 1TGO.  
 DR InterPro: IPR002064; DNA\_pol\_B.  
 DR InterPro: IPR003586; Hedgehog\_hinc.  
 DR InterPro: IPR003587; Hedgehog\_hinc.  
 DR InterPro: IPR002203; Interin.  
 DR InterPro: IPR004042; Interin\_endonuc.  
 DR InterPro: IPR004578; Pol2.  
 DR Pfam: PF00136; DNA\_pol\_B\_4.  
 DR Pfam: PF03104; DNA\_pol\_B\_exo; 1.  
 DR PRINTS: PR00379; INTERIN.  
 DR SMART: SM00305; Hinc. 3.  
 DR SMART: SM00306; Hinc. 3.  
 DR SMART: SM00486; POLB; 1.  
 DR TIGR: TIGR00592; pol2; 2.  
 DR PROSITE: PS00116; DNA\_POLYMERASE\_B; FALSE\_NEG.  
 DR PROSITE: PS50818; INTERIN\_C\_TER; 3.  
 DR PROSITE: PS50819; INTERIN\_ENDONUCLEASE; 2.  
 DR PROSITE: PS50817; INTERIN\_N\_TER; 3.  
 KW Transferrase: DNA-directed DNA polymerase; DNA replication;  
 KW DNA-binding; Hydrolase; Endonuclease; Autocatalytic cleavage;  
 KW Protein splicing.  
 FT CHAIN 1 409 DNA POLYMERASE, 1ST PART (POTENTIAL).  
 FT CHAIN 410 769 INTERIN I.  
 FT CHAIN 770 855 DNA POLYMERASE, 2ND PART (POTENTIAL).  
 FT CHAIN 856 1392 INTERIN II.  
 FT CHAIN 1393 1441 DNA POLYMERASE, 3RD PART (POTENTIAL).  
 FT CHAIN 1442 1598 INTERIN III.  
 FT CHAIN 1599 1829 DNA POLYMERASE, 4TH PART (POTENTIAL).  
 FT CHAIN 1829 211875 MW: A113A8BC57EB9C3 CRC64;  
 SQ SEQUENCE

Query Match 2.9%; Score 162; DB 1; Length 1829;  
 Best Local Similarity 20.8%; Pred. No. 0.13;  
 Matches 178; Conservative 101; Mismatches 294; Indels 284; Gaps 42;

QY 260 VGSVSGTLTKLRTSYSEMLETLSDDFVNVSFNSN----- 297  
 DB 492 LSGVKG---KIITTKL-----FKIAFEENKNSSEELKLGSLIAGTL 537  
 QY 298 -ADVSCF-----OHLVQANV-RNKVKLVADN-----NNTAKG----- 329  
 DB 538 LRKIDIEFDSRGKGRKISHQRYVEITIGENEKELLERILYFDKLGIRDSYKKGDTNA 597  
 QY 330 -INDYKGFGEFAPEOILNINVSANCKIIMLEPTDGEERAOEIPAKYKDKKRVYFTF 387  
 DB 598 LKTTAKAVYLOIEELK-NIESLYAPAVLRGF-----ERDITVAKISITIVT- 647  
 QY 388 SVGOHNYDRGPIQWAGENKGY---YIEPSIGARINTOEYLDVIGRPVYLAGDAKQV 444  
 DB 648 -QGNNMKKIDIVAKLDSIGIPYSREYKYIENGKELKHILEITGRD----- 695  
 QY 445 QMTNVTLDALGLVITGTLPFNITGNE-----KTNLKNOLLIGKGVDSLE 495  
 DB 696 -----GLITQTLVGFISSEKNEALEKAIEVERENRRLKNSFYNLSTFEVSSE 743  
 QY 496 DIKRLTPRTICPNQGYPAIDPNCVLLAPMLQPKNPQSEPTVLDFDLAELNDIRVEI 555  
 DB 744 YKGEVYDLTEGNPYTA---NG-ILTHNSLYSIIVTHN-VSPDLIER----- 789  
 QY 556 RNKMIDGSEGEKTFETLVKSODERYIDGNRTYTWTPVNGTDYSLALVLPYTSYIYAK 615  
 DB 790 -----GCKNVDAPIVG---YRFCKDPG---PIPSI 815  
 QY 616 IETITQARSKKGMKDETLKPNFEESG-----TFIAPROCDNLKISDNTE 666  
 DB 816 IGLITMQEIKKKM--ATDIPLEKMLDYRQRAVKLLANSILPNEW---LPIENG 870  
 QY 667 FILNNEFIDR-----KTPNPNSCNTDLINRYLDAGFTNELVYWSKQKINIGVARE 721  
 DB 871 KVKYKGEFIDRMEDQKQKRVTDVTEYLE---VDNIFAFSL-NKESKSEIKKKAL- 924  
 QY 722 VTDGGITRVRVKEGE 738  
 DB 925 -----IRHKYKGEAYE 935

RESULT 12  
 Y103-SYNY3  
 ID Y103-SYNY3 STANDARD; PRT; 420 AA.  
 AC Q55874;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Hypothetical protein s110103.  
 GN S110103.  
 OS Synchocystis sp. (strain PCC 6803).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.  
 OX NCBI\_TaxID=1148;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96127529; PubMed=8590279;  
 RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,  
 Sugita M., Tabata S.;  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 RT Synchocystis sp. strain PCC6803. I. Sequence features in the 1 Mb  
 RT region from map positions 64k to 92k of the genome.";  
 RL DNA Res. 2:153-166(1995).  
 CC -1- SIMILARITY: TO E.COLI YFBK.  
 CC -1- SIMILARITY: CONTAINS 1 VFPA DOMAIN.  
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 CC

CC -----  
 DR EMBL: D64004; BAA10635.1; -  
 DR InterPro: IPR002035; VWF\_A.  
 DR Pfam: PF00092; vwa; 1.  
 DR SMART: SM00327; vwa; 1.  
 DR PROSITE: PS0234; VWF\_A. 1.  
 KW Hypothetical protein; Complete proteome.  
 FT DOMAIN 43 215  
 SO SEQUENCE 420 AA; 45849 MW; E711B51478E74F3 CRC64;

Query Match 2.8%; Score 160.5; DB 1; Length 420;  
 Best Local Similarity 21.1%; Pred. No. 0.018;  
 Matches 86; Conservative 86; Mismatches 181; Indels 55; Gaps 16;

QY 251 PKMLIIIVDVGSGVSTLTILKIRTSVEMLETSDDEFNVAVSFNADVSCFOHLVQA 310  
 DB 41 PLNLCLVLHDSGMDGPLETVKSAALGLIDRLIEDRLSVIAFDHRAKIV-----IENG 95  
 QY 311 NVRRKVLKAVNNITAKGITDYKGFSPAFEDLLNVSRAKCNKIMLTGGERRAO 370  
 DB 96 QVNRGAIAIAIERKAEGETALDEGLKIGIQEAKGKEDRS--HIFLLTGENEHGD 152  
 QY 371 E----IFAKYNKKKVFETFSVGOHNYDRGIOMNACENK--YYEIPISGIRINTQ 424  
 DB 153 NDRCLKIGTVASDYKILVHTLFGGDH-WNQDVLKAIASQSLSTIENPS-EALTFPQ 210  
 QY 425 EYLDVGRPVYLAGDKAKQVQNTNYLDALELG---LVITGLPVFNITGONENKTNK 480  
 DB 211 LF-----QKRSNNGLTNAHL-LLELAPQAHAI--VKPAQVSPETMDLT-VQ 254  
 QY 481 NQILGVMGVDSLEDIKRLTPFTLCPPNGYPAIDPNGVLLHPMLQPKNKSOE----- 536  
 DB 255 NQAIIEVRGLDGLTDQERY-----LLNLXYDQLPGHVGIVQIRIDDPASGDTNL 309  
 QY 537 ----PTLDELDALENDIKVEIRNMIDGEGSEKT--FRTLVKSODERYIDKGNRTYT 590  
 DB 310 SDPLPLTIG-VQYQPSIDVQVESILYLAQRQIAETFKLKADRGAAATMLQTAK 368  
 QY 591 TPVNGDYSLALVLPYSFYIKAKIETITQARSKKGKMKSEITLP 638  
 DB 369 TALQMDKNGARTILQTN---TRLQSGEDLSEGRKRTKTMVSKTTLQ 413

RESULT 13  
 ITH2\_HUMAN  
 ID ITH2\_HUMAN STANDARD: PRT; 946 AA.  
 AC P19823; Q15484; Q14659;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy chain H2) (Inter-alpha-trypsin inhibitor complex component II)  
 DE (Serum-derived hyaluronan-associated protein) (SHAP).  
 GN ITH2 OR IGHEP2  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN RN  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE=88152237; PubMed=2450046;  
 RA Gebhard W., Scheitmueller T., Hochstrasser K., Wächter E.;  
 RT "Complementary DNA and derived amino acid sequence of the precursor of one of the three protein components of the inter-alpha-trypsin inhibitor complex."  
 RL FEBS Lett. 229:63-67(1988).  
 RN RN  
 RP SEQUENCE OF 384-865 FROM N.A.  
 RX MEDLINE=88068576; PubMed=2446322;  
 RA Sailer J.P., Diarra-Mehrpour M., Sessboue R., Bourguignon J.,  
 RT "Isolation and characterization of cDNAs encoding the heavy chain of human inter-alpha-trypsin inhibitor (I alpha II): unambiguous

RT evidence for multipolypeptide chain structure of I alpha II.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:8272-8276(1987).  
 RN RN  
 RP SEQUENCE OF 384-766 FROM N.A.  
 RX MEDLINE=89076497; PubMed=2462430;  
 RA Sailer J.P., Diarra-Mehrpour M., Sessboue R., Bourguignon J.,  
 RT "Human inter-alpha-trypsin inhibitor. Isolation and characterization of heavy (H) chain cDNA clones coding for a 383 amino-acid sequence of the H chain."  
 RL Biol. Chem. Hoppe-Seyler 369:15-18(1988).  
 RN RN  
 RP PARTIAL SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=88024442; PubMed=3663330;  
 RA Scheitmueller T., Hochstrasser K., Resinger P.W.M., Wächter E.,  
 RT "cDNA cloning of human inter-alpha-trypsin inhibitor discloses three different proteins."  
 RL Biol. Chem. Hoppe-Seyler 368:963-970(1987).  
 RN RN  
 RP SEQUENCE OF 55-74; 116-127; 224-246; 295-307 AND 365-385.  
 RX MEDLINE=89380192; PubMed=2476436;  
 RA Englid J.J., Thøgersen I.B., Pizzo S.V., Salvesen G.;  
 RT "Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-alpha-trypsin inhibitor, from human plasma. Polypeptide chain stoichiometry and assembly by glycan."  
 RL J. Biol. Chem. 264:15975-15981(1989).  
 RN RN  
 RP SEQUENCE OF 55-64.  
 RC TISSUE=Plasma;  
 RX MEDLINE=93039735; PubMed=1384548;  
 RA Malki N., Balduyck M., Maes P., Capon C., Han K.K.,  
 RT "The heavy chains of human plasma inter-alpha-trypsin inhibitor: their isolation, their identification by electrophoresis and partial sequencing. Differential reactivity with concanavalin A."  
 RL J. Biol. Chem. Hoppe-Seyler 373:1009-1018(1992).  
 RN RN  
 RP SEQUENCE OF 55-64 AND 681-702, CROSS-LINK STRUCTURE, AND CARBOHYDRATE-LINKAGE SITES T-691.  
 RX MEDLINE=93232026; PubMed=7682553;  
 RA Englid J.J., Salvesen G., Thøgersen I.B., Valnickova Z.,  
 RT "Presence of the protein-glycosaminoglycan-protein covalent cross-link in the inter-alpha-inhibitor-related proteinase inhibitor heavy chain 2/bikunin."  
 RL J. Biol. Chem. 268:8711-8716(1993).  
 RN RN  
 RP SEQUENCE OF 67-101, AND HYALURONAN BINDING.  
 RC TISSUE=Serum;  
 RX MEDLINE=94075371; PubMed=7504674;  
 RA Huang L., Yoneda M., Kimata K.;  
 RT "A serum-derived hyaluronan-associated protein (SHAP) is the heavy chain of the inter-alpha-trypsin inhibitor."  
 RL J. Biol. Chem. 268:26725-26730(1993).  
 RN RN  
 RP SEQUENCE OF 699-702, AND COVALENT LINKAGE WITH CHONDROITIN SULFATE.  
 RC TISSUE=Plasma;  
 RX MEDLINE=94229087; PubMed=7513643;  
 RA Morelle W., Capon C., Balduyck M., Sautiere P., Kouach M.,  
 RT "Chondroitin sulphate covalently cross-links the three polypeptide chains of inter-alpha-trypsin inhibitor."  
 RL Eur. J. Biochem. 221:881-888(1994).  
 RN RN  
 RP CARBOHYDRATE-LINKAGE SITES, AND MASS SPECTROMETRY.  
 RX MEDLINE=98343966; PubMed=9677337;  
 RA Flahaut C., Capon C., Balduyck M., Ricart G., Sautiere P., Mizon J.;  
 RT "Glycosylation pattern of human inter-alpha-inhibitor heavy chains."  
 RL Biochem. J. 333:749-756(1998).  
 RN RN  
 RP CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.

MEDLINE-98087700: PubMed-9425062:  
 RA Olsen E.H.N., Rahbek-Nielsen H., Thøgersen I.B., Roepstorff P.,  
 RA Engblid J.J.:  
 RT "Posttranslational modifications of human inter-alpha-inhibitor:  
 RT Identification of glycans and disulfide bridges in heavy chains 1 and  
 RT 2.";  
 RL Biochemistry 37:408-416(1998).  
 CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SPERM OR AS A  
 CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,  
 CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE  
 CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE  
 CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES.  
 CC -1- SUBUNIT: I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM  
 CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,  
 CC BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2  
 CC AND BIKUNIN. INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND  
 CC BIKUNIN. AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.  
 CC -1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN  
 CC 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARATE.  
 CC -1- MASS SPECTROMETRY: MW=76508; METHOD-MALDI; RANGE=55-702.  
 CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.  
 CC -----  
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 CC -----  
 DR EMBL: X07173; CAA30160.1; ALT\_SEQ.  
 DR EMBL: M18193; AAA60558.1; -  
 DR EMBL: M33033; AAA59195.1; -  
 DR PIR: S00346; ITHU2.  
 DR PIR: B34245; B34245.  
 DR GlycoSiteDB: P19823; -  
 DR Genew: HGNC:6167; ITIH2.  
 DR MIM: 146640; -  
 DR InterPro: IPR002035; VWF\_A.  
 DR Pfam: PF000692; VWF\_1.  
 DR SMART: SM00327; VWF\_1.  
 DR PROSITE: PS50234; VWFA; 1.  
 KW Serine protease inhibitor; Repeat; Signal; Multigene family;  
 KW Glycoprotein.  
 FT SIGNAL 1 18  
 FT PROPEP 19 54  
 FT CHAIN 55 702  
 FT  
 FT PROPEP 703 946  
 FT DOMAIN 308 468  
 FT DISULFID 261 264  
 FT DISULFID 650 651  
 FT CARBOHYD 118 118  
 FT  
 FT CARBOHYD 666 666  
 FT  
 FT CARBOHYD 671 671  
 FT CARBOHYD 673 673  
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 FT CARBOHYD 675 675  
 FT  
 FT CARBOHYD 691 691  
 FT  
 FT MOD\_RES 282 282  
 FT MOD\_RES 283 283  
 FT BINDING 702 702  
 FT CONFLICT 374 374  
 FT CONFLICT 674 674  
 FT CONFLICT 705 705  
 FT CONFLICT 729 729  
 FT CONFLICT 731 731  
 FT SEQUENCE 946 AA; 106436 MW; 1478CF3EBF3BA776 CRC64;

Query Match 2.8%; Score 155.5; DB 1; Length 946;  
 Best Local Similarity 19.8%; Pred. No. 0.12;  
 Matches 134; Conservative 106; Mismatches 249; Indels 189; Gaps 31;  
 33 IKSWDKQEDLVTLAKASGVNOLVIEKYQDLYTEPPNNAQV-----80  
 26 LSEFVD--YEDLVE--APGKFLVAENRRYQSL--PESEEMEEVDQVTLYSKYV 77  
 81 -----IAARIEKLRSKALVRLALEAKVQAQAHQWREDFASN-----120  
 78 GSTITSRMAKTIQSKVNNNSQPONVYFDVQIPGA-----FISNFMVVDGKTFSS 131  
 121 -----EYVYVNAK-----DDLPEKNDSE--PGSORIKPFVIDANQGRQ 158  
 132 IREKTVGALVYAQARAKGTAGLVRSSALDMENFTEVVLVIGAKVQFELHYQEKMRKL 191  
 159 ISYQH-----AAVHITDIEGSTIVLNLNMTSALD-----EYFKNRRE-----199  
 192 GSYEHRIYLQPRHLAKHLEVDVWVLEPQGLRFLVDPDFEGHFDGCVPIYSGQAKAHYSF 251  
 200 DESLQVFGSATGLARYYPASPVWVNSRTPNKKIDLYVRRP-----WYIQGA 249  
 252 KPTVAQ-----RIPCSC--ETAVDGLVYLVDYKREKAGELEVNGYFVHFFA 300  
 250 S-----PKDMLLDVSGSVSGTLIKLIRTSYSEMLETLSDDDPVNNAFNSNADQVSC 303  
 301 PDMLDIPKRIILEVIDVSSMGVKKQYVEAMKTLIDDLRAEDHSVIDFNQNR--TW 358  
 304 FOHLVQANRNKKVLDVANNITAKGITDYKKGF--SPAFQOLLNYSNRANCKIIML 360  
 359 RNDLISRTQVADAKRYIEKTOPSGGTINENMLRALFIILNEANNLGLDNRNSLIIL 418  
 361 FTDG-----GEPAQEIFARYKNDKRVVFTFSVGQ--HNYDRGPIQMACENGK-----408  
 419 VSDGDPVYGLKSLQKNVKNENIQNISLPSIGMGFDVYDLKRLSNENNGIAQRIYQ 478  
 409 -----YYEEL--PSIGAIRIN--TOEYIDLVL-----GRPVNLG--DKAQ 443  
 479 NODTSQLKRFYQVSTPLLRNQVFNYPHTSVTDVQNNFNHFGSGSEIVVAGKFDPAK- 537  
 444 VQMTNVLDALELGLVITGTLVPFNITGQENENTKNOILIGVMGVDSLEDI--RR 499  
 538 -----LDIE--SVYTA-----TSANTQVLETLAQMDLDQFLSKDKH 574  
 500 LTRPFTLCPGYGFALDPNGVYLHPNLOPKNKSQEPVTLDFLDALENDIVETIRNKA 559  
 575 ADPFTLR-KIMAYLTLIN--QLAERSLAP--TAAAKRRITRSLQMSLDHIVTPPLTSLV 629  
 560 IDSGSGKTRFTLVKSOD 577  
 630 IENEAGDERMLADAPPOD 647  
 RESULT 14  
 ATX1\_PLAFA  
 ID ATX1\_PLAFA STANDARD: PRT; 1956 AA.  
 AC 004936;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Probable cation-transporting ATPase 1 (EC 3.6.3.-).  
 OS Plasmodium falciparum.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 NCBI\_TaxID=5833;  
 RN NCBI [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=T9/96;  
 RX MEDLINE-9313070: PubMed-8421054;  
 RA Krishna S., Cowan G., Meade J.C., Wells R.A., Stringer J.R.,  
 RA Rodson K.J.:  
 RT "A family of cation ATPase-like molecules from Plasmodium  
 RT falciparum.";

RL J. Cell Biol. 120:385-398(1993).  
 CC -1- CATALYTIC ACTIVITY: ATP + H<sub>2</sub>O = ADP + phosphate.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2  
 CC ATPASES) SUBFAMILY V.  
 CC  
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 CC  
 DR EMBL, X65738; CAA46646.1; -  
 DR InterPro: IPR001757; ATPase\_E1-E2.  
 DR Pfam: PF00122; E1-E2\_ATPase; 1.  
 DR PROSITE: PS00154; ATPASE\_E1\_E2; 1.  
 KW Hydrolyase; Transmembrane; Phosphorylation; Magnesium; ATP-binding.  
 FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).  
 FT TRANSHEM 36 58  
 FT DOMAIN 59 61 EXTRACELLULAR (POTENTIAL).  
 FT TRANSHEM 62 80  
 FT DOMAIN 81 407 POTENTIAL.  
 FT TRANSHEM 408 427 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 428 440 POTENTIAL.  
 FT TRANSHEM 441 462 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 463 1818 POTENTIAL.  
 FT TRANSHEM 1819 1837 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 1838 1845 EXTRACELLULAR (POTENTIAL).  
 FT TRANSHEM 1846 1863 POTENTIAL.  
 FT DOMAIN 1864 1881 EXTRACELLULAR (POTENTIAL).  
 FT TRANSHEM 1882 1905 POTENTIAL.  
 FT DOMAIN 1906 1928 POTENTIAL.  
 FT TRANSHEM 1929 1952 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 1953 1956 CYTOPLASMIC (POTENTIAL).  
 FT MOD\_RRS 496 496 PHOSPHORYLATION (BY SIMILARITY).  
 FT METAL 1760 1760 MAGNESIUM (BY SIMILARITY).  
 FT METAL 1764 1764 MAGNESIUM (BY SIMILARITY).  
 FT DOMAIN 246 251 POLY-ASN.  
 FT DOMAIN 252 256 POLY-LYS.  
 FT DOMAIN 937 941 POLY-ASN.  
 FT DOMAIN 1344 1347 POLY-LYS.  
 FT DOMAIN 1363 1372 POLY-ASN.  
 FT DOMAIN 1680 1684 POLY-ASN.  
 SQ SEQUENCE 1956 AA; 230285 MW; AE708AAE9009335 CRC64;  
 Query Match 2.7%; Score 155; DB 1; Length 1956;  
 Best Local Similarity 17.2%; Pred. No. 0.37;  
 Matches 181; Conservative 141; Mismatches 357; Indels 372; Gaps 46;

Db 318 YTDCLIKKVEAISOKKII-----YSNED 342  
 QY IOWMACKENGGYEIPISGAIIRINTOEYLDLPRVLAG-----DAKQV 444  
 Db 343 INKMYLGGTYVLSLVNINIKIKNNKENRILGL-YIKGFIITTKGIVNNIYHKKEL 401  
 QY 445 QMTWVYDALELGLVITGLPVP---NITGONENKTNLKLILG----- 486  
 Db 402 NLINDSKYKFLII-LIYALFVSFILLIYITLSNNEYT---NHIIKCLDITDAIPALPT 457  
 QY 487 --YMGVDSLEDIKRLPRFTLCPNGYFA-----IDPNGVYLLHPNQ---PKNP 532  
 Db 458 TLVYGISIALSRLLKFKFSISCLCPHKINTAGQINTWFPDVG-TLENNLQFGLITQNK 516  
 QY 533 KSOEPTVLDLDALELNDIKVLEIRNKIDEGSEKTEFRLVYSODERYIDKNRYTWTP 592  
 Db 517 KNNKMLS-DFIHK-----EMTESYHISKDNMHNK----- 549  
 QY 593 VNGTDYSIALVLPYSGFYIKAKIETITQASKKKKMD-----SETLKPQNE 642  
 Db 550 -----SISEYIKDKMKMLHTSSK-KKSITERSNFLVOTIKSCLLDHYIK 596  
 QY 643 ESGYPIAPRDYCNLDKISDN-TEFLN-----FNEF-IDRKT PNNPSCDTLIRV 693  
 Db 597 EKKEEYTNNTYCNLDHINDSCSSYLLNSFTKDAVCEYINIDH-----LCD---INKK 647  
 QY 694 LIDAGTNELVQNYWKSQKINIGVAKRYVVDGITRVYPKAGENWOENPETYEDSPFK 753  
 Db 648 NMDINSKNELMGYSKNEMLGKTIKNEML-----GKXSK 681  
 QY 754 RSLDNDNVFTAPYFNKSGPAGYSGIYVSKAVEIYIOGKLKPAVVG-----IKIDVN 807  
 Db 682 NEL-----MKYSKNEMLGYSKNEMLGYSKNEMLGYSKNEMLGYSKNEMLGYSK 734  
 QY 808 STENFTKTSIND-PCAGVCDCKRNSDMCV-----ILDDGFLMANHDDYTNOIGRF 862  
 Db 735 IYHMCNDNDYNDYPCD---YNCNMCNDTYHRLYEHININKDMSFNIPEKKSVNISEH 791  
 QY 863 -----FGEIDPSLMRHLVNTSYAF-----NKSY 886  
 Db 792 IKINYPLEFALACHTLSKVNKKIMGVLEIMFNFTNCMLINNNSFIKERKKKCSY 851  
 QY 887 DYOSVCEPAPKQAGAGHRSAYVPSIADILHIGWATTAAMSIILOQFLSLTPRLLEAV 946  
 Db 852 DFQKI---DGDKNIGANDERCHLN-----NLVSYNIIKRF----- 884  
 QY 947 EMEDDFTASLSKSCITBQYFFDNDKS 977  
 Db 885 -----EFQSRLOKMSVIVKST-YGNNDNDN 909  
 RESULT 15  
 ITH2\_MESAU  
 AC P97279 STANDARD; PRT; 946 AA.  
 ID P97279  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUN-1998 (Rel. 36, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy  
 DE chain H2) (H02).  
 GN ITH2.  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Cricetinae;  
 OC Mesocricetus.  
 OX NCBI\_TaxID=10036;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=97420688; PubMed=9276673;  
 RA Nakatani T., Suzuki Y., Yamamoto T., Sinohara H.,  
 RT "Molecular cloning and sequencing of cDNAs encoding three heavy-chain  
 precursors of the inter-alpha-trypsin inhibitor in Syrian hamster";



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GenCore version 5.1.3  
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## OM protein - protein search, using sw model

Run on: February 10, 2003, 14:13:54 ; Search time 20.3466 Seconds  
(Without alignments)  
5050.861 Million cell updates/sec

Title: US-10-090-827-9

Perfect score: 5650  
Sequence: 1 MAAGCLALTLTLFQSLHIG.....NNALEDYDTCGVSHHHHHH 1069

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: PIR-73:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	5532	97.9	1091	2 JH0565	calcium channel al
2	5420	95.9	1091	2 A44147	calcium channel pr
3	5405.5	95.7	1106	1 CHBA2	calcium channel pr
4	1145.5	20.3	1091	2 T30256	calcium channel al
5	611	10.8	734	2 S44617	C50C3.11 protein -
6	587	10.4	1148	2 T18770	probable calcium c
7	196.5	3.4	886	2 S54355	inter-alpha-trypsi
8	190.5	3.3	1450	2 C86880	hypothetical prote
9	188	3.3	885	2 S30350	inter-alpha-trypsi
10	170.5	3.0	1819	2 D97033	uncharacterized pr
11	168.5	3.0	575	2 D64998	hypothetical prote
12	166	2.9	889	2 JC5576	inter-alpha-trypsi
13	165	2.9	459	2 F64688	protease (PC 3.4
14	160.5	2.8	420	2 S76691	hypothetical prote
15	160.5	2.8	2364	2 I40884	cytotoxin L - Clos
16	159	2.8	932	2 JC5953	inter-alpha-inhibi
17	158.5	2.8	918	2 E90542	lipoprotein (impor
18	155.5	2.8	946	1 TRH2	inter-alpha-trypsi
19	155	2.7	1315	2 T28679	fibronogen-binding
20	154	2.7	1884	2 A44396	P-type cation tran
21	153.5	2.7	688	2 D96930	methyl-accepting c
22	153.5	2.7	1426	2 A99580	hypothetical prote
23	153	2.7	946	2 JC5575	inter-alpha-trypsi
24	152.5	2.7	5005	2 F82884	hypothetical prote
25	152	2.7	1516	2 E71619	RAU2 endonuclease
26	150.5	2.7	680	2 A97331	membrane associate
27	149.5	2.6	654	2 A69656	methyl-accepting c
28	149.5	2.6	921	2 JC4625	inter-alpha-trypsi
29	149.5	2.6	926	2 D86897	hypothetical prote

30	149.5	2.6	3216	2 C90538	hypothetical prote
31	148.5	2.6	1285	2 B72420	hypothetical prote
32	148	2.6	2706	2 T28155	variant-specific s
33	147.5	2.6	689	2 F84811	probable retrolem
34	147.5	2.6	1237	2 AC1583	internalin protein
35	147	2.6	1087	1 S41797	cellulose 1,4-beta
36	146.5	2.6	676	2 T47637	hypothetical prote
37	146	2.6	1027	2 B90527	atp-binding protei
38	145	2.6	1385	2 D89824	hypothetical prote
39	145	2.6	1599	2 S22737	glucosyltransferas
40	145	2.6	1864	2 T18485	hypothetical prote
41	145	2.6	2401	2 T28676	thorpy protein -
42	144.5	2.6	929	2 I51027	type XII collagen
43	144	2.5	930	2 JX0368	inter-alpha-trypsi
44	144	2.5	1091	2 S33850	fibronectin-binding
45	143.5	2.5	1243	2 S60138	sex factor aggrega

## ALIGNMENTS

## RESULT 1

JH0565  
calcium channel alpha-2b chain precursor - human

C:Species: Homo sapiens (man)

C>Date: 30-Jun-1992 #sequence-revision 30-Jun-1992 #text-change 20-Aug-1999

C:Accession: JH0565

R:Williams, M.E.; Feldman, D.H.; McCue, A.F.; Brenner, R.; Vellicelbl, G.; Ellis, S.B.

Neuron 8, 71-84, 1992

A:Title: Structure and functional expression of alpha1, alpha2, and beta subunits of

A:Reference number: JH0564; PMID:92110010; PMID:1309651

A:Accession: JH0565

A:Molecule type: mRNA

A:Residues: 1-1091 <WIL>

A:Cross-references: GB:M76559; NID:q179761; PIDN:AA51903.1; PID:q179762

A:Experimental source: basal ganglia

A:Note: several conflicts are found between GenBank submission, authors' translation

C:Comment: This protein is a subunit of the voltage dependent calcium channel.

C:Superfamily: calcium channel alpha-2 chain

C:Keywords: glycoprotein; phosphoprotein

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-1067/Product: calcium channel alpha-2b chain #status predicted <CAL>

F:32-268/326,539,635,1087/Binding site: phosphate (Thr) (covalent) (by protein kinase

F:91,142,250,625,817/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #

F:92,136,184,324,348,468,475,585,594,663,682,769,812,876,883,973,986/Binding site: ca

F:833/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status pre

F:833/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status pre

Query Match 97.9%: Score 5532; DB 2; Length 1091;

Best local similarity 98.7%: Pred. No. 0;

Matches 1049; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY	1	MAAGCLALTLTLFQSLHIGSSQEPSPSAVTIKSWDKMOEDVTLAKTAGVNOAVDI 60	
DB	1	MAAGCLALTLTLFQSLHIGSSQEPSPSAVTIKSWDKMOEDVTLAKTAGVNOAVDI 60	
QY	61	YKRYDDLVTEPNNAROLVETIAARDIEKLNSRAVSLALDEAKVQAHOHREDPASN 120	
DB	61	YKRYDDLVTEPNNAROLVETIAARDIEKLNSRAVSLALDEAKVQAHOHREDPASN 120	
QY	121	EVVYNNAKDDLPKNDSEPSQSRIKPFVIDANFGROISYQHAHVHTIDYEGSTIVL 180	
DB	121	EVVYNNAKDDLPKNDSEPSQSRIKPFVIDANFGROISYQHAHVHTIDYEGSTIVL 180	
QY	181	NEIWNMTSALDEVFKKRNREDEPSLIMQVFGSATGLARYYPASFWVDSNRTPKKIDLYVRR 240	
DB	181	NEIWNMTSALDEVFKKRNREDEPSLIMQVFGSATGLARYYPASFWVDSNRTPKKIDLYVRR 240	
QY	241	RMWYIQAASPKDMLIVDVSGVSGITLKITRSVSEMLFTISDDPVVNAFSPNSNOD 300	
DB	241	RMWYIQAASPKDMLIVDVSGVSGITLKITRSVSEMLFTISDDPVVNAFSPNSNOD 300	
QY	301	VSCFOHLVQANVRNKKVLKDAVANNTAKGIDYDKGFSFAEQLLNNVNSRANCKIIML 360	

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|||||
Db 301 VSCFOHLVQANVRNKKVLDKAVANNITAKGTTDYKKGFSAFEOQLLVNVRANCKNTIML 360
QY 361 FTGGEERAEIIFAKYTKKDKKRVVFESYGOHNYDRGPLOMMACENKGYEELPSIGAIR 420
Db 361 FTGGEERAEIIFAKYTKKDKKRVVFESYGOHNYDRGPLOMMACENKGYEELPSIGAIR 420
QY 421 INTQEVLDVIGRPMVLADGAKAKOVMTNYYLDALDELGLVITGTLPEVNTGONENKTNLK 480
Db 421 INTQEVLDVIGRPMVLADGAKAKOVMTNYYLDALDELGLVITGTLPEVNTGONENKTNLK 480
QY 481 NOLILVGVYDVSLIEDIKRLTPFTLCPNGYFPAIDPNCYVLLHPMLQPKNPKSOEPVTL 540
Db 481 NOLILVGVYDVSLIEDIKRLTPFTLCPNGYFPAIDPNCYVLLHPMLQPKNPKSOEPVTL 540
QY 541 DFLDAELNDIKVEIKRNMKIDEGSEKTRTLVKSODERYIKGNNTYTWTPVNGTDSL 600
Db 541 DFLDAELNDIKVEIKRNMKIDEGSEKTRTLVKSODERYIKGNNTYTWTPVNGTDSL 600
QY 601 ALVLPYTSFYIYIAKIEETITQARSKKGMKDESEFLKPDNFEESGYTFIAPRDYCNDLKI 660
Db 601 ALVLPYTSFYIYIAKIEETITQARSKKGMKDESEFLKPDNFEESGYTFIAPRDYCNDLKI 660
QY 661 SDNTEFLNFEEDIDRKTTPNPNPSCNTDLINRVLLDAGFTNELVQNYMSKOKNIGYVAKR 720
Db 661 SDNTEFLNFEEDIDRKTTPNPNPSCNTDLINRVLLDAGFTNELVQNYMSKOKNIGYVAKR 720
QY 721 FVYTDGIGTRVYPKEAGENMOENPETEYDSFYKRSIDNDNRYFAPYFNKSGPAYESGI 780
Db 721 FVYTDGIGTRVYPKEAGENMOENPETEYDSFYKRSIDNDNRYFAPYFNKSGPAYESGI 780
QY 781 MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENTFTSTRDPCAGYVCCCKRNSDVMDCVI 840
Db 781 MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENTFTSTRDPCAGYVCCCKRNSDVMDCVI 840
QY 841 IDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRLHVNISYAFNKSXYDQSCPEGAAPKQ 900
Db 841 IDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRLHVNISYAFNKSXYDQSCPEGAAPKQ 900
QY 901 GAGHRSATVPSIADLIHIGWMTAAAMSILQOFLSTLTFPRLLAEVEMEDDFTASLSKQ 960
Db 901 GAGHRSATVPSIADLIHIGWMTAAAMSILQOFLSTLTFPRLLAEVEMEDDFTASLSKQ 960
QY 961 SCITEQOTQYFFDNDKSSFSGVLDGNCGRIFRHEKLMNTNLIFIMVESKGTCPDTRLLI 1020
Db 961 SCITEQOTQYFFDNDKSSFSGVLDGNCGRIFRHEKLMNTNLIFIMVESKGTCPDTRLLI 1020
QY 1021 QAEQTSQDPDPCDMVKQPRYRKGPVCPDNNALEDYTDGCGVS 1063
Db 1021 QAEQTSQDPDPCDMVKQPRYRKGPVCPDNNALEDYTDGCGVS 1063

RESULT 2
A44147
calcium channel protein alpha-2 chain precursor - rat
N:Alternate names: dihydropyridine-sensitive L-type
N:Contains: calcium channel alpha-2 chain
C:Species: Rattus norvegicus (Norway rat)
C:Date: 27-Jun-1994 #sequence, revision 27-Jun-1994 #text, change 20-Aug-1999
C:Accession: A44147
R:Kim, H.L.; Kim, H.; Lee, P.; King, R.G.; Chin, H.
Proc. Natl. Acad. Sci. U.S.A. 89, 3251-3255, 1992
A:Title: Rat brain expresses an alternatively spliced form of the dihydropyridine-sensit
A:Reference number: A44147; MUID:92228762; PMID:114363
A:Accession: A44147
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1091 <KIM>
A:Cross-references: GB:M86621; NID:q203954; PIDN:AAAA1088.1; PID:q203955
C:Superfamily: calcium channel alpha-2 chain
C:Keywords: calcium, glycoprotein, ion channel, transmembrane protein

Query Match 95.9%; Score 5420; DB 2; Length 1091;

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Best Local Similarity 96.2%; Pred. No. 3,66-317;
Matches 1024; Conservative 23; Mismatches 15; Indels 2; Gaps 2;
|||||
QY 1 MAAGCLLALITLTFOSLLIGPSQEPFSAVYIKSWDKMOEDLVTLAKTASGVNOYDI 60
Db 1 MAAGCLLALITLTFOSLLIGPSQEPFSAVYIKSWDKMOEDLVTLAKTASGVNOYDI 60
QY 61 YEKYODLYTVEPNNARQVLEIAADIEKLSNRSKALVRLALEKVOAAHOMREDFASN 120
Db 61 YEKYODLYTVEPNNARQVLEIAADIEKLSNRSKALVRLALEKVOAAHOMREDFASN 120
QY 121 EYVYVNAKDLDPEKNDSEPSQRIKPFIDDAWFGROISQAAVHLPIDYEGSTIVL 180
Db 121 EYVYVNAKDLDPEKNDSEPSQRIKPFIDDAWFGROISQAAVHLPIDYEGSTIVL 180
QY 181 NELMWTSLADEVFRKNEEDPSLLMOYFGSATGLARYPPASPWVNDSPRTNKTIDLYDVR 240
Db 181 NELMWTSLADEVFRKNEEDPSLLMOYFGSATGLARYPPASPWVNDSPRTNKTIDLYDVR 240
QY 241 RPYITOGAASPKDMLILVDVSGYSGLTLKILRTSVSEMLETISDDDFVAVASFNNAOD 300
Db 241 RPYITOGAASPKDMLILVDVSGYSGLTLKILRTSVSEMLETISDDDFVAVASFNNAOD 300
QY 301 VSCFOHLVQANVRNKKVLDKAVANNITAKGTTDYKKGFSAFEOQLLVNVRANCKNTIML 360
Db 301 VSCFOHLVQANVRNKKVLDKAVANNITAKGTTDYKKGFSAFEOQLLVNVRANCKNTIML 360
QY 361 FTGGEERAEIIFAKYTKKDKKRVVFESYGOHNYDRGPLOMMACENKGYEELPSIGAIR 420
Db 361 FTGGEERAEIIFAKYTKKDKKRVVFESYGOHNYDRGPLOMMACENKGYEELPSIGAIR 420
QY 421 INTQEVLDVIGRPMVLADGAKAKOVMTNYYLDALDELGLVITGTLPEVNTGONENKTNLK 480
Db 421 INTQEVLDVIGRPMVLADGAKAKOVMTNYYLDALDELGLVITGTLPEVNTGONENKTNLK 480
QY 481 NOLILVGVYDVSLIEDIKRLTPFTLCPNGYFPAIDPNCYVLLHPMLQPKNPKSOEPVTL 540
Db 481 NOLILVGVYDVSLIEDIKRLTPFTLCPNGYFPAIDPNCYVLLHPMLQPKNPKSOEPVTL 540
QY 541 DFLDAELNDIKVEIKRNMKIDEGSEKTRTLVKSODERYIKGNNTYTWTPVNGTDSL 600
Db 541 DFLDAELNDIKVEIKRNMKIDEGSEKTRTLVKSODERYIKGNNTYTWTPVNGTDSL 600
QY 600 IALVLPYTSFYIYIAKIEETITQARSKKGMKDESEFLKPDNFEESGYTFIAPRDYCNDLK 660
Db 600 IALVLPYTSFYIYIAKIEETITQARSKKGMKDESEFLKPDNFEESGYTFIAPRDYCNDLK 660
QY 660 ISDNTTEFLNFEEDIDRKTTPNPNPSCNTDLINRVLLDAGFTNELVQNYMSKOKNIGYVAKR 720
Db 660 ISDNTTEFLNFEEDIDRKTTPNPNPSCNTDLINRVLLDAGFTNELVQNYMSKOKNIGYVAKR 720
QY 720 RPYITOGAASPKDMLILVDVSGYSGLTLKILRTSVSEMLETISDDDFVAVASFNNAOD 779
Db 720 RPYITOGAASPKDMLILVDVSGYSGLTLKILRTSVSEMLETISDDDFVAVASFNNAOD 779
QY 780 IMVSKAVEIYIOGKLLKPAVVGIKIDVNSWIENTFTSTRDPCAGYVCCCKRNSDVMDCVI 839
Db 780 IMVSKAVEIYIOGKLLKPAVVGIKIDVNSWIENTFTSTRDPCAGYVCCCKRNSDVMDCVI 839
QY 840 IIDDGFLLMANHDDYTNOIGRFFGEIDPSLMRLHVNISYAFNKSXYDQSCPEGAAPK 899
Db 840 IIDDGFLLMANHDDYTNOIGRFFGEIDPSLMRLHVNISYAFNKSXYDQSCPEGAAPK 899
QY 900 GAGHRSATVPSIADLIHIGWMTAAAMSILQOFLSTLTFPRLLAEVEMEDDFTASLSK 959
Db 900 GAGHRSATVPSIADLIHIGWMTAAAMSILQOFLSTLTFPRLLAEVEMEDDFTASLSK 959
QY 960 QSCITEQOTQYFFDNDKSSFSGVLDGNCGRIFRHEKLMNTNLIFIMVESKGTCPDTRLLI 1019
Db 960 QSCITEQOTQYFFDNDKSSFSGVLDGNCGRIFRHEKLMNTNLIFIMVESKGTCPDTRLLI 1019
QY 1020 IQAEQTSQDPDPCDMVKQPRYRKGPVCPDNNALEDYTDGCGVS 1063
Db 1020 IQAEQTSQDPDPCDMVKQPRYRKGPVCPDNNALEDYTDGCGVS 1063

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Db      14 ASADLA--TALLYALGDVVRSEGOIPLSV--VKIMASAFGEIKSIKAKYSGSOLLQKKY 71
Qy      63 KYODLYVEPNARQLEIARQIEKLLSNRSKALVRLAEKVYQAQAHOMREDFASNEV 122
Db      72 EYEDVAIEERIDGLOLVAKKLAKIMEFHKKEAVRLVAAEBAHLKHEFDAL--QY 128
Qy      123 VYNAK--DDLDPEKNDSEPSQRIKIPVETIDANFGROISYOHAAVHLPDIYEGSTVL 180
Db      129 EYFNAVLINERDKGNFLGKEFT--LAPNDHFNPLPVNLSLSDVQVFNMYNKKDPAIV 186
Qy      181 NELMTSALDEVEKKNNEEDPSLLMOYFGSATGLARYPASPWVDSRTNKKIDLYVR 240
Db      187 NGVWSSSLNKVFVNDPDRPSLLMOYFGSAKGFRRQYPLKWPDE--NGVIAFPCRN 243
Qy      241 RPYTIOGASPKDMLIVDVSAGSVGTLKIRTSVSEMLETSDDEFFVAVSNAQD 300
Db      244 RKMTIOATSPKDVYLLIVDVSAGSKGLRLTAKOTVSSIIDTLDDDFENIITYNEFLAY 303
Qy      301 VS-CFO-HLVOANYRNKRVLKDAVANNITANGITDYKKGSFAEQLNLYNVRAN--CNK 356
Db      304 VEPCLNGTIVQADRTNKEHREHLDFAGIGMLDIALNBAFNLISDFNHTGGGSIQ 363
Qy      357 IIMLPTGGERRAOETRAKYN-KKKKRVTFPSYGHNTRGPIQWACENKGYEYIP 415
Db      364 AIMLITIGADVDTYITIAKYNMPPDRKVRIFTYLLIGREAFADNLKMAKANKGFFTOIST 423
Qy      416 IGAIRIMOXYEYLDVIGRPMYLAGDAKAOYOMTNYLD-----ALEIGLY--TGT 464
Db      424 LADVQENVMEIHLVSRKRY--DQENHYVTEAYIDSTLPOAKLADDOGLVMTVTAM 481
Qy      465 PVFNITGONENKTNLKNOLILGVGVDSLEDIKRLPRFLCPNGYFPAIDPNGVYLH 524
Db      482 PVFS-----KONETRSKG--ILGVGVDTVPYKELKLTIPKTKLIGHYAFATINNGYLTH 536
Qy      525 PNLOP---KNPKSOEP--VITDPIADLENDIKYEIRNKALIDSGSKTRTLVKSODER 579
Db      537 PELRPLYEKGKRRKPKYSSVDSEVMEQEDV-LRNAAVNRKTKG--FSMEVK---K 589
Qy      580 YIDGKNT-----YTWPVNGDYSLALVLP--YSFYIYIKAK--IEETIOAKSKGKM 630
Db      590 TYDGKRVLWNTNYTDTDKGTFSLGVALSRGHGKTFRRGNTIREGL----- 639
Qy      631 KDSETLKPDNEESGYFIAPRDYCN-DLKISDNTEFLLNFNEEIDRKTNNPNSCNTLD 669
Db      640 -----HDLHEDVSLADEMSYCNLDLPEHRHLSQLDAIKLYLKGKPE--LLQCDKEL 690
Qy      690 INRYLLDAGFTNELVQWYMS-----KOKNKGKARFVYTDGITRVYP----- 733
Db      691 IOEVLFPDA-VVSAPLEAWTSLALNKSNSDKGEVAFGLTGLSKRIINLFPVGAEOULTNQ 749
Qy      734 --KEAGENMOENPEYEDSEFYKRSLDN--DNYVYFARY-----FNKSGPAGAYESGIMVSKA 785
Db      750 DFLAAGKKNENFNDHPRMWRRAEQIAGSPYSIFPSFGTVKNS-----NVYVASTS 803
Qy      786 VEYIOGKLKPAVAVGIKIDVNSWIEFNFTTSTIRDPACAGVCDCKRNSDVMDVCIILDDG 845
Db      804 IOLDERKSPVYAAVGIOMKLEFFQKRFWASRQASLDKCSISCDDEFTVNCYLIDNNG 863
Qy      846 FLTMANDDYTNQIGREFGEIDPSLMHILVNSIYAFNKNKYDVOSVECPGAAPROGAGR 905
Db      864 FILVS--EDYT-QTGDFEGEGAVNMKLLTMSFKRITLYDYOAMCR--ANESSDSA 917
Qy      906 SAYVPSIADILHIGMWATAAASILQOFLSLTFPRLLAEVEMDEDFATSLSK-----Q 960
Db      918 HGLLDPRYKAF-----SAAKWIMTELVFLVE--NCSMWHSMITAKAKKIKOTLE 967
Qy      961 SCITEQIYFPDNDKSESGVLDGCGNSRIFHEKLMNTULIFIVESKTCPCDT--R 1017
Db      968 PCDEYFAFVSERTIKETGTGACEDSKSFVIOIPSSNLFVWVDS--SCICESVAPI 1025
Qy      1018 LLLIAEQTSQDPDPCDMVKQPRYRKRGDVCENNALLDYIDCGVS 1063

```

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Db      1026 TWAPIEIRYNESLKCERLKAQKIRRRPESCHGFHEENARECGAS 1071
RESULT 5
S44617
C50C3.11 protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 30-Jun-2001
C:Accession: S44617
R:Ravello, A.D.
submitted to the EMBL Data Library, May 1993
A:Description: Sequence of the C. elegans cosmid C50C3.
A:Reference number: S44627
A:Accession: S44617
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-734 <FAV>
A:Cross-references: EMBL:U14433; NID:g289649; PID:g289650
C:Genetics:
A:Introns: 24/2; 87/3; 175/1; 259/1; 290/3; 346/3; 460/3; 538/3

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Query Match      10.8%; Score 611; DB 2; Length 734;
Best Local Similarity 26.5%; Pred. No. 9.7e-29;
Matches 179; Conservative 127; Mismatches 261; Indels 108; Gaps 19;

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Qy      47 LAKTASGVNQLVDIYEKYODLYVEPNARQLEIARQIEKLLSNRSKAL--VALALEA 104
Db      36 MKETFSKIHETILKQNTYKELVEEQQFOPRAELKSKHRIEDLYLVRSQFAYKAKISLEA 95
Qy      105 EKVQAQAHQREDFASNEVYVYNAKDLDPEK--NDSEPSQRIK-----VFIDANF-G 156
Db      96 RSVRNDSTVNDQSKSFIFMSAKQNDGTTIYESNHLGKRLKLVETKSFNLTQANFYT 155
Qy      157 ROISYQAAVHIPTDIEGSTIVLELMTSALDEVEKKNREEDPSLLMOYFGSATGLAR 216
Db      156 LPTSSVSAVHIPTLYDNEEDLKRKID-SDIDAVYIKRNETYDOLFOLPESAGATMR 214
Qy      217 YYPASFWV--DNSRTPNKIDLYVRRRPWYIOGAAPKMLILVDVSGVSGITLKLIFTS 275
Db      215 YYPASFWMDNQ--DEHLDLFCORNTEMYINSATNSKNVLLIMLDMSGMLGQRYEVAKOT 272
Qy      276 VSMLETLSDDDPYNVAVASNSNA-----QVYSCPHLYQAVNRRKKVILKAVNNTAKGTTD 332
Db      273 TEALLETLSHNDYFNIMTFSKMTFLDGCNGTNGLLQATMRKKALRRKMDYOSSEGA 332
Qy      333 YKGFSEFAEQLLNTN-----VSRANCKIIMLFTDGEERAOETFAKYNKKDKYRVTF 387
Db      333 YERALPLAESVLLDINGGDNRRGACENVIMLTDGAPNAKRTIPDMYTNADKRYRVTF 392
Qy      388 SVGQHNDRGPIQWACENKGYEYIPISTIGAIRINTOYL---DVLGRPMVLAGDKAKQ 443
Db      393 LVGDEAIDENEYEMACNRRGYMVHANADVDEKIHYYIRMSHYVRHKESGOLS-- 450
Qy      444 VQMTNYLLDALDELGL--VITGLLPFNITGONENKT----- 478
Db      451 -WMTGYRRELYLPRPELFAEPVLPITNOSFAVNMWASRRKIRLOKSEARSMEYTVTSY 509
Qy      479 --LKNOLILGVGVDSLEDIKRLTPREFLCPNGYFALDPNGVYLHPNLOPKNP----- 532
Db      510 PVIYNTEFPVAAVNPILPTEVAKSHIPANIGSKSFEMLDQNGFMTGRPOLRIPDPFRKY 569
Qy      533 KQOEPLYLDFLD-----ALELNDIKVEIRNKMIDGE 563
Db      570 HKQNYNMMDLLELEVQONVRSQSAVSDLVCESGANVACEVDLRKAVRKMIIDCD 629
Qy      564 SGKGTFRILYKODEXY-----IDK---GNRTYTWIPVNTDVSIALVLPYTSFYIYAKI 616
Db      630 NSD-----VOOLDVLYATNELLDRVYPTGTNYAECINHANVIGLAVAKGDYRVVRK- 682
Qy      617 EETIOARSKKGMK 631
Db      683 -----OKKTFDGRVK 692

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Db 174 QL-VRH--FEIDAHIEPQGI-----SMLD-----AEASFITNDLGSALTRKFS 215  
 QY 213 GLAAYVSPWVNSRT-PNKID-----LYDVRBP-----WYI-----QG- 247  
 Db 216 GKKGHSFKSLDQGRSCPTDLSLNGDFTIYDVNRKESPVQVYNGVFVFEAPQGL 275  
 QY 248 AASKKMLIIVYSGVSGITLKLRTSVSEMLETSDDFVAVASNSAQCFO-H 306  
 Db 276 PVYFKNIYFVIDVSGSGRRIQOTREALKILDDVEDDYLNFIEST--DYTWKOH 332  
 QY 307 LVOANVNRKVLDAVNITAKGITYKKGFSAFQOLNANVRAN-----CNKIML 360  
 Db 333 LVQATPRLKAEATPVKNIHDSMTNINDGLKIEML--NKARDHVPENKSTIIM 389  
 QY 361 FTDC---GEBAQEIFAKYN--DKRVYTFPSVQOHYDRGPIDMACENKGYEIP 414  
 Db 390 LITGDANTGSRPEKIOENVRNAGKFPVLYNGFG--NMLNMFETLLENHGLARKY 448  
 QY 415 SIGAIFINQEVLDVGRPVVLAGDAKOVQNTVYLDLLEGLVITGTPVFNITGONE 474  
 Db 449 EDSANLQIQGFEEVYANPL-----TNVEVEPENA-----LIDLTRNGY 489  
 QY 475 NKTNLNOLIGVGVDSLEDIKLTPRTLCPNGYFAIDPNGVLLHPMLQPKRPS 534  
 Db 490 PHEPDSSEIYVAGRLVDRMND-----PKADYKGHGALN-----DLTF 527  
 QY 535 QEVYITDFDALENDIKVEIRNKMIDGSEK--TFRTLVKSODERYIDKGNRTYTWP 592  
 Db 528 TEEDVMEENDALK-----EGGYIFGDYIERLMAVYLIIEQLERKKADEKENT- 579  
 QY 593 VNGTDSLAL--LYLPTYSFYIKAKIEETIQARSKGKMKSER-----LKPDNEBSG 645  
 Db 580 AEMDLSTLKHHTYPLTSNVYTRPEDNEQISADNAGEARAEITMSFLTQOSSSP 639  
 QY 646 YTFIAPRDYCNLDKISDNTEFLNFEIRDKTPNNSCNTDLNRYLDAGFTNEIYO 705  
 Db 640 YYYV-----DCDPRFIQI-----PKNDISCFENIDKRGVYLRILQ 676  
 QY 706 NYWSQKNIKGYKARFVYTDGKITVYPRKAGEENQENPEYEDSFYRSLDNDNYFTA 765  
 Db 677 D-----PVT--GIT--VTGQIIGD-----KRS--NASSRTGK 702  
 QY 766 PYENKSGPVRSGIMVSKAVEIYQKILKRAVYGIKIDVNSWIENTKISINPCGP 825  
 Db 703 TYFGKLGITNAMDRVEVTEKILG-----TGAELSTFPMIDYTVTQ-----TGL 750  
 QY 826 VQDCRNSDVADCVILDYG-GEFLMAN-----HDDYTNQIGRFEGLDPSIMRHLVN 876  
 Db 751 SVTINRKKNMV--VSFGGISFVILHQQVMKKHVNQDFLG-----FYVDSSHMSAQTH 803  
 QY 877 ISVYAFNKSVDYQSY-CEPGAAP 898  
 Db 804 GILGQFPQPPDPKVGIRGSDP 826  
 RESULT 8  
 C86880  
 hypothetical protein yvcc [imported] - lactococcus lactis subsp. lactis (strain IL1403)  
 C:Species: Lactococcus lactis subsp. lactis  
 C:Date: 23-Mar-2001 #sequence: revision 23-Mar-2001 #text: change 03-Aug-2001  
 C:Accession: C86880  
 R:Biological, A: Wincker, P.; Mauger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrlich  
 Genome Res. 11, 731-753, 2001  
 A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss  
 A:Reference number: A86625; MUID:2125186; PMID:11337471  
 A:Accession: C86880  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1450 <STO>  
 A:Cross-references: GB:AE005176; PID:912725093; PIDN:AAK06141.1; GSPDB:GN00146  
 A:Experimental source: strain IL1403  
 A:Genetics:  
 A:Gene: yvcc

Query Match 3.4%; Score 190.5; DB 2; Length 1450;  
 Best Local Similarity 19.4%; Pred. No. 0.005;  
 Matches 203; Conservative 148; Mismatches 359; Indels 339; Gaps 51;  
 QY 37 VDKMEDLVTLAKTASVQVQVLDIYKQVQDYTPENPNAROLVETIARDIEK-----L 89  
 Db 69 IKTEDEDELKIKTFSEGNQPLEIE--NESWTLKKNNT-----IISDFEKNRGKIVL 120  
 QY 90 ISNRKALVRLAEAKVQAAHQR--EDFA-----SNRVYYNA 127  
 Db 121 RANNSISILNLEIQADALINDEQVISEDLLAKKESTIESLYTPENNKADSKDKNKT 180  
 QY 128 KQDLDPEKNDSEPGQRKRP--VFIDANFGROI SYOHAH----- 167  
 Db 181 BEVLNNESSQEBYSQLKQDQLAFYSYNSNGIKASFNDAQYENISPEYQDETGISP 240  
 QY 188 ---IPTDYSGSTVLNLELWNTSALDEVFKKNEEDPSILMQVFGSATGLARTYSPW 223  
 Db 241 NWSWIP-----GNTTVVNHQGNPF-----SSQMDGVNSWN--GRATNLENSYIEYAG 287  
 QY 224 VDN-----SRTPKRIDY-DVRRRPWYIQAASPKMLIIVYSGVSGITLK 270  
 Db 288 VNNPVPFALKRYAKETETPGLYVYLVNRCN--VQNPTRPVQIVLYIDMSGMGAKET 344  
 QY 271 LIRTSVSEMLETSDD--DFVNV--ASFNSNADVSCFOHLYOANVRNKKVYLDK----A 321  
 Db 345 AVRCGVSDFLSTIONTAYADVNVGVIGYSSPGNYVYAGSAGYITVPI--DKVSESSEHYKS 402  
 QY 322 VNNTA--KQITDYKGFSAFQOLNANVRANCKIIMLFDDGEBAQEIFPAKYNK 378  
 Db 403 INQALAPQSGCFPTQGLRKTEML--RQDSSDNQKMMIIMTGD--VPPFSTKIVNS 455  
 QY 379 DKYR--VFIFSVQAHYDRG--PIQ--WMAECNKGYEYI--PSIGAIRINTOE 425  
 Db 456 ASKDVNVIYQGSFASRDEBQNTSKIOSPYVYKIDNGSNIETRDMAATLGAERISQE 515  
 QY 426 YLDVGRPVYLAGD-----KAKOVQNTVYLDLLEGLVITGTPVFNITGONE 474  
 Db 516 ISEIHITGIGLNDGSLVSEYKSRSLIATITGLYODANSAN-----DITDYLK 565  
 QY 475 NKTN-----LKNOLIGVGVDSLEDIK----- 498  
 Db 566 NOANVYLSRNTTNGILDLPLGAQFEYKDYKFEITSVGSDSIDNLPQKINKEGLEISN 625  
 QY 499 -----RTPRTLCPNGYFAIDPNGVLLHPMLQPKRKSQ----- 535  
 Db 626 LINGKQDEVOIHYQVRLNETDDEFTKNYWM--NGETTLTPN--GSNDKRVNFGVPSA 681  
 QY 536 --BPVTLDFDALENDIKVEIRNKMIDG--SGEKTFRILVKSODERYIDKGNRTY 588  
 Db 682 KSSGIMLTLEKQWLANSENIPENVELLIGRRSQISSDITKTYVLEKDE----- 731  
 QY 589 TWTPVNGTDYSLAVLYPTS-----FYIKAKI-----EETIQARSKRGK 629  
 Db 732 -WR-----SOLENPKSLIGEEFYIEIKDEIYVILNSEIYDITIGEDKTTIANIEKFR 783  
 QY 630 MKDSETLKPDNEESGYTFIAPRDYCN--DLKISDNNEFL-----LNNE--FIDKKT 679  
 Db 784 LQIKTSNNDNEISSLVEYVRLKNSQGEEDKAVYNEKGEHILPDKTRLNNGEYQULHEKS 843  
 QY 680 PNN-----PSCNTD-----LINRYLDAGFTNEI--VOYMSKQKNI 714  
 Db 844 PGHSLGEPKIRKITEFENQPIIKYQGEQIALDEHNKFMISLNTINDNVEEF--RNS 899  
 QY 715 KGKARAFVYT--DQGITRYVPKRA--GENQENP-----ETVEDSEFK 753  
 Db 900 VTIIDKRAVDSEKLDCAVFNLIQIESVDDELQQLPLEITNNLLPGYALQESVSPNGY 959  
 QY 754 RSLDNDNYFTA-----PYENKSGPAGVYESGIWYKAV--EITYGGLL 795  
 Db 960 R--DDEVHFFRYKFNKSGIYALGSEIDLPFDENESG--KNGLVNREENGDLHLTLIFY 1015

QY 796 KPAVGIKIDVNSWENETKTSIRDPGAG 824  
 Db 1016 NQAVPPIQLVETDKIDDPFT-----SPLAG 1039

## RESULT 9

Inter-alpha-trypsin inhibitor heavy chain 3 precursor - human  
 S30350  
 C:Species: Homo sapiens (man)  
 C:Date: 03-May-1994 #sequence-revision 20-Feb-1995 #text-change 04-Feb-2000  
 C:Accession: S30350; S34123; S02141; D34245; A39079; S50133; B53642; A59167  
 R:Bourguignon, J.; Diarra-Mehrpour, M.; Thiberville, L.; Bost, F.; Sesboue, R.; Martin, E.  
 A>Title: Human pre-alpha-trypsin inhibitor precursor heavy chain cDNA and deduced amino-  
 A:Reference number: S30350; MUID:93215656; PMID:7661778  
 A:Accession: S30350  
 A:Molecule type: mRNA  
 A:Residues: 1-885 <BOU1>  
 A:Cross-references: EMBL:X67055; NID:9288562  
 R:Bourguignon, J.  
 Submitted to the EMBL Data Library, June 1992  
 A:Reference number: S34123  
 A:Accession: S34123  
 A:Molecule type: mRNA  
 A:Residues: 1-310, 'K', 312-343, 'R', 345-885 <BOU2>  
 A:Cross-references: EMBL:X67055; NID:9288562; PIDN:CAA47439.1; PID:9288563  
 R:Diarra-Mehrpour, M.; Bourguignon, J.; Sesboue, R.; Mattei, M.G.; Passage, E.; Saller, E.  
 A>Title: Human plasma inter-alpha-trypsin inhibitor is encoded by four genes on three ch  
 A:Reference number: S02141; MUID:89137072; PMID:2465147  
 A:Accession: S02141  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 341-356, 'G', 358-845, 'H', 847-885 <DIAM1>  
 A:Cross-references: EMBL:X14690; NID:935464; PIDN:CAA32821.1; PID:935465  
 R:Englind, J.J.; Thogersen, I.B.; Pizzo, S.V.; Salvesen, G.  
 J. Biol. Chem. 264, 15975-15981, 1989  
 A>Title: Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-  
 A:Reference number: A92736; MUID:89380192; PMID:2476436  
 A:Accession: D34245  
 A:Molecule type: protein  
 A:Residues: 30-49 <ENG1>  
 R:Englind, J.J.; Salvesen, G.; Hefta, S.A.; Thogersen, I.B.; Rutherford, S.; Pizzo, S.V.  
 J. Biol. Chem. 266, 747-751, 1991  
 A>Title: Chondroitin 4-sulfate covalently cross-links the chains of the human blood prot  
 A:Reference number: A39079; MUID:91093267; PMID:1898736  
 A:Accession: A39079  
 A:Molecule type: protein  
 A:Residues: 631-647 <ENG2>  
 R:Diarra-Mehrpour, M.; Bourguignon, J.; Sarafan, N.; Bost, F.; Sesboue, R.; Muschio-Bot  
 Biochim. Biophys. Acta 1219, 551-554, 1994  
 A>Title: Tandem orientation of the inter-alpha-trypsin inhibitor heavy chain H1 and H3 g  
 A:Reference number: S50132; MUID:95002176; PMID:7522574  
 A:Accession: S50132  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-27 <DIA2>  
 A:Cross-references: EMBL:X75318  
 R:Slusniwski, H.G.; Burgess, W.H.; Oppenheim, J.D.; Vilcek, J.  
 Biochemistr 33, 7423-7429, 1994  
 A>Title: TSG-6, an arthritis-associated hyaluronan binding protein, forms a stable comp  
 A:Reference number: A53642; MUID:94271799; PMID:7516184  
 A:Accession: B53642  
 A:Molecule type: protein  
 A:Residues: 30-34, 'X', <WIS>  
 R:Jensen, T.E.; Paarvang, K.L.; Ploug, M.  
 FEBS Lett. 250, 193-200, 1988  
 A>Title: Carbohydrate as covalent crosslink in human inter-alpha-trypsin inhibitor: a no  
 A:Reference number: S02431; MUID:88167187; PMID:2450785  
 A:Accession: A59167  
 A:Molecule type: protein  
 A:Residues: 30-32, 'GEKQAVDT' <JES>

C:Comment: As pre-alpha-inhibitor, this protein is covalently cross-linked by chondro  
 C:Genetics:  
 A:Gene: GDB:ITIH3  
 A:Cross-references: GDB:120109; OMIM:146650  
 A:Map position: 3p13-3p12  
 C:Superfamily: Inter-alpha-trypsin inhibitor complex component II  
 C:Keywords: Chondroitin sulfate proteoglycan; glycoprotein; heterodimer; proteinase I  
 F:1-19/Domain: signal sequence #status predicted <PRO>  
 F:20-29/Domain: propeptide #status predicted <PRO>  
 F:30-647/Product: inter-alpha-trypsin inhibitor heavy chain 3 #status experimental <M  
 F:648-685/Domain: carboxyl-terminal propeptide #status predicted <CTR>  
 F:87-576/Binding site: carboxylate (Asp) (covalent) #status predicted  
 F:647/Modified site: chondroitin sulfate ester carboxyl end (Asp) (in mature form) #s  
 Query Match 3.3%; Score 188; DB 2; Length 885;  
 Best Local Similarity 21.5%; Pred. No. 0.0033;  
 Matches 138; Conservative 112; Mismatches 243; Indels 150; Gaps 36;  
 QY 45 VTLAKTSGVNLVDYIEKQDLYTPVNNARQLVEIADIRKLSNRKALVRLALEA 104  
 Db 77 VELPKRTAFITNFTLTI-----DGVTY-NGVKE-KEYAKQYKAVSQGTAGL----- 123  
 QY 105 EKVQAAHOWREDF-----ASNEVYVYNAKDDIDPEKNDSEPGSORIKPVFIDANFGR 157  
 Db 124 --VKAQGRKLEKFTVSVNVAAGSKVTTELYEELKHKRKYEMLYKQP-----K 172  
 QY 158 QISYQHAHVLIPDIYEGSTIVLNMWTSALDEVFKNREDEPSLIMOVGSA-----T 212  
 Db 173 QL-VKHFIEIV--DIFEPQGI-----SWLD-----AEASFITNDLGSALTQKFS 214  
 QY 213 GLATYRPSFVNDKSR-PKID-----LYDVRRP-----NYI-----QG- 247  
 Db 215 GKXKHSRFPRLDOQRSCPTCTDLSLNGDFTTYDVNRSPGNVQVINGFVHFPAQGL 274  
 QY 248 AASPEDMLIVDVGSGVGLTLKLRISVSEMLETSDDDFVNVPNSAODVSCF-QH 306  
 Db 275 PVKRNKNAFVIDISGSMAGKRLKEQTKELRLIEDQEDLYNLTLFSG---DVSATKEH 331  
 QY 307 LVQANVRNKKVLKDAVNNTAKGITDYKKGFSFPEOLLNNTNSR-----ANCKITML 360  
 Db 332 LVQATPEMLQEAQKTFVKSMEDEKMTNINDGLRISGM---NKAREHRIRPERSTIVIM 388  
 QY 361 FTDG-----GEERAOEIFAKYK--DKKYRVTFFVSGHNDRGPIDMACENKGYEIP 414  
 Db 389 LTDDGAVNGEERPEKIQGNVNAIGKPLYNLPG--NMLYNFLNMALENHCFARITY 447  
 QY 415 SIGAIRINTQEYLDVLRPNVLACGAKAKOVQWTVNYLDALP-----LGLVITGLP 465  
 Db 448 EDSADADLQGFYEYEVANPL-LTGVEKMPY--NAILDLTQNTYQHFFYDGESEIYVAGRLV 504  
 QY 466 VFNITGQNEKNTNLK-----NOLLGVNGVDVSLIEDIKRLTPRTLCNPGYFAIDPN-- 518  
 Db 505 DEDM---NSFADVYGHGATNDL--PTEYEDMKEMK-----ALDERDVIYG--NYI 550  
 QY 519 ----GYVLLHPRLQPK---NPKSQEPVTLDFLDALENDIKVEIRNKKMIDSESGEKTEFT 571  
 Db 551 ERLMAVLTITQELLEKRNKAHGEKENLTPARALDLSLKTHFTPLPSWVTPK----- 603  
 QY 572 LVKSODERYI-DKGNRTYTTPVN-CTDYSLALVLPYTSFYI 612  
 Db 604 --DNEDERAILDKPEGDAEATFVSPAMSYLTSYGPQNPYYV 644  
 RESULT 10  
 D97033  
 uncharacterized protein, probably surface-located [Imported] - Clostridium acetobutyli  
 C:Species: Clostridium acetobutylicum  
 C:Date: 14-Sep-2001 #sequence-revision 14-Sep-2001 #text-change 14-Sep-2001  
 R:Noelling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L  
 J. Bacteriol. 183, 4823-4838, 2001  
 A>Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium



Query Match	3.0%;	Score 170.5;	DB 2,	Length 1619;
Best Local Similarity	18.8%;	Pred. No. 0.11;		
Matches 194;	Conservative 153;	Mismatches 334;	Indels 351;	Gaps 53

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QY 717 VKARVYVDDGIIITVYKPKGENMOENPEDESKFLDNNDNYFTAPYKNGSGPAY 776
Db 941 EATVYVYRSLTETGV-----TKENLIFNTYIKE--GQY 972
QY 777 ESGIVSKAVET-----YIO--GKLLKPAVYGIKIDVNSMIENFTYTSIRDCAPV 826
Db 973 FDLTSLKSSVELEKEKYEAVIKITSGK--AYVG-----DYIKVGIKIDYENI 1018
QY 827 CDCRKNSSVYMC 838
Db 1019 AYININDLQNG 1030

```

hypothetical protein b2270 - Escherichia coli (strain K-12)  
C:Species: Escherichia coli

C:Species: Escherichia coli  
C:Date: 12-Sep-1997 #sequon

C;Accession: D64998  
#sequence\_revision 1/-sep-1997  
#text\_change 01-Mar-2002

R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Rose, D.I.; Mau, P.; Shao, Y.

Science 277, 1453-1462, 1997

A:Reference number: A64720: M11D:97426617: PMID:8328503  
A:title: The complete genome sequence of Escherichia coli K-12.

A: Accession: D64998

status: preliminary; nucleic acid sequence not shown; translation not shown  
A; molecule type: DNA

A;Residues: 1-575 <BLAT>

A; Experimental source: strain K-12, substrain MG1655

Query Match	3.0%	Score 168.5;	DB 2;	Length 575;
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Matches 111; Conservative 94; Mismatches 205; Indels 105; Gaps 24;

QY 71 EPNNARQLVEIARDIEKLLSNRSKALVRLALEAEKVOAHOWREDFASNEVYYNAKDD 130

22 OPENKES0000BPTDFECCVY AAOOATY - - FAECCGAA  
| | : : | : : ||| : ||  
| | : : | : : ||| : ||

[illegible]

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0Y      131  LDPEKD-----SEPGSQRKRPVFIDDANFGRGQISYQHAA---VHIPTDI 172

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Db 76 LOGRLOEAPTFARAKAKATHIANPGTARYQOF--DDNPVKQVAQNPLATESLDVDTGS 132

QY 173 YEGSTIVLNE-----LNTSALDEVEKKNBREDPSIJMOVEGSATGIARVY 218

133 VANPPEI NOCI DDDDAVVEETIVVDDCPVDT  
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ADNVOJFASDNFJFFHMKLEA --- 18/

219 PASFWVUNSKRTPNKIDLYDVRRRRPWYIQGAASPKDMLILDVSGS-VSGTLKLIRTSVS 277

Db 188 PA-PW-NEORTLLKVDILAKDRKSEELPAS-----NLVFLIDTSGSMISDERLPLIQSSLK 241

QY 278 EMEETLSDDDEFVNVASFNSNAODVSCFOHLYOANVRNKKVY.KDAYNNITAKGTIDYKKE 337

[illegible]

LPSISGSHKAEINAAIDSLDPAEGSINGAGL 296

QY 338 SFAFEQLLNYSRANCNKIIMFTD-----GEERAQEIFAKYNKDKKVRVFTFSVGQ 391

Db 297 ELAYQATK-GFIKGINR-ILLATDGFENVGIDDPKSIESMWKKQRESGVTLSTFGVN 354

392 HNYDRGPTOWMACENKGYVETPSGATBINTOEVDH CBPMU - - - - - 445

[illegible]

333 SNINEMVRIADVGNNGNSYIDTLLS---EAQKVLNSEMRQMLITVAKDKVKAQIEFNPA 410

QY 446 WTNVYLDALEGLVITGTLPVFNITGONENKTNLKNQLILGVMGD-VSLEDI---KRLT 501

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Db      411 WTEY---RQIGYE-----KROLVEHENNDNYDAGDIGAKHIT 447
          | | : | | | | | | | |

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503 BRESTI CBNCEVERA TDDYQWUT I HWT CBNCEVERA EEC

[illegible]

DB 448 LFFELTNGÖKASIDKLRYA--PDNKLAKSDKTYE 480



## RESULT 12

JC5576

Inter-alpha-trypsin inhibitor heavy chain 3 - golden hamster

C:Species: Mesocricetus auratus (golden hamster)

C:Date: 23-Sep-1997 #sequence\_revision 23-Sep-1997 #text\_change 17-Mar-1999

C:Accession: JC5576; PC4486

R:Nakamori, T.; Suzuki, Y.; Yamamoto, T.; Shinohara, H.

J. Biochem. 122, 71-82, 1997

A:Title: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precursors

sin inhibitor heavy chain family.

A:Reference number: JC5574; MUID:97420688; PMID:9276673

A:Accession: JC5576

A:Molecule type: mRNA

A:Residues: 1-889 &lt;NAK&gt;

A:Cross-references: DDBJ:D89287

A:Experimental source: liver

A:Accession: PC4486

A:Molecule type: protein

A:Residues: 34-53/449-475/509-526 &lt;NA2&gt;

C:Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3 were

that the complexes play important role for pancreatic cancer.

C:Superfamily: Inter-alpha-trypsin inhibitor complex component II

F:236-239, 664-865/Disulfide bonds: #status predicted

Query Match 2.9%; Score 166; DB 2; Length 889;

Best Local Similarity 23.2%; Pred. No. 0.068;

Matches 66; Conservative 57; Mismatches 111; Indels 51; Gaps 11;

QY 202 SLMOVFGSATGLARYYPASPWVNSRT-PNKID-----LYVRRR-PWYIOGA-- 248

Db 211 SALTFSFGKKGKGVSEF---LDQKSCPTCTDILLNGFTIYVYVNRSPENQVVG 267

QY 249 -----ASPKDMLLVHSGSVSGSLTLKIRTSVSEMLETSLDDDEVNVAVSNS 296

Db 268 YVHFHFAPOGLPVYVKNIVFVIDISGSMAGRKIQOTRVALLKTIIDMKDDYINLFEST 327

QY 297 NAQVSCFOHLVQVYVNRKVKLDAVNNITAKGITDYKGFSPAFQQLN---YVNSA 352

Db 328 GV--TWKMSLVQATPANLEAATFYKRSISDQMTNINDGLGIMTLDAEQHTVPER 385

QY 353 NCKKIIMLTLDG---GEERAOEIFAKYKDKKRVFTESVG-QHNYDRGPLOMACENK 407

Db 386 STSIITML-TDGDANNGESPEKIEGVNRKATIEGRPLVNLGFGNNLNFLETALLENH 444

QY 408 GYVEIPSGAIRINQVEYLDVIGRPMVLAGDKAKOVONTNYLD 452

Db 445 GVARRTYEDSDANLQLOGFYEYANPL-----TNEVE 478

## RESULT 13

F64688

Proteinase (EC 3.4.-.-) - Helicobacter pylori (strain 26695)

C:Species: Helicobacter pylori

C:Date: 09-Aug-1997 #sequence\_revision 15-Aug-1997 #text\_change 29-Sep-1999

C:Accession: F64688

R:Tomb, J.F.; White, O.; Kierlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodex, A.; McKen-

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.K.; Fujii, C.; Bowman, C.; Wathey, L.

Nature 388, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.

A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A:Reference number: A64520; MUID:97394467; PMID:9252185

A:Accession: F64688

A:Molecule type: DNA

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Residues: 1-459 &lt;TON&gt;

A:Cross-references: GB:AE000636; GB:AE000511; NID:g2314517; PIDN:AD08394.1; PID:g231452

C:Genetics:

A:Start codon: GTG

C:Superfamily: carboxyl-terminal processing proteinase

C:Keywords: hydrolase

Query Match 2.9%; Score 165; DB 2; Length 459;

Best Local Similarity 22.2%; Pred. No. 0.028;

Matches 138; Conservative 69; Mismatches 198; Indels 216; Gaps 30;

QY 6 LMLTLTLPQSLIGSSQEPFSAVITKSWDKMOEDLVTLAKTASGV-----NDLV 58

Db 3 LMTLRRLKGLLAVALSLHSGEVEKPKVPKVEDQQLA--AKREARSRSNNVS 60

QY 59 DIERYODLYTVEPPNAROLVEIARDIEKLNSRSKALVRLALEKQAQAHQREDPA 118

Db 61 EIKKKYVDKIS-----ELMTAIGLSNLD-----AHS----- 91

QY 119 SNEVYVNAKDDLPKNDSEPSQRIKPEVITDANFGHOISQHAANHIPDIESTI 178

Db 92 ---AYLN-----EKKFKE-----FQQTGEFGGLGITGMNDVLT 125

QY 179 VLNELMWTSL-----DEVKKNEEDPSLMOVFGSATGLARYYPASPWVNSRPN 231

Db 126 VIAPELGTAYKAGVSGNIIKINNE---STLSMSIDAIMMGKPRTP----- 173

QY 232 KIDLVDVRRRPMWYIOGAAPKMDL--ILVDVSGVSGTLKIRTSVSEMLETSLDDPFV 289

Db 174 -IGITVYRN-----EPKPLVFNITDI-----IKLPYVKKIKET--PYLYV 214

QY 290 NVASFNMAQVSCFOHLVQVYVNRKVKLDAVNNITAKGITDYKGFSPAF----- 341

Db 215 RVSGFDKNYTK-SVLEGL-KANPKAKGIYLDLGN--PGLLNQAVGLSNLFKRGVLS 270

QY 342 -----EOLNTNVSRN-----CNKIIMLTLDGGEERAOEIFAKYKDKKRVFTESVG 390

Db 271 QKGRKKEEMLEY--KANRADYTNLPIAVLVNVSASASELVAGALDDHRAVI---IG 324

QY 391 QHNYDRGPLOMACENKGYVEIPSGAIRINQVEYLDVIGRPMVLAGDKAKOVONTNY 450

Db 325 EKTFFGSGVQMLLPVKNK-----EAKITTAIYLPSCR-----TIOAKIT 366

QY 451 LDALGLVITTLPEVFNITGONENKTNKQLILGVGVDSLEDIKRLTPRFTLCPNG 510

Db 367 PDI---VYLPKVP-----ENENKFSLE-----ADLKH----- 392

QY 511 YFEAIDPNQVYLH-----PNLOPKNPKSQEPVITDLDALENDIKVEIKNKMIDG-- 563

Db 393 -----HLEOLKTKIDDTPNKSK-----ADKOKKEEKEIIPKMIINDIQ 433

QY 564 -----SGERTPTLVKSODER 579

Db 434 LKTAIDSLKTSIVDEKMDK 454

## RESULT 14

S76691

Hypothetical protein - Synechocystis sp. (strain PCC 6803)

C:Species: Synechocystis sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 08-Oct-1999

C:Accession: S76691

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamitsu, E.; Nakamura, Y.; Miyajima,

O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys

s.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S76691

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-420 &lt;KAN&gt;

A:Cross-references: EMBL:U064004; GB:AB001339; NID:g1001701; PIDN:BA01635.1; PID:d101

A&gt;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match

Best Local Similarity 2.8%; Score 160.5; DB 2; Length 420;

Matches 86; Conservative 86; Mismatches 181; Indels 55; Gaps 16;

QY 251 PKDMLLVDSVSGVSGTLKIRTSVSEMLETSLDDDEVNVAVSNSNAQVSCFOHLVQA 310

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      1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95
Db 41 PLMLCLVLDHSSMGOPLLEYKSAALGLIDLEEDDLRSVAFPHRKIV-----IENQ 95
Qy 311 NVNRNKKVLDAVNNITAKGIDYKGFSAFEBOLLNVNVRANKIMLFTDGEERAO 370
Db 96 QVRNGAAIKALIERLKAEGGTALIDGLIKIGDAKGRKEDRVS---HIFLLTDCHEHGD 152
Qy 371 E-----IFAKYNDKKYRVTFVSGOHNDRGFIOMMACENKNG--YYEIPISGIRINMO 424
Db 153 NDRCKLGTVASDYKLTHTTIGGDH-WMOQDVLEAIASAGSLSTIENPS-EALHTTRQ 210
Qy 425 EYLDVLRPMVLADGAKOVMTNVLDALELG---LVTTGTLPEVFNITGONENKTNL 480
Db 211 LF-----QMSNVGGLNMAHL-LLELAPQAHIAL-VKRYAQVSPETMDLT-VQ 254
Qy 481 NDLILGVMGVDSLEDIKRLTPFTLCPNGYFAIDPNCYVLLHPMLQPKNKSOE----- 536
Db 255 NGAIEFVRLGDMTDOEHV-----LLNLMLYLDOLLPGOHVIGOVQIRYDPAASQOTNLL 309
Qy 537 ----PYLDFPLAELENDIKVEIRNKMIDGEGSEKT--FRTLVKSODERYIDKGRNTYTW 590
Db 310 SDBPLFTIQ-VOTOTPTSDVOVESITLTLAKYRQIOLAKETLKKAGDRGAATMLQTAAK 368
Qy 591 PTYNGTDSLALVLPYTSFYIKAKIETITTOARSKKGMKDSSETLKP 638
Db 369 TALQMGDKKAGATILQTN---TRLQSGEDLSREGDKRKTMTNVSKTTLQ 413

RESULT 15
140884
Cytotoxin L - Clostridium sordellii
C:Species: Clostridium sordellii
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 15-Oct-1999
C:Accession: I40884
R:Green, G.A.; Schue, V.; Montell, H.
Gene 161, 57-61, 1995
A:Title: Cloning and characterization of the cytotoxin L-encoding gene of Clostridium sc
A:Reference number: I40884; MUID:95369733; PMID:7642137
A:Accession: I40884
A:status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2364 <RES>
A:Cross-References: EMBL:X82638; NID:g1000694; PIDN:CAAS7959.1; PID:g1000695
C:Superfamily: cpl repeat homology
C:Keywords: cytotoxin

Query Match 2.8%; Score 160.5; DB 2; Length 2364;
Best Local Similarity 18.0%; Pred. No. 0.68;
Matches 219; Conservative 142; Mismatches 346; Indels 513; Gaps 58;

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Qy 292 ASFNSNAQDVSCFOHLYOAVNRNKKVLDAVNNITAK---GIDYKGFSAFEBOLLNVN 348
Db 1372 -----LSKLNIEDKIL---LNHTINFYDIDENSRFISLFTSLEDIN 1413
Qy 349 -----VSRA-----NCKNITMLFTD-----GGEERAOEIRA-----KYN- 377
Db 1414 IIRIDVLSYSKILLSGNCKMLIENSDDIOQKIDHIGFNGEHOKYIPVSYIDNETRYNG 1473
Qy 378 ---KDKYRVTFVSGOHNDRGFIOMMACENKNGYYEIPISGIRINMOEYLDVLRPM 434
Db 1474 FIDYSKKEGFTAEFSNESIIRN---ITMPPSNLFIYSSKDLDIRLINK-----GDVK 1525
Qy 435 VLADGKAKQ-----VQWNTNVLDALELGIVTGLPYFNITGONENKTNL 479
Db 1526 LLIGNYRKDDMKVSLSTIEDNTIKLNGVYLD-----NGVAQILKEMNNAKSLNT 1578
Qy 480 KNOILGVMGVDSLEDIKRLTPFTLCPNGYFAIDPNCYVLLHPMLQPKNKSOEPTV 539
Db 1579 SNSLMNPLESINIK-----NIFVNNIDPNIETIILDTNF----- 1611
Qy 540 LDFLDALEENDIKVEIRNKMIDGEGSEKTFTLVKSODERYIDKGRNTYTWTPVNGTYS 599
Db 1612 -----LISGSNSIGQFE-LICBMDKN----- 1631
Qy 600 LALVLPYTSFYIKAKIETITTOARSKKGMKDSSETLKPNEFESGYTFLAPRDYCNLDK 659
Db 1632 ---IQP---YFINPKIKET-----SYTLVGNRQV---LIVEPSYHLD-- 1666
Qy 660 ISDNTEFLAMPNE---FIDR---KTPNPNSCWTDLIN-----RYLDAGF 699
Db 1667 -SGNISSTVINFSQYLYGIDRYVNAKYIAPNLTYTDELINTTPYKPNYICPEVYIILDANY 1725
Qy 700 TNE-----LYQNYV-----SKQKNIRKARFVYTDGITRYVPKEAGE 738
Db 1726 INEKINNVINOLSTRYVWVNDNGSDILLIANSEONQPVKIRFV-----NVFKSDTAA 1778
Qy 739 -----NMOENDE-----TYDSFYKR-----SIDNNYVFTAPYFKSKPGA 775
Db 1779 DKLSFNFSDKQDVSVSKLIISTFSLAAYSDFEYDFGLVSLDND-----YFINSFGN 1831
Qy 776 YESSGIMSKAVEIYIOGKL-LKP---AYVGI-KIDVSNWIEFTKTSIRDCAGPVCD 828
Db 1832 MVSGL-----IYINDSLYFKPKPKNNLITGFTTIDGNKRIFFDPTNSG-----AASL-- 1877
Qy 829 CKRNSDVMDCVLLDDGGLMANHDDYTN---QIG-----RFF---GEIDPSLMR 872
Db 1878 -----GETTIDGKDYFNKOGIIOVGIVINTSDGLKYFAPAGTLDENLEG 1921
Qy 873 HLYVNI-----SYAANKSYDVQSVCEPGAAPKQGGHRSAYVPSIADILHIGWATA 924
Db 1922 ESNVFTIGKLNIDGKIITYEDN-----RAA 1946
Qy 925 AAMSIIQGFILSLTPRLLAEVEMEDDFTASLSKQSCITPOTOFEPDNDKSPFSGVLD 984
Db 1947 VEMKLLD-----DETYFFNKKTEGALKGHLQI 1973
Qy 985 GNCSTRIFHEVKIMTNLIFI 1004
Db 1974 GDNKYFFDNGCIMQGTGFI 1993

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Search completed: February 10, 2003, 14:22:10  
 Job time : 26.346 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2003, 14:22:34 ; Search time 7.90442 Seconds  
(without alignments)  
2998.192 Million cell updates/sec

Title: US-10-090-827-9

Perfect score: 5650

Sequence: 1 MAAGCLALTLTLFQSLIG.....NNALDYDCCGSHHHHHH 1069

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 129505 seqs, 22169297 residues

Total number of hits satisfying chosen parameters: 129505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications, AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
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7: /cgn2\_6/ptodata/2/pubpaa/PCUS\_PUBCOMB.pep:\*  
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12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5532	97.9	1091	US-09-875-423-4	Sequence 4, Appl1
2	1145.5	20.3	1091	US-09-875-423-5	Sequence 5, Appl1
3	1140.5	20.2	1091	US-09-875-423-2	Sequence 2, Appl1
4	470.5	8.3	223	US-10-005-168-2	Sequence 2, Appl1
5	272	4.8	51	US-09-864-761-44281	Sequence 44281, A
6	272	4.8	53	US-09-864-761-38267	Sequence 38267, A
7	190	3.4	35	US-09-864-761-38318	Sequence 38318, A
8	185	3.3	35	US-09-828-423-5	Sequence 5, Appl1
9	182	3.2	35	US-09-864-761-16461	Sequence 36461, A
10	160.5	2.8	790	US-09-850-351A-4	Sequence 4, Appl1
11	160.5	2.8	790	US-09-828-423-3	Sequence 3, Appl1
12	157.5	2.8	790	US-09-850-351A-6	Sequence 6, Appl1
13	157.5	2.8	790	US-09-850-351A-8	Sequence 8, Appl1
14	152	2.7	1349	US-09-815-242-5898	Sequence 5898, Ap
15	152	2.7	1349	US-09-815-242-13137	Sequence 13137, A
16	146.5	2.6	1781	US-09-995-749A-2	Sequence 2, Appl1
17	140	2.5	3169	US-10-114-170-257	Sequence 257, App
18	133.5	2.4	764	US-10-105-695-4	Sequence 4, Appl1
19	133.5	2.4	764	US-10-105-694-4	Sequence 4, Appl1

20	133.5	2.4	764	US-09-747-521-4	Sequence 4, Appl1
21	133.5	2.4	764	US-10-106-014-4	Sequence 4, Appl1
22	131.5	2.3	2125	US-09-919-172-29	Sequence 29, Appl1
23	131.5	2.3	3712	US-10-108-605-103	Sequence 103, App
24	130.5	2.3	1323	US-09-801-368-34	Sequence 34, Appl1
25	127.5	2.3	956	US-10-121-032-63	Sequence 63, Appl1
26	126	2.2	876	US-09-815-242-12623	Sequence 12623, A
27	124.5	2.2	151	US-10-050-786-10	Sequence 10, Appl1
28	124	2.2	2285	US-09-932-183A-2	Sequence 45, Appl1
29	118.5	2.1	1183	US-09-870-759-45	Sequence 9, Appl1
30	118	2.1	103	US-10-050-786-9	Sequence 12610, A
31	118	2.1	5795	US-09-815-242-12610	Sequence 4, Appl1
32	117	2.1	3594	US-10-150-821-4	Sequence 4, Appl1
33	117	2.1	3594	US-09-911-842-4	Sequence 4, Appl1
34	116	2.1	911	US-09-828-423-4	Sequence 190, App
35	114	2.0	549	US-09-712-363-190	Sequence 4, Appl1
36	114	2.0	698	US-09-801-220-4	Sequence 6, Appl1
37	113.5	2.0	1430	US-09-740-274-6	Sequence 2, Appl1
38	113.5	2.0	3571	US-10-150-821-2	Sequence 2, Appl1
39	113.5	2.0	3571	US-09-911-842-2	Sequence 3, Appl1
40	113	2.0	1066	US-09-423-126-3	Sequence 5, Appl1
41	113	2.0	1066	US-09-280-197-5	Sequence 4, Appl1
42	112	2.0	2835	US-09-885-535-4	Sequence 10, Appl1
43	111.5	2.0	836	US-09-858-525A-10	Sequence 10, Appl1
44	111.5	2.0	871	US-09-858-525A-2	Sequence 2, Appl1
45	111.5	2.0	881	US-09-850-351A-32	Sequence 32, Appl1

## ALIGNMENTS

RESULT 1	US-09-875-423-4	Sequence 4, Application US/09875423
1	Patent No. US20020081657A1	
2	GENERAL INFORMATION:	
3	APPLICANT: Curtiss, Roy A.J.	
4	TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF	
5	FILE REFERENCE: 10448-059001	
6	CURRENT APPLICATION NUMBER: US/09/875,423	
7	CURRENT FILING DATE: 2001-06-05	
8	PRIOR APPLICATION NUMBER: US 60/209,257	
9	PRIOR FILING DATE: 2000-06-05	
10	NUMBER OF SEQ ID NOS: 6	
11	SOFTWARE: FastSeq for Windows Version 4.0	
12	SEQ ID NO 4	
13	LENGTH: 1091	
14	TYPE: PRT	
15	ORGANISM: Homo sapiens	
16	US-09-875-423-4	
17	Query Match	97.9% ; Score 5532; DB 10; Length 1091;
18	Best Local Similarity	98.7% ; Pred. No. 0;
19	Matches 1049; Conservative	6; Mismatches 8; Indels 0; Gaps 0;
20	QY	1 MAAGCLALTLTLFQSLIGSSQEPSPAYTISWDMKQEDLVTLAKTASGNQVLDI 60
21	DB	1 MAAGCLALTLTLFQSLIGSSQEPSPAYTISWDMKQEDLVTLAKTASGNQVLDI 60
22	QY	61 YEKYODLVTEVBNNAKQVETIARDIEKLISNRKALVRLALEAKVOAHOHREDFASN 120
23	DB	61 YEKYODLVTEVBNNAKQVETIARDIEKLISNRKALVRLALEAKVOAHOHREDFASN 120
24	QY	121 EYVYVNAKDDLDPEKNDSEPSQRIKPYFIDANFGROISTQHAANHPTIYGSTIVL 180
25	DB	121 EYVYVNAKDDLDPEKNDSEPSQRIKPYFIDANFGROISTQHAANHPTIYGSTIVL 180
26	QY	181 NGLNMTSALDEVEFKKNNREDEPSLIMQVGSATGLARYYPASPMWNSRTPPKIDLYVRR 240
27	DB	181 NGLNMTSALDEVEFKKNNREDEPSLIMQVGSATGLARYYPASPMWNSRTPPKIDLYVRR 240
28	QY	241 RRMVYIGAGSPKMDLILVDVSGVSGTLTKLIRTSVSEMLETLSDDDFVNVAFPNSNAQD 300

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Db 241 RPYTIOGAASPKDMLILVYSSVSGLTILRTSVSEMLETLSDDDFYNVASFNSMAD 300
Qy 301 VSCFOHLVQANVRNKKVLDKAVANNITAKGITYKKGFSAFQOLLNYSVRNCKKIIML 360
Db 301 VSCFOHLVQANVRNKKVLDKAVANNITAKGITYKKGFSAFQOLLNYSVRNCKKIIML 360
Qy 361 FPDGGERROELFAFVYNDKRYVTFVSQGHNYRGPLOMACENKGYEIPISGAIR 420
Db 361 FPDGGERROELFAFVYNDKRYVTFVSQGHNYRGPLOMACENKGYEIPISGAIR 420
Qy 421 INTQETLDVLRPMVLADGAKAQQVMTVYLDALGLVITGTPYVNTQGNENKTKML 480
Db 421 INTQETLDVLRPMVLADGAKAQQVMTVYLDALGLVITGTPYVNTQGNENKTKML 480
Qy 481 NQILIGWGVVSLDILKRLPRFTLCPNGYFAIDPNGVYLHPNLOPKNPKSQEPVTL 540
Db 481 NQILIGWGVVSLDILKRLPRFTLCPNGYFAIDPNGVYLHPNLOPKNPKSQEPVTL 540
Qy 541 DELDAELNDIKVEIRNKMIDGSEGEFTFLVKSQDERYIDKGRITYTTPVNGTDSL 600
Db 541 DELDAELNDIKVEIRNKMIDGSEGEFTFLVKSQDERYIDKGRITYTTPVNGTDSL 600
Qy 601 ALVLPYTFYIYKAKIETITQARKSKGKMDSETIKPDNEESGYTFIAPRDYCNLDKI 660
Db 601 ALVLPYTFYIYKAKIETITQARKSKGKMDSETIKPDNEESGYTFIAPRDYCNLDKI 660
Qy 661 SDNTEFLNNEFTIDRTPNPNSCNDLIRVLLDAGFTNELVQANVWSKOKIKGVAR 720
Db 661 SDNTEFLNNEFTIDRTPNPNSCNDLIRVLLDAGFTNELVQANVWSKOKIKGVAR 720
Qy 721 FVVTIDGTRIRYPRKAGENNQENETEDSFYKSLNDNDVYFAFPNKSGBPAYSGI 780
Db 721 FVVTIDGTRIRYPRKAGENNQENETEDSFYKSLNDNDVYFAFPNKSGBPAYSGI 780
Qy 781 MVSAAVEIYIOGKLKPAVVGIKIDVNSWIENTFKTSIRPCAGPYDCCKRNSDVMCVI 840
Db 781 MVSAAVEIYIOGKLKPAVVGIKIDVNSWIENTFKTSIRPCAGPYDCCKRNSDVMCVI 840
Qy 841 LDDGFLIMANHDTYNOIGRFEEDPSLMRHVNSVYAFNKSVDYOGVCEPGAAPK 900
Db 841 LDDGFLIMANHDTYNOIGRFEEDPSLMRHVNSVYAFNKSVDYOGVCEPGAAPK 900
Qy 901 GAGHRSAYVPSIADILHIGWATAAAMSILQFLSLTFPRLEAVEMEDDDTASLSK 960
Db 901 GAGHRSAYVPSIADILHIGWATAAAMSILQFLSLTFPRLEAVEMEDDDTASLSK 960
Qy 961 SCITEGQYFEDNDKSFSGVLDGNCSTRIFHEKLMNTLIFIMVESKGTCTDRLII 1020
Db 961 SCITEGQYFEDNDKSFSGVLDGNCSTRIFHEKLMNTLIFIMVESKGTCTDRLII 1020
Qy 1021 QABQTSIDGPDPCDMVKOPRYRKGPVCEFDNNALEDYTDGGSV 1063
Db 1021 QABQTSIDGPDPCDMVKOPRYRKGPVCEFDNNALEDYTDGGSV 1063

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; TYPE: PRI
; ORGANISM: Mus musculus
US-09-875-423-5
Query Match 20.3%; Score 1145.5; DB 10; Length 1091;
Best Local Similarity 28.6%; Pred. No. 2, 5e-72;
Matches 322; Conservative 234; Mismatches 437; Indels 133; Gaps 40;

Qy 3 AGCLLALTILFOSGLIGPSQEPFSAVYIKSWMDKQBDVLTAKTASGVNQLDIYE 62
Db 14 ASALLA-TALLIYALGDVRSQEIPLSY-VKLMAFAGEIKSIYAKYSGQLDKKKK 71
Qy 63 KYODLYVEPNRNAROLYEIARDIEKLSRSKALVRLIAEAKYQAAQWREDPAFANEY 122
Db 72 EYENDVAIEEDIGQVLYKLAKEEFHKSQSAVRVLVAAEAHLKHEFDADL---QY 128
Qy 123 VYTNAA--DDLDEKNDSEFGSQRIRPVFLDANFGQISYQAAVHIFTDIYEGSTYL 180
Db 129 EYENAVLINERDKDGNFELGKEFI--LAPNDFHNNLPVNIISLSDVQYFTNMYNDPAIV 186
Qy 181 NELNMTSALDEVPKRRREDDPSLLNQVFGSAGLARYYPASPVWDSRTPNKIDLYDVR 240
Db 187 NGVYWSLKNKVVVDNDRDPSLIWQYFSGAKGFQYQGIWEPDE---NGVIAFDCKN 243
Qy 241 RPYTIOGAASPKDMLILVYSSVSGLTILRTSVSEMLETLSDDDFYNVASFNSMAD 300
Db 244 RMYTIOGAASPKDMLILVYSSVSGLTILRTSVSEMLETLSDDDFYNVASFNSMAD 303
Qy 301 VS-CFO-HLVQANVRNKKVLDKAVANNITAKGITYKKGFSAFQOLLNYSVRNCKKIIML 360
Db 304 VEPCLNGTLVQADRUKKEHREHLDKLFAKGIMDLIALNEAFNLTSPDNHGGQISIQ 363
Qy 357 IIMLFDDGGEERROELFAFVYNDKRYVTFVSQGHNYRGPLOMACENKGYEIPISGAIR 420
Db 364 ALMLITDGAVDYDITFAFYTNMPDKRVLFYTLIRGEAFAFADNKKMCAKNGFTQIST 423
Qy 416 IGAIRINTQETLDVLRPMVLADGAKAQQVMTVYLDALGLVITGTPYVNTQGNENKTKML 480
Db 424 LADVQENVAEYIHLVSRPKVI--DQEHVWTEAATIDSTLQAOGLADOGILVMTTYAM 481
Qy 465 PYENITQGNENKTKMLNQLILGWSGVSLDILKRLPRFTLCPNGYFAIDPNGVYLHPNLOPKNPKSQEPVTL 540
Db 482 PYFS---KQNTSRSG--ILGAVGTDPVYKELTIKRYKILGIGHYAFATNNGYILTH 536
Qy 525 PNLQD---KNPSQBP--VTLDLDAELNDIKVEIRNKMIDGSEGEFTFLVKSQDERYIDKGRITYTTPVNGTDSL 600
Db 537 PELRPLYEGRKKRRKPNVSSVDLSVEWEDRDV-LRANAVNRKTKG--FSMEYK---K 589
Qy 589 YIDKGNRT---YTMTPVNGTDSLALVLPY--YSFYIRAK--IEETITQARKSKGKMDSETIKPDNEESGYTFIAPRDYCNLDKI 660
Db 590 TVDKGRKRVLYMTNDYYNDIKGTPEFSLGVALSRHGKGYFRCGVNTIEGQ----- 639
Qy 631 KDSEFLKPDNEESGYTFIAPRDYCN-DLAKISDNNTTEFLNENFIDRKTPPNPNSCNDLIRVLLDAGFTNELVQANVWSKOKIKGVAR 720
Db 640 -----HDEHPVSLADEMSTICNTDLRHEHRLQLEAIKLYLKGEKP-LLOCDKEL 690
Qy 690 INRVLLDAGFTNELVQANVWSKOKIKGVARFVYDQGITRVPY----- 733
Db 691 IOEVLFLDA-VVSADPLEAWTSLALNKSNSDKGYEAVFLGRGLSLINLFCVAGQOLLNQ 749
Qy 749 --KEAGENQENPETEDSFYKSLDN--DNYVTIAPY---FNKSGPAYESGIMVSKA 785
Db 750 DELKAGDENENFADHPPLWRRAAEQIASFPVSIPIPSGVYVNS-----NVVTFSTS 803
Qy 786 VEIYIOGKLKPAVVGIKIDVNSWIENTFKTSIRPCAGPYDCCKRNSDVMCVI 840
Db 804 IQLLDERKSPVVAVVGQMLLEFPQRKFTASQCASLSDCKSICDDETVNCTYLIDNNG 863
Qy 864 FLMAHNDYTNQIGRPFGEIDPSLMRHVNSVYAFNKSVDYOGVCEPGAAPKQAGHR 905
Db 864 FILVS--EDYT-QTGDFGEVGAVMNKLTLGMSFKRITLYDQAMCR--ANKSSDSA 917
Qy 906 SAAVPSIADILHIGWATAAAMSILQFLSLTFPRLEAVEMEDDDTASLSK-----Q 960

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Db 918 HGLIDPYKAFI-----SAKWIIMTELVLVEF-----NLCSMWHSMDTKAKOKLTLE 967  
 QY 961 SCTEDTOFFENDSKSFGVLDGNCSTRIFHEKELMTNLIPIVESGTCPCDT---R 1017  
 Db 968 PCDETPAFVSEETIKETGNTACEDCSKSFYIOQLPSSNLEWVYDS--SCLCESVAPIT 1025  
 QY 1018 LLLQAEQTSDDGPDPCDMVKOPRYRKGPVYCFDNNALDEYTDGCGVS 1063  
 Db 1026 TMPIELRYNESLKCERLAKOKIRRRPESCHGFHPENARECGAS 1071

RESULT 3  
 US-09-875-423-2  
 ; Sequence 2, Application US/09875423  
 ; Patient No. US20020081657A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CURTIS, ROY A.J.  
 ; TITLE OF INVENTION: 21/84, A NOVEL HUMAN CALCIUM CHANNEL.  
 ; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF  
 ; FILE REFERENCE: 10448-059001  
 ; CURRENT APPLICATION NUMBER: US/09/875,423  
 ; CURRENT FILING DATE: 2001-06-05  
 ; PRIOR APPLICATION NUMBER: US 60/209,257  
 ; PRIOR FILING DATE: 2000-06-05  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 1091  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-875-423-2

Query Match 20.2%; Score 1140.5; DB 10; Length 1091;  
 Best Local Similarity 28.4%; Pred. No. 5,7e-72;  
 Matches 318; Conservative 234; Mismatches 442; Indels 127; Gaps 39;

QY 3 AGCLLALTLFOSLLIGPSSQEPFPPSAVITKSNVDMKQEDLYLATASGVNQLDIYE 62  
 Db 14 ASALLAAL-LYAALGDVYRSEQIPLSY-VKIMASAFEGGEIKSIKAKYSGSOLLKKYK 71  
 QY 63 KYODLYTEPNNALQVETIARDIEKILSNRSKALIVRLAEKVAQOAHQWREDFASNEV 122  
 Db 72 EYKDOVAIEEDIGLQLYKKLAKNHEMKHKSSEAVRLVEAEALHKLHEFDAL---QY 128  
 QY 123 VYNNK--DDLDPEKNDSEPSQRIKPYFIDANFGROISYQOAHVHPIDYEGSTIVL 180  
 Db 129 EYFNANVLNEDKQGNFLELGEKFI--LAPNDHEFNLPVNISTSDVQVPTMNMKDPATV 186  
 QY 181 NELMNTSALDEYFKKKNREDEPSLMQVYGSATGLARYTPASPVWDNSTPKNKIDLYDVR 240  
 Db 187 NGVYSESLNKVYFNDNFRDPSLIMQYFGSAKGFRRQYFGIKWEPDE---NGVIAFDGRN 243  
 QY 241 RMYVIOGAASPPDMLIVDVSGSVSGTLFKLIRTSVSEMLTSLDDDFVNAVAFSNSAOD 300  
 Db 244 RMYVIOGAATSPRDVYTLVDYSGSMGLALTYLAKQVSSILDTGDDDFNIIAVNEELHY 303  
 QY 301 VS-CFQ-HLYOANVRNKKVLDVANNITAKGITDYKKGSFPAEQLLNYNSRAN--CNK 356  
 Db 304 VEPCLNGTLVQADRTNKEFHREHLDKLEPAKGMIDIALNEFAFNILSPNTGOGSICSO 363  
 QY 357 TMLFTDGGEEAQLFPAKYN-KDKKVRVETPESVGOHNYDRKPIOMMACENKGYEELPS 415  
 Db 364 ATMLTIDGAVDYDTITFAKYNPDKKVRITFYLLIGREAPADNKLWMAKANKGFTQIST 423  
 QY 416 IGAIRINQOEYLDVLRPVLVLAGDKAKOVMTNVTYLDAL-----ELG--LVITGTL 464  
 Db 424 LADVOENWEVETLHVLSRPRVI--DQEHVYVTEAVYIDSTLPQAKILTDGQGVLTVMAM 481  
 QY 465 PVFNITGQNEKNTNLKNQULIGVAGVDSLEDIKRLPRFTLCPCGYAFADIPNGLYVLH 524  
 Db 482 PVFS-----KQNETRSKG-ILIGVGTGVYVKKELLTIPRYKYLGIHGAYAFATINNGYLTH 536

QY 525 PNLQ---PKNPKSQRP--VTILDIAELENDIKVEIRNKMLIDGSGEKTFTLVKSODER 579  
 Db 537 PELRLYEGRKKRRKPNVSSVDLSEVEDDDV-LRNAMNRRKTKG--FSEMKR-----K 589  
 QY 580 YIDKGNRT-----YTWTPVNGTIDYSLALVPT-YSFYIRAK--IEETITQARKSKGM 630  
 Db 590 TYDKCKRVLVMTNDYYIDIKGTPTSLGVALSRGKGYFPGNVTIIEBGL----- 639  
 QY 631 KQSEFLKPDNFEESYTTIAPRDYCN-DLKSIDNTEFLANFNEIDIKTNNNSCNTDL 689  
 Db 640 -----HDLHPDVSLADEWSYCNLTDLHPEHRLSOLEAIKLYLKKEP-LIQDDEL 690  
 QY 690 INRVLLDAGFTNELVONWS-----KOKNIKVAFRVYVDGTRVYP----- 733  
 Db 691 IODEVLDA-VVSAPLEAVTSLALNKSENSDKGVEVALGRTGTSLRNLTVGAEOQLNQ 749  
 QY 734 --KEAGENMOENPETEYEDSFYRSIDN--DNYVTAPYFNKSGPAGYSGLVSKAVEIY 789  
 Db 750 DFLKAGDKENIFNADHFLMYRRAEQIPGSFVYSIPE--STGPVKNKSNVYVASTIOL 807  
 QY 790 IQGKLKPAVVGIKIDVNSWNIENFTKTSIRDPACAGVCDCKRNSDMCVILDDGFTLM 849  
 Db 808 DERKSPVAVAGIOMKLEFFORKFWTASRQASLDKCSISCDDEFTVNCYLDNNGFILV 867  
 QY 850 ANHDVYTNQIGRFGEDPSLMKHLVNIISVAFNKSVDYOSVCEPGAAPKQGA-GHRSAY 908  
 Db 868 S-EDYT-OTGDFPGIEGAVNKKLLTMSFKRITLYDQAMCRANKESSDGAHGLDYP 924  
 QY 909 VPSIADILHIGWATAANSIILOQLLSTLTFPRLLEAVEMEDDTFASLSK-----QSCI 963  
 Db 925 -----NAPLSAVKMIIMTELVLVEF-----NLCSMWHSMDTKAKOKLTLEPDD 970  
 QY 964 TEOYTOFFENDSKSFGVLDGNCSTRIFHEKELMTNLIPIVESGTCPCDT---RLLI 1020  
 Db 971 TEPVAVSEETIKETGNTACEDCSKSFYIOQLPSSNLEWVYDS--SCLCESVAPITMA 1028  
 QY 1021 QAEQTSDDGPDPCDMVKOPRYRKGPVYCFDNNALDEYTDGCG 1061  
 Db 1029 PDIRYNESLKCERLAKOKIRRRPESCHGFHPENARECGG 1069

RESULT 4  
 US-10-005-168-2  
 ; Sequence 2, Application US/10005168  
 ; Patient No. US20020133840A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brennan, Thomas J.  
 ; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING DISRUPTIONS  
 ; TITLE OF INVENTION: IN GENES ENCODING A2D2 CALCIUM ION CHANNEL SUBUNIT PROTEINS  
 ; FILE REFERENCE: R-10  
 ; CURRENT APPLICATION NUMBER: US/10/005,168  
 ; CURRENT FILING DATE: 2001-12-04  
 ; PRIOR APPLICATION NUMBER: US 60/299,668  
 ; PRIOR FILING DATE: 2001-06-19  
 ; PRIOR APPLICATION NUMBER: US 60/282,685  
 ; PRIOR FILING DATE: 2001-04-09  
 ; PRIOR APPLICATION NUMBER: US 60/254,802  
 ; PRIOR FILING DATE: 2000-12-11  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 223  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 ; US-10-005-168-2

Query Match 8.3%; Score 470.5; DB 12; Length 223;  
 Best Local Similarity 44.3%; Pred. No. 6.3e-26;  
 Matches 81; Conservative 38; Mismatches 63; Indels 1; Gaps 1;

QY 878 SVYAFNKSVDYOSVCEPGAAPKQAGHRSAYVPSIADILHIGWATAANSIILOQLLST 937  
 Db 2 SFYTRKESYDQACAPQPNGLGAARGVYVPIADPLNLAMWTSAANSLRQOLLXGL 61



QY 45 VTLAKTASGVNOLVDIYEKYODLYTVEPNNAQOLVEIARDIEKLISNRSKALVRLALEA 104

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Db 77 VELPKATITNFTLTI-----DGVYV -PGNWK- KEVAKQYEVASGCKTAGL----- 123
QY 105 EKVQAAHOMREDF-----ASNEVYVYNARDLDPEDKNDSEPSQRIKPFVIDANEGR 157
Db 124 --VKASGKRLEKFTVSVMVAGSKVTFELTYELLKRIKGYEMVIAKQP-----K 172
QY 158 QISYHAAVHPDIYESTIVLNLNMTSALDEYFKKRNREDDSLMQVFGSA-----T 212
Db 173 QL-VKHEIEV--DIFEPQGI-----SMID-----AEASFTINDLGSALTQSFS 214
QY 213 GLARYPPSPWVNSRT--PNKID-----LYDVRRRP-----WYI-----OG- 247
Db 215 GKKGIVSKRPSLDQORSCPCTDLSLINDFTITTDVNRSGNQVYNGVHFHFAPOGL 274
QY 248 AASPRDMLILVDVSGVSGTLTKLRISVSEMLETLSDDEPVNVAFSNADVSCF--QH 306
Db 275 PVVKNVAVFIDISGSMAGRKLEQTKREALRILEDMKEEDYLNFLPSG---DYSTWKEH 331
QY 307 LVQANVRKKYKLVKAVNNITAKGTTDYKKGFSFAEQLNANVR-----ANCNKIIML 360
Db 332 LVQATPEMLQARTFVSKMEDKGMTINDGLRISML--NKAREHRIPERSTSIIVM 388
QY 361 FTLDG---GEERAOEIFAKYK--DKRVYFTFSVGOHNYDRGPIOMACENKGYEIP 414
Db 389 LITDGDANVGSERPEKIQENNVNNAIGCKFPLYNLQFG--NLNLYNLFENMALENHGFARIV 447
QY 415 SIGAIRITQOYLDVGRPVYLAGDKAKQVQWNTVYDALE-----LGVITGTL 465
Db 448 EDSADADLOLQFYEVAANPL--LTGVEMEYPR--NAILDLTQNTQHFYDGSSEIYVAGRLV 504
QY 466 VENITGQENKTNLK-----NQLLGWGVQVYSIEDIKRLTPRTLCPCNGYTFADIN-- 518
Db 505 DEDM---NSFADYKKGHGANIDL--TFTEVDKMEK-----ALDERDYIFG---NYI 550
QY 519 ---GYVLLHPNLOPK--NPKSOEPTLDFDALELNDIKVEIRNKMIDGESSEKFTFT 571
Db 551 ERLWAVITLQELLKRNNAHGEKENITARALDSLAKYHPTVPLTSMNVIKPE----- 603
QY 572 LVKSQDERIT--DKGNRTYTTTPVN--GTDYSLALVLPYTSFYI 612
Db 604 --DNEDERALADKPGDEAETPVSPAMSYLTSYQPPONPYVV 644

RESULT 9
; Sequence 36461, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 36461
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC008283.2
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.67
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.7
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.8
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.6
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
; OTHER INFORMATION: EST_HUMAN HIT: AW051735.1, EVALUE 3.00e-04
; OTHER INFORMATION: SWISSPROT HIT: P54290, EVALUE 6.00e-15
US-09-864-761-36461

Query Match 3.2%; Score 182; DB 10; Length 35;
Best Local Similarity 97.1%; Pred. No. 7.7e-07;
Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 141 GSORIKPVIDANFGROISYQAAVHIPPTDIYEG 175
Db 1 GSORIKPVIDANFGROISYQAAVHIPPTDIYEG 35

RESULT 10
US-09-850-351A-4
; Sequence 4, Application US/09850351A
; Patent No. US2002010080A1
; GENERAL INFORMATION:
; APPLICANT: Pettelson, Gerald S.
; APPLICANT: Schnepf, H. Ernest
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stockhoff, Brian A.
; APPLICANT: Schmeltz, James
; APPLICANT: Loewer, David
; APPLICANT: Dullum, Charles Joseph
; APPLICANT: Muller-Cohn, Judy
; APPLICANT: Stamp, Lisa
; APPLICANT: Morrill, George
; TITLE OF INVENTION: Sequences which Encode These Toxins and Nucleotide
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESS: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606-6669

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## COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/850,351A

FILING DATE: 07-May-2001

CLASSIFICATION: &lt;unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/073,898

FILING DATE: 06-MAY-1998

APPLICATION NUMBER: US 08/960,780

FILING DATE: 30-OCT-1997

APPLICATION NUMBER: US 60/029,848

ATTORNEY/AGENT INFORMATION:

NAME: Sanders, Jay M.

REGISTRATION NUMBER: 39,355

REFERENCE/DOCKET NUMBER: MA-708CD1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 352-375-8100

TELEFAX: 352-372-5800

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 790 amino acids

TYPE: amino acid

STRANDEDNESS: single

MOLECULE TYPE: linear

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: 36a

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-850-351A-4

Query Match 2.8%; Score 160.5; DB 10; Length 790;

Best Local Similarity 19.7%; Pred. No. 0.0024;

Matches 138; Conservative 103; Mismatches 216; Indels 245; Gaps 35;

231 NKIDLYDVRPRWYIOGASPKDMLIVDSVSGSLTLKLRITVSSEMLLETLSD-DFV 289  
 105 NMLDINTMLRYLL-----PKITSMLSDMKQNALSLIQI--EYLSKQLOEISDKLII 156  
 290 NY-ASEFNSAODVS-----CFQHLVQANRNKKVYLKDA-----VANNIT-----A 327  
 157 NVNVLINSLLEITTPAYORIKIVNKEFEELTSPAEFTSSKVKKDGSPANILDELLELLEIA 216  
 328 KQITDYKKGFSFAEFDLIN--YVNSRANCKIMLFTDGEERAOEIRAKYNNKKQKVRVF 385  
 217 KSVT---KNDVDGFEFYINTFHDVAVGN-----NLFGRSALKATASELITKEN---VATS 264  
 366 TFSVQO-HNYDRGPIQOMACENKGYEIPISGAIIRINTOEYLDVIGRPVLAQDKANQV 444  
 265 GSEVGNVYNE---LIVLTALQAKAFLLTTCRKLGLADIDYTSIMNEHL-----NKEEE 317  
 445 QMTNYLDALELGLVITGLPVENITGONENKTNLKN-----QILT-----GWAGVUS 493  
 318 FRVNI-----LPLLSNTFSNPYAKVKSDEDAKMLVEAKPGHALIGFEIS 363  
 494 LEDI-----KRLTPRF-----TLCPNG-----YVF--AIDPNGYVLL 523  
 364 NDSITVLKVEAKLKONQVODKSLSEVITGDMOKLLOPPDSEQIYYINNNIVFREYIIT 423  
 524 HPNLOPKPKGOEPTVLDLFLAELNDIKVEIRNMKIDGSEGEKTFRTLVKSODEKRYIDK 583  
 424 KIDFTKKKTKLRYETANFYDSSTG---EIDLNNKKV--ESSEAEYKLLSANDGVVYPL 478  
 584 GNRITYT-TPVNGDYSLALVLPYSFYIYAKIEETITQARSKKKKKKSKSETLKPNEF 642  
 479 GVISTFTFLTPINGC-----LQAD--E 498  
 643 ESGYFIAPRDYCNLDKISDNTEFLNFNEIDRKTNNPNSCMTDLNR-----VLDAG 698

DB 499 NSRLITLCKSYRLLELLA-----TDSNKEFKLIIPPSSG 533  
 QY 699 FNNELVON-----YMSKOKN-----IKGVARFVVDGCTTRVYPRAGEBNW 740  
 DB 534 FLSNIVEGSLIEDNLEFPKANNKNAVYDHTGVGTALYVHKDGGISQF-----IGDNL 589  
 QY 741 QENPEY-----EDSFYKRSLDNDNYVETAFYFNK----- 770  
 DB 590 KKEETVYIQTYYKKKPSLHLDENGTGIHYEDTNNNLEDYQITNKRFTGTDLKGVYLL 649  
 QY 771 ---SGPGAVESGIMVSKAVEIYIOGKLKPAVVGIKIDVNSW 809  
 DB 650 KSONGDEAMGDNFI---LEISPSEKILSPEL---INTNMW 684

## RESULT 11

US-09-828-423-3

Sequence 3, Application US/09828423

Patent No. US20020099178A1

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

Guegler, Karl J.

Patterson, Chandra

TITLE OF INVENTION: GROWTH-ASSOCIATED TRYPSIN-TYPE

INHIBITOR HEAVY CHAIN PRECURSOR

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: Word Perfect 6.1/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/828,423

FILING DATE: 05-Apr-2001

CLASSIFICATION: &lt;unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/388,774

FILING DATE: &lt;unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Cerrone, Michael C

REGISTRATION NUMBER: 39,132

REFERENCE/DOCKET NUMBER: PF-0505 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

TELEX: &lt;unknown&gt;

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 946 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GENEBANK

CLONE: q133985

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-828-423-3

Query Match 2.8%; Score 160.5; DB 10; Length 946;  
 Best Local Similarity 19.8%; Pred. No. 0.0031;  
 Matches 134; Conservative 107; Mismatches 248; Indels 189; Gaps 31;

QY 33 IKSVNDKQEDVILVITKAGVQVLDIYERKQDLYTVEPNNAKOLV----- 80  
 DB 26 LSEFVD--YEDIVEL---APGKQVLAENRRYORSL---PGESEEMEEVDVTLTSYRV 77

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1      OPERATING SYSTEM: PC-DOS/MS-DOS
2      SOFTWARE: PatentIn Release #1.0, Version #1.30
3
4      CURRENT APPLICATION DATA:
5      APPLICATION NUMBER: US/09/850,351A
6      FILING DATE: 07-May-2001
7
8      CLASSIFICATION: <Unknown>
9
10     PRIOR APPLICATION DATA:
11     APPLICATION NUMBER: US 09/073,898
12     FILING DATE: 06-MAY-1998
13     APPLICATION NUMBER: US 08/960,780
14     FILING DATE: 30-OCT-1997
15     APPLICATION NUMBER: US 60/029,848
16     FILING DATE: 30-OCT-1996
17
18     ATTORNEY/AGENT INFORMATION:
19     NAME: Sanders, Jay M.
20     REGISTRATION NUMBER: 39,355
21     REFERENCE/DOCKET NUMBER: MA-708CD1
22
23     TELECOMMUNICATION INFORMATION:
24     TELEPHONE: 352-375-8100
25     TELEFAX: 352-372-5800
26
27     INFORMATION FOR SEQ ID NO: 6:
28     SEQUENCE CHARACTERISTICS:
29     LENGTH: 789 amino acids
30     TYPE: amino acid
31     STRANDEDNESS: single
32     TOPOLOGY: linear
33     MOLECULE TYPE: protein
34     ORIGINAL SOURCE:
35     INDIVIDUAL ISOLATE: 81F
36
37     SEQUENCE DESCRIPTION: SEQ ID NO: 6:
38     US-09-850-351A-6

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Query Match          2.8% ; Score 157.5 ; DB 10 ; Length 789 ;
Best Local Similarity 20.1% ; Pred. No. 0.0038 ;
Matches 188 ; Conservative 103 ; Mismatches 231 ; Indels 215 ; Gaps 35 ;

QY      231 NKDDIDVRRRRPYIGGASPRKMDLIYDVSSVSGILTKLRFSVSEMETLSDD -DFY 289
      ||| : : : : || : : : : || : : : : || : : : : || : : : : || : : : :
Db      105 NKDDAINTMTLRVYL-----PKITSMELSDVMKONYATSLQI--EYLSKQLOEISDKLIDII 156
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      290 NV-ASFNSNAQDS-----CFQHLVOAANRNNKTVLKDA-----VNNIT-----A 327
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      157 NVANVLINSTITLTPNAYQRIKTVNNEKFELTPATETSSKVAKKQSPADIIDELTELTELA 216
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Qy	328	KGIIDYKKGSEAFEOULL--YNVSPANCKIIMLEFDGGERROELFPAANYMKDKRYAF	385
Db	217	KSIV----KNVDDEFEYLTFPHVMGN-----NLFGRSAULTASELITKEN-----VKTS	264
Qy	386	TFSTGO-HNYDRGPLOMACENKGGYVEITPSGIRINTOEVLVLRLPRMLAGDKAKOV	444
Db	265	CEGVGVNVRN---ITVTPALOKAKETITTCCKIKGIDNTIYTSIMENHI-----NKKRPE	317

[illegible]

QY 524 HPNIQAPNPKSQEPVTLDFLDAELENIDKVEIRNMKIDGESGEFTERTLYKSODERYIDK 563  
 Db 424 KIDPTKCMKTLREVTANFYDSSTG---EIDLNKKV--ESSEAEYRLSDNDGGVYML 478  
 QY 564 GNRITYTM-TYVNG---TDYSLALVLPYTSFYIYAKAEIHTIQAQSKKCKMKMSETLKP 638  
 Db 479 GVISEFTLFTPIINGGLQADENSRLIYLTCTKSYLRELLATDLSN-----KTKTLIVP 530

```

OY 639 ---DNEESGSGTFLAPRDYCDMLKLSNNNE--FLNFLEPFIDRKTPNNSCNTDLIN 691
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 531 PSCGTKNIVENG-----SLEEDNLEPMAKNNKNNRYVDH----- 563
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 692 RVLIDAGFTMLDYONWKSOKNTKGAKAFVYTDGSI-----RYRK----- 734
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Db 564 -----EAG-----EAGWENPETYEDSFYKRSIDNDNYFTAFYFNKSGPAGYESSIMV 782  
 QY 735 -----EAG-----EAGWENPETYEDSFYKRSIDNDNYFTAFYFNKSGPAGYESSIMV 782  
 Db 605 PSIHAKDENGCIYIHEPDNNLEQYITRKFTGTDLKGYLLKSGNDDEAMGDNFI 664  
 QY 783 SKAVEIYIOGKLKPAVYGVKIDVNSW 809  
 Db 665 ---LEISPEKLSPEL---INTNMW 684

## RESULT 13

US-09-850-351A-8  
 ; Sequence 8, Application US/09850351A  
 ; Patent No. US2002010080A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Feteleson, Jerald S.  
 ; Schnepf, H. Ernest  
 ; Narva, Kenneth E.  
 ; Stockhoff, Brian A.  
 ; Schneits, James  
 ; Loewer, David  
 ; Dullum, Charles Joseph  
 ; Muller-Cohn, Judy  
 ; Stamp, Lisa  
 ; Morrill, George  
 ; TITLE OF INVENTION: No. US2002010080A1 Pesticidal Toxins and Nucleotide  
 ; Sequences Which Encode These Toxins  
 ; NUMBER OF SEQUENCES: 144  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
 ; STREET: 2421 N.W. 41st Street, Suite A-1  
 ; CITY: Gainesville  
 ; STATE: FL  
 ; COUNTRY: US  
 ; ZIP: 32606-6669  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/850,351A  
 ; FILING DATE: 07-May-2001  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 09/073,898  
 ; FILING DATE: 06-May-1998  
 ; APPLICATION NUMBER: US 08/960,780  
 ; FILING DATE: 30-Oct-1997  
 ; APPLICATION NUMBER: US 60/029,848  
 ; FILING DATE: 30-Oct-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Sanders, Jay M.  
 ; REGISTRATION NUMBER: 39,355  
 ; REFERENCE/DOCKET NUMBER: MA-708CD1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 352-375-8100  
 ; TELEFAX: 352-372-5800  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 790 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; ORIGINAL SOURCE:  
 ; INDIVIDUAL ISOLATE: Jay90  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
 ; US-09-850-351A-8  
 ; Query Match 2.8%, Score 157.5; DB 10; Length 790;

Best Local Similarity 19.7%; Pred. No. 0.0039;  
 Matches 138; Conservative 102; Mismatches 217; Indels 245; Gaps 35;

QY 231 NKIDLYVRRRPPYIOGAASPKMDILVDSGVSGLTKLIRTSYSEMLTSLDD-DEV 289  
 Db 105 NKIDALINTMLRYLL-----PKITSLSDVMQNVNLSIQI--EYLSKLOQESKLDII 156  
 QY 290 NV-ASRNSNAQDVS-----CFQHLVQANVKNKVLKDA-----VNNIT-----A 327  
 Db 157 NVNVLINSTLEITPAYORIKYVNEKEFEELTETSSKVKDKGSPADILDELTELTELA 216  
 QY 328 KGITDYKKGSPAFEDQLN--VNSRANCKIMLPTDGEFEBAOEIPAKYKDKVRPF 385  
 Db 217 KSVT---KNDVDFEFLYLNFDHVMGN---NLGRSALKTASBELTKEN---VKTS 264  
 QY 386 TFSVGO-HNYDRGPIOMACENKGYEYIETSGAIRINTOEYLDVGRPMVLGKAKQY 444  
 Db 265 GSEVGNVYNF--LYVLTALQAKAFLLTTCRLLADLADITSINNEHL-----NKEKEE 317  
 QY 445 QMTNVIYDALEGLVITGLPVPENITGONENKTNLKN-----OLIL-----GVMGVDS 493  
 Db 318 FRVNI-----LPTLSNTEFSPNRYAKVGSDEDAKMIYEAAPGHALLIGFEIS 363  
 QY 494 LEQI-----KRLTPRF-----TLCPNG-----YF--AIDPNGVYL 523  
 Db 364 NDSITVLKYEAELKONYOYDKDSLSEVYIGDMKLLCPQOSEQIYTNVIVPNEYVIT 423  
 QY 524 HPLDOPNPKSQPVTLDFLDALENDIKVEIRNKMIDSEGEKPTLVKSODERYIDK 583  
 Db 424 KIDFTKMKTLRYEVANFVDSSTG--EIDLNKKV--ESSAEERTLSANDGVYIML 478  
 QY 584 GNRITYW-TPVNGTDVSLALVLPYSPYYIKAKIETITQARSKGKMDSETLKPDNE 642  
 Db 479 GVISEFTFPIINGF-----LQAD--E 498  
 QY 643 ESGYTFIAPRDYONDKISDNTFELNFEFIDRKTNNPNSCNDLINR---VLLDAG 698  
 Db 499 NSRLITLTCKSYLRELLA-----TDLSNKETKLYIPPSG 533  
 QY 699 FTNELVON-----YWSKQKN-----IKGVKAFVYTDGIRVYPKEAGENW 740  
 Db 534 FISNIYNGSIEEDNLEPMKANKNAVYDHTGCVNGKALYVHKDGIQSF--IGDKL 589  
 QY 741 QENDEY-----EDSEFKSLDNDNYFTAFYFNK----- 770  
 Db 590 KPTEYIYQYTVKXPSIHLDKENTGXIHYEDYNNLEQYITRKFTGTDLKGYLL 649  
 QY 771 ---SGPAGESGIMVSKAVEIYIOGKLKPAVYGVKIDVNSW 809  
 Db 650 KSONDEAMGDNFI---LEISPEKLSPEL---INTNMW 684

RESULT 14  
 ; US-09-815-242-5898  
 ; Sequence 5898, Application US/09815242  
 ; Patent No. US20020061569A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Haselbeck, Robert  
 ; APPLICANT: Ohlsen, Karl L.  
 ; APPLICANT: Zyskind, Judith W.  
 ; APPLICANT: Wall, Daniel  
 ; APPLICANT: Trawick, John D.  
 ; APPLICANT: Carr, Grant J.  
 ; APPLICANT: Yamamoto, Robert T.  
 ; APPLICANT: Xu, H. Howard  
 ; TITLE OF INVENTION: Identification of Essential Genes in  
 ; TITLE REFERENCE: ELITRA.011A  
 ; CURRENT APPLICATION NUMBER: US/09/815,242  
 ; CURRENT FILING DATE: 2001-03-21  
 ; PRIOR APPLICATION NUMBER: 60/191,078  
 ; PRIOR FILING DATE: 2000-03-21  
 ; PRIOR APPLICATION NUMBER: 60/206,848



Db 91 NOK-----EMASSQNETSNKNGK-----LIEKESVOST-----TGKKEVSTAKSD-- 132  
QY 133 PEKNDSEPGSORIKPEVIDANFGROISYQHAAVHIPTDIYEGSTIV----- 179  
Db 133 ---E0ASPKSTN-----EDLNTKOTISNCEA---LQPDLOENKSVVNVQPTNEKNKVD 180  
QY 180 -----LN-----ELNWTSALEDFKKNREDEPSLLM-----QYFGSATGLARYPA 220  
Db 181 AKTSTLTLNVSDAIKSNDETLVDNNSNSNENNADIIIPKSTAPKRLNTRMRIAQOPS 240  
QY 221 SPWVDN-----SRTPNKIDLYVRRRPWYIOGAASPKDMLIIVDVSQVSGLTFLKLRIT 274  
Db 241 STEAKNVNDLTSNTTLTYVADAKNNKIYPAQDYLISLSQITVDKYSQDFTIKY--- 297  
QY 275 SVSEMLETLSDDDFVNVASFN--SNAQDVSCFOHLVOANVRNKKVLKDAVNNITAKGTTD 332  
Db 298 SDTVOYVGLNPEDEIKNIGIDIKPNNGETIATAKH-----DTANNLITYTFTD 344  
QY 333 YKKGFSFAEBQLNLYNY-----SRANC-----NK 356  
Db 345 YVDFRN--SVQMGITVSTIYMDADTIPVSKNDVEFNVTIGNTTKTANIQYPDYVNVNEKNS 403  
QY 357 IIMLETD-----GGEER-----AOEIFAKYNNKD-----KVRVTFP-----SVGOHNYDRG 397  
Db 404 IGSAFTETVSHVGNKENPGYKOTIYVNPSENSTNAKLKQVQVHSSYPNNIGQINKDVT 463  
QY 398 PIOMMACE-----NKGYYETPISGAIKIRINTQETLDVLRPM--VLAGDKAKOV----- 444  
Db 464 DIKIYQVPGKYTLNKG-----DVNTKELTDTNQLKITYGDNNNSAVIDFGNA 513  
QY 445 -----QWNTN----- 448  
Db 514 DSAVYVNVNTRKFOYTNESEPTLVOMATLSTGKNSVSTGNALGFTNNQSGAGQEVYKIG 573  
QY 449 --VYLDALGLVITGTLPEVNIT--GONENKTNLKNOLILGVMGVDVSEDIKRLTPRFT 505  
Db 574 NYWEDENKNGVOELGEGKGVNTVTFEDNNTYTK-----VGEAVTKEDGSYLLIPNL- 625  
QY 506 LCPNGYV---FAIDPNGYVLLHNLQPKNK-----SQEPVTLDFLDAELNDIKVEIRN 557  
Db 626 --PRGDIYRVEFSNLPKGYEY--PSKOGNNEELDSNGLSVITVNGKD-NLSADLGIYKPK 681  
QY 558 KMIDGESGEKTFRTLVKSODERYIDKGNRTYTWPVNGTDYSLALVLPYSFYIRAKIE 617  
Db 682 YNLCDYVWEDTNKNGIQDDEKGI--SGVTVTLKDENG-----DVL 720  
QY 618 ETTTQARSKKGMKDESETLKPDPNEBSGYTFIAPRDYCNDLKISDNNTEFLNPFNFI 677  
Db 721 KTVTTADGKFKFTD---LHNGNYK---VEFTTPEGTYPTTVSGSDIE----- 763  
QY 678 KTPNPNFSCNTDLN---RYVLDAAGFTN---ELVQNTW-----SKOKNIKCY--- 717  
Db 764 -KDSNGITTTGVINGADNMTLDSGFYKTPRYKNGVWEDTNKNGQDSTEKIGISGVTV 822  
QY 718 -----KARFVVTGIGITRV-----YPREAGENMOE----- 742  
Db 823 LKNEGEVLQTTKTDKQKQFTGLENGIVKVFETPSCGYTPQVQVSGTDEGIDSGTST 882  
QY 743 -----NPEYEDSFYKRSLSLNDNTVFTAPYFNKSGPQAYE---SGIMVSKAWEIYITQ 791  
Db 883 TGVYIKDKNDTIDSGFYKPYLNGDYVWEDT--NKNGVQDKDEKIGISGVTVTLKDE---N 937  
QY 792 GKLLK 796  
Db 938 DKVLK 942

Search completed: February 10, 2003, 14:49:03  
Job time : 11.9044 secs

4-1-1

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2003, 14:22:34 : Search time 7.86006 Seconds  
(without alignments)  
2998.192 Million cell updates/sec

Title: US-10-090-827-8

Perfect score: 5602  
Sequence: 1 MAAGCLLALTLTLFQSLILG.....PDVCFDNNALDYDCGVS 1063

Scoring table:  
BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 129505 seqs, 22169297 residues

Total number of hits satisfying chosen parameters: 129505

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCU\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubpaa/PCUUS\_PUBCOMB.pep:\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
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12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5532	98.8	1091	US-09-875-423-4	Sequence 4, Appli
2	1145.5	20.4	1091	US-09-875-423-5	Sequence 5, Appli
3	1140.5	20.4	1091	US-09-875-423-2	Sequence 2, Appli
4	470.5	8.4	223	US-10-005-168-2	Sequence 2, Appli
5	272	4.9	51	US-09-864-761-44281	Sequence 44281, A
6	272	4.9	53	US-09-864-761-38267	Sequence 38267, A
7	190	3.4	35	US-09-864-761-38318	Sequence 38318, A
8	185	3.3	35	US-09-828-423-5	Sequence 5, Appli
9	182	3.2	35	US-09-864-761-36461	Sequence 36461, A
10	160.5	2.9	790	US-09-850-351A-4	Sequence 4, Appli
11	160.5	2.9	946	US-09-828-423-3	Sequence 3, Appli
12	157.5	2.8	789	US-09-850-351A-6	Sequence 6, Appli
13	157.5	2.8	790	US-09-850-351A-8	Sequence 8, Appli
14	152	2.7	1349	US-09-815-242-5898	Sequence 5898, Ap
15	152	2.7	1349	US-09-815-242-13137	Sequence 13137, A
16	146.5	2.6	1781	US-09-995-749A-2	Sequence 2, Appli
17	140	2.5	3169	US-10-114-170-257	Sequence 257, App
18	133.5	2.4	764	US-10-105-695-4	Sequence 4, Appli
19	133.5	2.4	764	US-10-105-694-4	Sequence 4, Appli

20	133.5	2.4	764	US-09-747-521-4	Sequence 4, Appli
21	133.5	2.4	764	US-10-106-014-4	Sequence 4, Appli
22	131.5	2.3	2125	US-09-919-172-29	Sequence 29, Appli
23	131.5	2.3	3712	US-10-108-605-103	Sequence 103, App
24	130.5	2.3	1323	US-09-801-368-34	Sequence 34, Appli
25	127.5	2.3	956	US-10-121-032-63	Sequence 63, Appli
26	126	2.2	876	US-09-815-242-12623	Sequence 12623, A
27	124.5	2.2	151	US-10-050-786-10	Sequence 10, Appli
28	124	2.2	2285	US-09-932-183A-2	Sequence 45, Appli
29	118.5	2.1	1183	US-09-870-759-45	Sequence 45, Appli
30	118	2.1	103	US-10-050-786-9	Sequence 9, Appli
31	118	2.1	5795	US-09-815-242-12610	Sequence 12610, A
32	117	2.1	3594	US-10-150-821-4	Sequence 4, Appli
33	117	2.1	3594	US-09-911-842-4	Sequence 4, Appli
34	116	2.1	911	US-09-828-423-4	Sequence 4, Appli
35	114	2.0	549	US-09-712-363-190	Sequence 190, App
36	114	2.0	698	US-09-801-220-4	Sequence 4, Appli
37	113.5	2.0	1430	US-09-740-274-6	Sequence 6, Appli
38	113.5	2.0	3571	US-10-150-821-2	Sequence 2, Appli
39	113.5	2.0	3571	US-09-911-842-2	Sequence 2, Appli
40	113	2.0	1066	US-09-423-126-3	Sequence 3, Appli
41	113	2.0	1066	US-09-280-197-5	Sequence 4, Appli
42	112	2.0	2835	US-09-885-535-4	Sequence 4, Appli
43	111.5	2.0	836	US-09-858-525A-10	Sequence 10, Appli
44	111.5	2.0	871	US-09-858-525A-2	Sequence 2, Appli
45	111.5	2.0	861	US-09-850-351A-32	Sequence 32, Appli

## ALIGNMENTS

RESULT 1  
US-09-875-423-4  
Sequence 4, Application US/09875423  
Patent No. US20020081657A1  
GENERAL INFORMATION:  
APPLICANT: Curtiss, Rory A.J.  
TITLE OF INVENTION: 21764, A NOVEL HUMAN CALCIUM CHANNEL  
FILE REFERENCE: 10448-059001  
CURRENT APPLICATION NUMBER: US/09/875,423  
CURRENT FILING DATE: 2001-06-05  
PRIOR APPLICATION NUMBER: US 60/209,257  
PRIOR FILING DATE: 2000-06-05  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 1091  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-875-423-4

Query Match	Score	DB ID	Length
Best Local Similarity	98.8%	US-09-875-423-4	1091
Matches 1049; Conservative	98.7%	US-09-875-423-4	1091
Mismatches	6;	US-09-875-423-4	Indels 0; Gaps 0;
1	MAAGCLLALTLTLFQSLILGSSQPPPSATYIKSVNKKMEDLVYTLAKTASGVNOLVDI	60	
1	MAAGCLLALTLTLFQSLILGSSQPPPSATYIKSVNKKMEDLVYTLAKTASGVNOLVDI	60	
1	MAAGCLLALTLTLFQSLILGSSQPPPSATYIKSVNKKMEDLVYTLAKTASGVNOLVDI	60	
61	YKYYODLVYVEFNNAKDDLPKNDSEPGSORIKPVFIDDAFNGROISQHAHVHPTDIESTIVL	180	
61	YKYYODLVYVEFNNAKDDLPKNDSEPGSORIKPVFIDDAFNGROISQHAHVHPTDIESTIVL	180	
61	YKYYODLVYVEFNNAKDDLPKNDSEPGSORIKPVFIDDAFNGROISQHAHVHPTDIESTIVL	180	
121	EVVYNAKDDLPKNDSEPGSORIKPVFIDDAFNGROISQHAHVHPTDIESTIVL	180	
121	EVVYNAKDDLPKNDSEPGSORIKPVFIDDAFNGROISQHAHVHPTDIESTIVL	180	
121	EVVYNAKDDLPKNDSEPGSORIKPVFIDDAFNGROISQHAHVHPTDIESTIVL	180	
181	NEIWMNSALDEYFKKREDEPSLIMQVGSAGLARYYPASPVVNSRTPKIDLYDVR	240	
181	NEIWMNSALDEYFKKREDEPSLIMQVGSAGLARYYPASPVVNSRTPKIDLYDVR	240	
181	NEIWMNSALDEYFKKREDEPSLIMQVGSAGLARYYPASPVVNSRTPKIDLYDVR	240	
241	RPWYIQAASPPYDMLTLVDVSGSVSGLTKLIRTSVSEMLTLLSDDFVNAFNSNAOD	300	
241	RPWYIQAASPPYDMLTLVDVSGSVSGLTKLIRTSVSEMLTLLSDDFVNAFNSNAOD	300	
241	RPWYIQAASPPYDMLTLVDVSGSVSGLTKLIRTSVSEMLTLLSDDFVNAFNSNAOD	300	

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Db 241 RPYVIGGAASPKDMLILVYSGSVSGLTLKLRITVSEMLETLSDDDFVNVAFSNMAOD 300
Qy 301 VSCFOHLVQANVRANKKVLKDAVANNITAKGIDYKKGESFAFOLLNANVRANKKITML 360
Db 301 VSCFOHLVQANVRANKKVLKDAVANNITAKGIDYKKGESFAFOLLNANVRANKKITML 360
Qy 361 FPDGGERAEOELFPAKYKNDKAVRFESVQHNDRGPLOMACBNKGYEIPSGAIR 420
Db 361 FPDGGERAEOELFPAKYKNDKAVRFESVQHNDRGPLOMACBNKGYEIPSGAIR 420
Qy 421 INTQETLDVGRPVLAGKAKOVMTNYLDALEGLVITGTLVFNITQGFENKTMK 480
Db 421 INTQETLDVGRPVLAGKAKOVMTNYLDALEGLVITGTLVFNITQGFENKTMK 480
Qy 481 NOLLIGVGVDSLEDIKRLPRFTLCNGYFFAIDPNGYVLLHPNLOPKPKKSOEPTVL 540
Db 481 NOLLIGVGVDSLEDIKRLPRFTLCNGYFFAIDPNGYVLLHPNLOPKPKKSOEPTVL 540
Qy 541 DFLDAELNDIKVELIRNKMIDGSESEKTFRLVKSODERYIDKGNRTYWTVPNGTDSL 600
Db 541 DFLDAELNDIKVELIRNKMIDGSESEKTFRLVKSODERYIDKGNRTYWTVPNGTDSL 600
Qy 601 ALVLPYTFYIYKAKIETITQASRSKGMKDSFTLKPDNFESGYTFIAPRDYCNLDKI 660
Db 601 ALVLPYTFYIYKAKIETITQASRSKGMKDSFTLKPDNFESGYTFIAPRDYCNLDKI 660
Qy 661 SDNNTFELNNEFIDRKTPNNPSCNTDLINRVLLDAGFTNELVQNTWSKOKNIKGVAK 720
Db 661 SDNNTFELNNEFIDRKTPNNPSCNTDLINRVLLDAGFTNELVQNTWSKOKNIKGVAK 720
Qy 721 FVVTIDGRTIRYPRKAGNMOENPEYEDSPKRSJLNDNVFPAFPNKSQCAVYSGI 780
Db 721 FVVTIDGRTIRYPRKAGNMOENPEYEDSPKRSJLNDNVFPAFPNKSQCAVYSGI 780
Qy 781 MYSKAVEITYQGLKLLKDAVYGIKIDVNSWLENFTKTSIRPDCAPVDCCKRNSVMDCVI 840
Db 781 MYSKAVEITYQGLKLLKDAVYGIKIDVNSWLENFTKTSIRPDCAPVDCCKRNSVMDCVI 840
Qy 841 LDDGGLLMANHDYTNQIGFSEIDPSLMRLVNI SVYAFNKSVDYQSCVCEGAPAKQ 900
Db 841 LDDGGLLMANHDYTNQIGFSEIDPSLMRLVNI SVYAFNKSVDYQSCVCEGAPAKQ 900
Qy 901 GAGHRSAYVPSIADLIHIGMMATAAAMSILOQFLSTFRLLEAVEMEDDFTASLSKO 960
Db 901 GAGHRSAYVPSIADLIHIGMMATAAAMSILOQFLSTFRLLEAVEMEDDFTASLSKO 960
Qy 961 SCITEQYQYFPDNDKSFSGVLDGNCSTRIFHEKLMNTNLIPIWESKGTCTPTRLII 1020
Db 961 SCITEQYQYFPDNDKSFSGVLDGNCSTRIFHEKLMNTNLIPIWESKGTCTPTRLII 1020
Qy 1021 QAEQTSIDGPPCDMVKOPRYRKGPVDCFNNALEDYTDGCGVS 1063
Db 1021 QAEQTSIDGPPCDMVKOPRYRKGPVDCFNNALEDYTDGCGVS 1063

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RESULT 2
US-09-875-423-5
; Sequence 5, Application US/09875423
; Patent No. US20020081657A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, ROY A.J.
; TITLE OF INVENTION: 21/84, A NOVEL HUMAN CALCITONIN CHANNEL
; FILE REFERENCE: 10448-059001
; CURRENT APPLICATION NUMBER: US/09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,257
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1091

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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-875-423-5
Query Match
Best Local Similarity 28.6%; Pred. No. 5.7e-74;
Matches 322; Conservative 234; Mismatches 437; Indels 133; Gaps 40;
20.4%; Score 1145.5; DB 10; Length 1091;
Qy 3 AGCLLALTLFOSLLIGSSQEPFSAVTKSVWDMKQEDVLTAKTAGVNOVDIYE 62
Db 14 ASALLA-TALLYALADGVRSQOIPLSV-VKLMAFAFGESIRIAKSSGOLLQKKK 71
Qy 63 KYODLVTEPPNMAKOLVETIARDIEKLSNRSAIYRIALAEKVOAQAOMRDEPANEY 122
Db 72 EYKDVAFIEIDGLQVKKLAKIMEEFHKSVAERLVAAEALKEHFFADL---OY 128
Qy 123 VYVNAK---DDLDEKNDSEPGSQRIRKVFETDPAFROISYQAAVHIPTDIESTIYL 180
Db 129 EYFNAVLINRDQGNFELGKEFI--LAPNDHFNNLPVNIISLDYQVPTNMTNKPDAIV 186
Qy 181 NELNMTSALDEYKKNREEDPSILMOVFGSANGLARVYASPVWNSRTPNKIDLYDVR 240
Db 187 NGVYWSIESLNKRVVDNEFRDPSLIMQYFSAKGFQYQGIKWEPE---NGVIAFDCKN 243
Qy 241 RPYVIGGAASPKDMLILVYSGSVSGLTLKLRITVSEMLETLSDDDFVNVAFSNMAOD 300
Db 244 RMYVIGGAASPKDMLILVYSGSVSGLTLKLRITVSEMLETLSDDDFVNVAFSNMAOD 300
Qy 301 VS-CFO-HLVQANVRANKKVLKDAVANNITAKGIDYKKGESFAFOLLNANVRANK 360
Db 304 VEPCLNGTIVQADRTNKEHREHLDFAKGIGMIDIANENFNLISDPNHTGOSISQ 363
Qy 357 IMLFTDGEERAEQELFAKYN-KDKKRVYFTSVQGHNTDRGPLOMACBNKGYEIP 415
Db 364 AIMLTIDGAVDITDTIFAAYNMPDRKVRITFYLRGAEAFADNLKMAKANGFTQIST 423
Qy 416 ISAIRINTQYLDVGRPVLAGKAKOVMTNYLDALEGLVITGTLVFNITQGFENK 464
Db 424 LADVGENVAYELVHSRPRVI--DQEHVYVTEAIDISTLPQACGLADOGVLTMTVAM 481
Qy 465 PYENITGQENKTNLKNOLLIGVGVDSLEDIKRLPRFTLCNGYFFAIDPNGYVLLH 524
Db 482 PVFS---KQNTSRKSG-ILLGAVGTDPVVKELTIKYKLGIGHYAFALITNGYILTH 536
Qy 525 PNLQF---KNPSQEP--VTDLFLDAELNDIKVIRNKMIDGSESEKTFRLVKSODER 579
Db 537 PELRPLYEGRKRRKPNSSVDLSVEWEDRDV-LRNAVNNRRTGK--FSMEVK---K 589
Qy 580 YIDKGNRT---YTPVPNGTDSLALVLPY-VSPYIYKAK--IERTITQASRSKGM 630
Db 590 TVDKGRVLYMTNDYYTIDIKTPSLGVALSRGHGKFFRGVNTIEGCL----- 639
Qy 631 KDSFTLKPDNFESGYTFIAPRDYCN-DLKSIDNNTFELNNEFIDRKTPNNPSCNTDL 689
Db 640 -----HLEHPDVSLADEWSTCNTDLHPHHRLLQLEAIKLYLKGKEP-LIQCKEL 690
Qy 690 INRVLLDAGFTNELVQNTWS-----KQNKIKGVAKRVVTDGRTIRYPRKAGNMO 733
Db 691 IOEVLFLDA-VVSAPLEAVWTSIALINKSENSDKGEVAFGLGRTLSLNTLFGVAGOLTNQ 749
Qy 734 ---KEAGENWOENPEYEDSPKRSJLNDNVFPAFPNKSQCAVYSGI 785
Db 750 DFLKAGDENIFNDHPEPLWYRAAEQIAGSFYSIPIFSGTGVNKS-----NVTASTS 803
Qy 786 VEIYIQGLKLLKDAVYGIKIDVNSWLENFTKTSIRPDCAPVDCCKRNSVMDCVI 845
Db 804 IQLDERKSPVYAAVGIOMKLEFFQKFWTASRQASLSDKCSISCDDEFTVNOYLLDNNG 863
Qy 846 FLMAHNDYTNQIGFSEIDPSLMRLVNI SVYAFNKSVDYQSCVCEGAPAGHGR 905
Db 864 FILVVS--EDYT-QTGDFGEVAGVNMKLLTMSFKRITLYDQAMK---AKESSDSA 917
Qy 906 SAVVPSTADLIHIGMMATAAAMSILOQFLSTFRLLEAVEMEDDFTASLSK-----Q 960

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Db 918 HELIDYKAF-----SAKIMTELVLVEF-----NLCSWMSHSDMTAKOKLTLE 967  
 Qy 961 SCITEOTQYFNDKSFSGVLDGNCGRIFHEKLMNTLIFIMESKGTCPDPT---R 1017  
 Db 968 PCDETPAVVSRTIKETTGNTACEDCSKSFYIOQIPSSNLEMYVYDS--SCLCESVAPI 1025  
 Qy 1018 LLIQAQTSDDGPDPCDMYKQPRYRKGPDYCFDNNALDEYTDGGS 1063  
 Db 1026 TWAPIEIRYNESIKCERLAKOKIRRRPESCHGFHEENARECGAS 1071

## RESULT 3

US-09-875-423-2  
 ; Sequence 2, Application US/09875423  
 ; Patent No. US20020081657A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Curtis, Rory A.J.  
 ; TITLE OF INVENTION: 21784, A NOVEL HUMAN CALCIUM CHANNEL  
 ; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF  
 ; FILE REFERENCE: 10448-053001  
 ; CURRENT APPLICATION NUMBER: US/09/875, 423  
 ; CURRENT FILING DATE: 2001-06-05  
 ; PRIOR APPLICATION NUMBER: US 60/209, 257  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 1091  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-875-423-2

Query Match 20.4%; Score 1140.5; DB 10; Length 1091;  
 Best Local Similarity 28.4%; Pred. No. 1.3e-73;  
 Matches 318; Conservative 234; Mismatches 442; Indels 127; Gaps 39;

Qy 3 AGCIALTLTLEFSSQEPFPPSAVITKSWDKQEDLVTLAKTAGSVNOLVDIYE 62  
 Db 14 ASALIAAAL-LYALGDVYRSEQIPLSV-VKLMAAFGEIKISAKYSGSOLQKKYK 71  
 Qy 63 KYODLYTEPPNNAQVEIARDEIKELNSRKALVLRLEAEKYQAQAHOREDFASNEV 122  
 Db 72 EYKQVAIEEDIGQLVYKLLAKNMEEMHKSSEAVRLEYEAELNKHEDADL---QY 128  
 Qy 123 VYNAK--DLDPEKNDSEPSQRIKPEYIDANFGQISYQAAVHIPTDIYEGSTVL 180  
 Db 129 EYFNAVILNERDKGNLELGEFT--LAPNDHFNLLPVNISLDVOYPTMYKKDPAIV 186  
 Qy 181 NELMWTSLDEVEFKKNEDEPSILMOYFGSATGLARYYPASPVWVNSRTPKIDLYVRR 240  
 Db 187 NGVWSESLKAVFYDNFDRDSLWQYFGSAKGFROYPGIKWEPDE---NGVIAFPGRN 243  
 Qy 241 RPWTIOGAAPKMDLIVDVSYSVGLTLKIRTSVSEMLETSLDDDFVNVASNSNAOD 300  
 Db 244 RKWYIOATSFKDQVLLIVDVSYSKGLRLTIAKQTVSIIIDTLDGDFNNIAINELHY 303  
 Qy 301 VS-CFO-HIVQANRKNKVLKDAVNNTIANGITDYKKGSPAEQOLLNVYNSRAN--CNK 356  
 Db 304 VEPCLNGTLVQADRTNHEHREHLKFLANGIMDLALNEAFNLLSDFNHTGGGSCISQ 363  
 Qy 357 IIMLTGGEERAOEIFAKTN-KDKRYVTFESVGHNYRGPIONMACENKGYIIPS 415  
 Db 364 AIMLTGCAVDYDTITAKTNMPPRKRYITFYILGREAPADNLKMWACANKGFPQIST 423  
 Qy 416 IGAIRINTOEYLDVGRPNVLADGKAKQOVMTNYLDAL-----ELG--LVITGL 464  
 Db 424 LADVOENVMELVLSRPYI--DQEHVYVTEAYIDSTLPQAKQLTDDGQVPLMTVAM 481  
 Qy 465 PVENITQONKTNLKNQOLLGWSGVDSIEDIKRLTPRTLCPCNGYFAIDPNGVYLH 524  
 Db 482 PVES---KONETRSKG-ILGAVGTDVPVKEELTKIPKYKLGHVAFATITNGYILTH 536

Qy 525 PNLQ---PKNRKQEP--VTIDFLDAELENDIKYEIRKMKIDGSGEKTRTITKSDER 579  
 Db 537 PELRLIYEEGKKRRKRNSSVDLSLEVEDREDV-LRNAMNRKTG--FSMEVK---K 589  
 Qy 580 YIDKGNRT-----YWTVPNGTDYSLALVLPY-YSEYTIKAK--IEETITQARSKGKM 630  
 Db 590 TVDKGRFLVMTNDYYTYDIDKGTPEFSLGVALMSRCHGKGYFFRGNTIIEGL----- 639  
 Qy 631 KDSITLKDNEEGSGYFIARDCN-DLAKISDNTEFLNFEIDRKTPNNPNSCFDL 669  
 Db 640 -----HDLHPDVSILADEMSYCNFDLHPEHRHLSQLEAIKLYLKGKEP-LLOCKEL 690  
 Qy 690 INRYLDAGFTNELVQWYS-----KOKNIKGKARFVYTDGKITVYF----- 733  
 Db 691 IQEVLFDA-VSAPILEAVTISLANKSENSKGYEAVFLGTGRLSRINI-FVGAEOLTNQ 749  
 Qy 734 --KTAGEMOENPTEYEDSPYKSLDN--DNYVTAAPYKSGGPAVSEGIWASKAVEIY 789  
 Db 750 DFLKAGDKENIFNADHPPLWYRAAEQIPGSFYISYF--STGPNKSNVYVASTISQTL 807  
 Qy 790 IQGKLPAVYGIKIDVNSMIENFTKTSINDPCAGPYCDCKRNSDWCYIIDDGFLM 849  
 Db 808 DERKSPVVAAGIDMKLEFFORKEFTWASRQCASLDGKCSISCDDEVNCLIDNNGFIV 867  
 Qy 850 ANHDYTNQIGRFGEDIPSLMRHLVNI SYAFENKSYDYOSVCEPGAAPKGA-GHRSAY 908  
 Db 868 S-EDYT-QTGDFEGELGAVMNKLLTNGSFKRTIYDYAMKRAKESDGAHGLDIPY 924  
 Qy 909 VPSTADILHIGWATTAAMSITLQFLISTLFPRLLEAVEMEDDFTASLSK-----QSCI 963  
 Db 925 -----NAFLSAKWKIMTELVLVEF-----NLCSWMSHSDMTAKOKLTQLEPDD 970  
 Qy 964 TEOTQYFNDKSFSGVLDGNCGRIFHEKLMNTLIFIMESKGTCPDPT---RLLI 1020  
 Db 971 TEYAFSERTIKETTGNTACEDCSKSFYIOQIPSSNLEMYVYDS--SCLCESVAPI 1028  
 Qy 1021 QAQTSDDGPDPCDMYKQPRYRKGPDYCFDNNALDEYTDGGS 1061  
 Db 1029 PIEIRYNESIKCERLAKOKIRRRPESCHGFHEENARECGG 1069

RESULT 4  
 US-10-005-168-2  
 ; Sequence 2, Application US/10005168  
 ; Patent No. US20020133840A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brennan, Thomas J.  
 ; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING DISRUPTIONS  
 ; TITLE OF INVENTION: IN GENES ENCODING A2D2 CALCIUM ION CHANNEL SUBUNIT PROTEINS  
 ; FILE REFERENCE: R-10  
 ; CURRENT APPLICATION NUMBER: US/10/005, 168  
 ; CURRENT FILING DATE: 2001-12-04  
 ; PRIOR APPLICATION NUMBER: US 60/299, 668  
 ; PRIOR FILING DATE: 2001-06-19  
 ; PRIOR APPLICATION NUMBER: US 60/282, 685  
 ; PRIOR FILING DATE: 2001-04-09  
 ; PRIOR APPLICATION NUMBER: US 60/254, 802  
 ; PRIOR FILING DATE: 2000-12-11  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 223  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 ; US-10-005-168-2

Query Match 8.4%; Score 470.5; DB 12; Length 223;  
 Best Local Similarity 44.3%; Pred. No. 1.4e-26;  
 Matches 81; Conservative 38; Mismatches 63; Indels 1; Gaps 1;

Qy 878 SYAFENKSYDYOSVCEPGAAPKQAGHRSAVYVPSTADILHIGWATTAAMSITLQFLIST 937  
 Db 2 SFITRKESYDQAAKAPQPPGNLGAAPRGVFTIADFLNLAWMTSAAWSILFQOLLVGL 61

QY 938 TEPRLLEAVEMEDDFTASLSKOSCIITQYFFPDNDSKSPSSVLDGNSRIPIHVKIM 997  
Db 62 IYHSWFQADPPEABG-SEPTRESSCYMKQTYFGSVASYNALIDGNSRLEHQAOLT 120  
QY 998 NTNLIIFIVESKGPCTCTRLIIAEOGSDGPDCDWKKOPRYKGGPDVCHDNALIEDYT 1057  
Db 121 NTNLIIFVAEKPICSGCAGRLIKETHSDGPGCELVORRNRGRHCHICDYATEDTS 180  
QY 1058 DCG 1060  
Db 181 DCG 183  
RESULT 5  
US-09-864-761-44281  
; Sequence 44281, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aecomica-X-1  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US/09/864,761  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263,6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 44281  
; LENGTH: 51  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AC006145.2  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.86  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.91  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.93  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.81  
; OTHER INFORMATION: SWISSPROT HIT: P54289, EVALUO 4.00e-25  
; OTHER INFORMATION: EST\_HUMAN HIT: H86016.1, EVALUO 1.00e-02  
US-09-864-761-44281  
Query Match 4.9%; Score 272; DB 10; Length 51;  
Best Local Similarity 100.0%; Pred. No. 2.8e-13;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 859 IGRFGEIDPSLIRHLVNISVAFNKSYPDQSYCEGAPAKOGAGHSAYV 909  
Db 1 IGRFGEIDPSLIRHLVNISVAFNKSYPDQSYCEGAPAKOGAGHSAYV 51  
RESULT 6  
US-09-864-761-38267  
; Sequence 38267, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO  
; FILE REFERENCE: Aecomica-X-1  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US/09/864,761  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263,6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 38267  
; LENGTH: 53  
; TYPE: PRT

ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC008283.3  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.86  
OTHER INFORMATION: EST HUMAN HIT: AL134437.1, EVALUE 3.00e-24  
OTHER INFORMATION: SWISSPROT HIT: P54289, EVALUE 4.00e-25  
US-09-864-761-38318

Query Match  
Best Local Similarity 4.9%; Score 272; DB 10; Length 53;  
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 294 FNSNADVSCFQHLVQANVRNKKVLDKAVNNTTANGTIDYKGFSAFQQLN 346  
DB 1 FNSNADVSCFQHLVQANVRNKKVLDKAVNNTTANGTIDYKGFSAFQQLN 53

## RESULT 7

US-09-864-761-38318  
Sequence 38318, Application US/09864761  
Patent No. US2002048763A1  
GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: Aecomica-X-1  
CURRENT FILING DATE: 2001-05-23  
PRIORITY FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/224,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 38318  
LENGTH: 35  
TYPE: PRT

ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC008283.2  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.84  
OTHER INFORMATION: EST HUMAN HIT: AW051755.1, EVALUE 1.00e-14  
OTHER INFORMATION: SWISSPROT HIT: P54289, EVALUE 2.00e-15  
US-09-864-761-38318

Query Match  
Best Local Similarity 3.4%; Score 190; DB 10; Length 35;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 WTSALDEVFKKRNREDPSLWQVGSATGLARYP 219  
DB 1 WTSALDEVFKKRNREDPSLWQVGSATGLARYP 35

## RESULT 8

US-09-828-423-5  
Sequence 5, Application US/09828423  
Patent No. US20020099178A1  
GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.  
APPLICANT: Guegler, Karl J.  
APPLICANT: Patterson, Chandra

TITLE OF INVENTION: GROWTH-ASSOCIATED TRYPSIN-TYPE  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: Word Perfect 6.1/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/828,423  
FILING DATE: 05-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/388,774  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Certone, Michael C  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PF-0505 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 885 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENEBANK  
CLONE: 91288563  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-828-423-5

Query Match  
Best Local Similarity 3.3%; Score 185; DB 10; Length 885;  
Matches 137; Conservative 113; Mismatches 243; Indels 150; Gaps 36;

QY 45 VTLAKTASGVNDLVIEKYQULYVEPNARQIVEIARDIEKLISRSKALVRLALEA 104

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Db 77 VELPRTAFITNFTLTI-----DGYTY-PGANYKE-KEYAKKOYEKAVSOGKTAGL----- 123
OY 105 EKVQAAHOMREDF-----ASNEVYVYNAKDDIDPEKNOSPESSQIKKPYFIDANFGR 157
Db 124 --VAVASGKLEKFTYVSVNAGSVTELELYEELKKRHKGYEMYLAVQP-----K 172
OY 158 QISOHVAHIPTIIEGSTIVLWELNMTSALDEVFKKNREDESLIMOVGSA-----T 212
Db 173 QI-VKHEIEY--DIFERQGI-----SMLD-----AEASFITNDLGSALTMSFS 214
OY 213 GLARYPPASPVVDSRT--PKID-----LYDVRRRP-----WTI-----QG- 247
Db 215 GKKGVSEKPSIDQORSCPTCTDILNNGDTITTYDVNKPESGNOYIYNGVFHFEPQGL 274
OY 248 AASPDMLILVDVSGSVGLLKLIRTSVSMLETLSDDDVNVNAPFSNADVSCF-OH 306
Db 275 PVVKNVAVFVIDISGSMGKRIEOTKEALKLILEDKMEEDILNLLISG--DYSTMKH 331
OY 307 LVQANVRKKYLKDAVNNITAKGITDYKKGFSEAFEOQLNYSR-----ANCKITML 360
Db 332 LVQATPEMLQEARFTVVKSMEDKCMNINDGLRGISML--NKAREHRIPERSTIYIM 388
OY 361 FTDG-----GEBAOETFAKYNK--DKKRVFTFSVGOHNYRGPLOMACNKGYYEIP 414
Db 389 LTDDGANVGESEPRKIQENVRNATIGKFPYLNLGFG--NNLNYNPLENNALNHFARIRY 447
OY 415 SIGARINTOEYLDVIGRPVYLAGDKAKOVQWTVNYIDALE-----GLVITGTLP 465
Db 448 EDSADLOLOQGYEEVAVNPL-LTGYEMEYPE--NAILDITONTYOHFDSGEIYVAGLY 504
OY 466 VENITGONENKTNLK-----NOLIGVAGVDSLEDIKRLPRTLCNGYYFAIDPN-- 518
Db 505 DEEDM--NSFKADYVGHGATNDL--TTEYDMKEMEK-----ALQBDYIFG--NYI 550
OY 519 ----GYVLHPLOQK--NKSQEPVLDPLDALENDINVEIRKMKIDESGKTRPT 571
Db 551 ERLMAYLITLEQLERKRNHGEKENLTPARALDSLKYHEVTPPLTSMVYTPK----- 603
OY 572 LVKSODERYI-DKGNRTYTWTPVN-GTDYSLALVLPYTSFYI 612
Db 604 --DNEDERAIADKPGEDAEATVSPAMSYLINSYOPPONPYIV 644

RESULT 9
US-09-864-761-36461
; Sequence 36461, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 36461
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC008283.2
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.67
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.7
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.8
; OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
; OTHER INFORMATION: EST HUMAN HIT: AM051755.1, EVALUATE 3.00e-04
; OTHER INFORMATION: SWISSPROT HIT: P54290, EVALUATE 6.00e-15
US-09-864-761-36461

Query Match 3.2%; Score 182; DB 10; Length 35;
Best Local Similarity 97.1%; Pred. No. 4.5e-07;
Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 141 GSGRIKPYFIDANFGQISYQNAVAHIPTDIYEG 175
Db 1 GSGRIKPYFIDANFGQISYQNAVAHIPTDIYEG 35

RESULT 10
US-09-850-351A-4
; Sequence 4, Application US/09850351A
; Patent No. US20020100080A1
; GENERAL INFORMATION:
; APPLICANT: Feltelson, Jerald S.
; APPLICANT: Schnepf, H. Ernest
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stockhoff, Brian A.
; APPLICANT: Schmeltz, James
; APPLICANT: Loewer, David
; APPLICANT: Dullum, Charles Joseph
; APPLICANT: Muller-Cohn, Judy
; APPLICANT: Stamp, Lisa
; APPLICANT: Morrill, George
; TITLE OF INVENTION: NO. US20020100080A1el Pesticidal Toxins and Nucleotide
; Sequences Which Encode These Toxins
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606-6669

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QY 81 -----IAARDIEKLNSKALVRLALAEKVQAHQWREDEFSN----- 120  
 DB 78 QSTTSMATMTIOSKVVNNSPQONVVDVQJPKGA-----FISNFSMTVCKTFRSS 131  
 QY 121 -----EYVYNNK-----DLDPEKNDSE-----PGSQRKPFVIFDANFGQ 158  
 DB 132 IKETVGALYQAARAGKTAGLVRSALDMENRETVNLPGAKVOFELHYQEVKMRKL 191  
 QY 159 ISYOH-----AAVHPDIIYEGSTIVLNLMTSALD-----EYFKKNRE----- 199  
 DB 192 GSYEHRIYLOPGRLLAKHLEVDVWIEPOGLNFIHVPDTEFGHEDGVPIISKQOKAHVSF 251  
 QY 200 DPSILMOVFSATGLARYPASPWDSRTPNKIDLYDVRRP-----WYIOGAA 249  
 DB 252 KPTVAQO-----RICEPCR-----ETAVDGLVVLKIDVREKAGLELVFNGVFFHFA 300  
 QY 250 S-----PKDMLILVDVSGSVGLTLKILRTVSSEMLETUSDDPFVAVASFNNAQVSC 303  
 DB 301 PDNLDPIPKNILEVIVDVGSMGVKMKQTVAMKTIILDDLEADHFSVIDENQIR--TW 358  
 QY 304 FOHLVQANVRKKVYLKDAVNMTAKGITYDKKF-----SFAEQLLNVNSRANCKITML 360  
 DB 359 RNDLFOLQKHRLQIAKRIETQPSGGTINLEALLRALFILLNEANNGLDLPNSVSLIL 418  
 QY 361 FTDG-----GEERAOEIFAKYKDKKVRVTFPSVQ--HNYDRGPLOMACENKG----- 408  
 DB 419 VSDGDPYVGLKLSKIQKNVENIQDNISLPSLGMFPVDYDLKRLSENHGIQRIYQ 478  
 QY 409 -----YYEYI--PSIGAIRIN--TOEYLDVL-----GRPMVLAG--DKAKO 443  
 DB 479 NODTSSQLKKFYNOVSTFLRNVOFNPHSTVDTYONNHNFGGSEIVVAGKFDPAK- 537  
 QY 444 VQWTVVYDALEGLVITGTLPEVFNITGQENKTNLKNQLILGVMGVDSLEDI-----KR 499  
 DB 538 -----LDQIR--SVITA-----ISANTQVLELTLAQDDLDQDLSKMKH 574  
 QY 500 LTRPRLCPNGYFFAIDENGVYLLHPNLQPKNPSQSEFVTLDFDAELENDIKYEIRNKK 559  
 DB 575 ADPDPTR-KIMAYITLIN--QLAERSLAP--TAAKRRTITSIILOMSIDHHIVPLTSLV 629  
 QY 560 IDGSEKTEFRTLVKSD 577  
 DB 630 IENAGDEHMLADAPPOD 647

RESULT 12  
 US-09-850-351A-6  
 : Sequence 6, Application US/09850351A  
 : Patent No. US2002010080A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Feltelson, Jerald S.  
 : Schnepf, H. Ernest  
 : Narva, Kenneth E.  
 : Stockhoff, Brian A.  
 : Schmeits, James  
 : Loewer, David  
 : Dullum, Charles Joseph  
 : Muller-Cohn, Judy  
 : Stamp, Lisa  
 : Morrill, George  
 TITLE OF INVENTION: NO. US2002010080A1el Pesticidal Toxins and Nucleotide  
 Sequences which Encode These Toxins  
 NUMBER OF SEQUENCES: 144  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
 STREET: 2421 N.W. 41st Street, Suite A-1  
 CITY: Gainesville  
 STATE: FL  
 COUNTRY: US  
 ZIP: 32606-6669  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/850,351A  
 FILING DATE: 07-May-2001  
 CLASSIFICATION: <unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 09/073,898  
 FILING DATE: 06-MAY-1998  
 APPLICATION NUMBER: US 08/960,780  
 FILING DATE: 30-OCT-1997  
 APPLICATION NUMBER: US 60/029,848  
 FILING DATE: 30-OCT-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sanders, Jay M.  
 REGISTRATION NUMBER: 39,355  
 REFERENCE/DOCKET NUMBER: MA-708CD1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 352-375-8100  
 TELEFAX: 352-372-5800  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 789 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 ORIGINAL SOURCE:  
 INDIVIDUAL ISOLATE: 81F  
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
 US-09-850-351A-6

Query Match 2.8%; Score 157.5; DB 10; Length 789;  
 Best Local Similarity 20.1%; Pred. No. 0.0026;  
 Matches 138; Conservative 103; Mismatches 231; Indels 215; Gaps 35;

QY 231 NKIDIVRRRPYIGGASPKMILIVYSSVSLTLKILRTVSSEMLETUSDD-DFV 289  
 DB 105 NKIDALNTMLRYL-----PKITSMDSVMKONVLSLQI--EYISKQLOEISDKDLII 156  
 QY 290 NV-ASFNSNAQDVS-----CFQHLVQANVRKKVYLKDA-----VNNT-----A 327  
 DB 157 NVNVLINSLTLETPAQRIRKYVNEKPELTFATETSSKYKKGSPADILDELTELTELA 216  
 QY 328 KGITDYKKGFSFAEQLLN--YVNSRANCKIITMLPTDGEERAOEIFAKYKDKKVRVRF 385  
 DB 217 KSVY--KNVDGEFEFLNPFHVMGN-----NLGFSALKTASLITKEN-----VKTS 264  
 QY 386 TFSYQO--HNYDRGPLOMACENKGYEYIETPSIGAIRINTQEYLDVLRPMVLAGDKAKOV 444  
 DB 265 GSEGVGNYNF--LIVITALQAKAFLLITCRKLLGLADIYTSINNEHL-----NKEKEE 317  
 QY 445 QWTVVYDALEGLVITGTLPEVFNITGQENKTNLKN-----OLIL-----GVMGVDVS 493  
 DB 318 FRVNI-----LPTLSNFPSPNRYAKVKGSDAKMIYEAKGHALVGEIS 363  
 QY 494 LEDI-----KRLTRPE-----TLCPNG-----YVF--AIDPNGYVLL 523  
 DB 364 NDSITVLKYEAKLKQYOVQDKSLSEVIYGDMDKLCPQOSQIYITNNIYFNPNEYVIT 423  
 QY 524 HPNLQPKNPSQSEFVTLDFDAELENDIKYEIRNKMIDGSEKTEFRTLVKSODERYIDK 583  
 DB 424 KIDYTKMKKTLRYEVYANFVDSSTG--EIDLNNKKV--ESSEAEKRYTISANDGVYVPL 478  
 QY 584 GNRITYW-TPVNG--TDVSLVLPFTYSFYIKAKIETITQANSKKKKMDSETLKP 638  
 DB 479 GVISETEFLPIINGLOADENSRLITLTKSYRELLELADLSN-----KETKLIIV 530  
 QY 639 -----DNFEESGYFIAPROVCNDLKTSDNNTG--FLNPNFEFDRTKTPANNPCNDLILN 691  
 DB 531 PSGFIKNIVENG-----SIEBDNLEPMKANNKNEYVDH----- 563  
 QY 692 RVLIDAGFTNELVONYMSKOKINIKVAKARFVYVDGIT-----RYDK----- 734

Db 564 -----TGCVNGTAKALVYHKDGGISQFIGKLRKTEYVQYTVKGR 604  
 QY 735 -----EAG-----EMWQENPEYEDSEFYKRSIDNDNYFTAPYFKSGPAGAYESGIMV 782  
 Db 605 PSILKDENTGYIHEDTNNLEDYQITRKFTTGDLKGVYLLKSQNDDEAMGDNFI 664  
 QY 783 SKAVEIYIOGKLRKPAVVGKIKIDVNSW 809  
 Db 665 ---LEISPSERKLSPEL---INTNMW 684

## RESULT 13

US-09-850-351A-8  
 ; Sequence 8, Application US/09850351A  
 ; Patent No. US20020100080A1  
 ; GENERAL INFORMATION:

APPLICANT: Feltelson, Gerald S.  
 Schnepf, H. Ernest  
 Narva, Kenneth E.  
 Stockhoff, Brian A.  
 Schmeits, James  
 Loewer, David  
 Dullum, Charles Joseph  
 Muller-Cohn, Judy  
 Stamp, Lisa

TITLE OF INVENTION: No. US20020100080A1 Pesticidal Toxins and Nucleotide  
 Sequences Which Encode These Toxins

NUMBER OF SEQUENCES: 144

CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
 STREET: 2421 N.W. 41st Street, Suite A-1  
 CITY: Gainesville  
 STATE: FL

COUNTRY: US  
 ZIP: 32606-6669

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC Compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/850,351A

FILING DATE: 07-May-2001

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/073,898

FILING DATE: 06-May-1998

APPLICATION NUMBER: US 08/960,780

FILING DATE: 30-Oct-1997

APPLICATION NUMBER: US 60/029,848

FILING DATE: 30-Oct-1996

ATTORNEY/AGENT INFORMATION:

NAME: Sanders, Jay M.

REGISTRATION NUMBER: 39,355

REFERENCE/DOCKET NUMBER: MA-708CD1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 352-375-8100

TELEFAX: 352-372-5800

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 790 amino acids

TYPE: amino acid

STRANDEDNESS: single

MOLECULE TYPE: linear

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: Jay90

SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-09-850-351A-8

Best Local Similarity 19.7%; Pred. No. 0.0026;  
 Matches 138; Conservative 102; Mismatches 217; Indels 245; Gaps 35;

QY 231 NKIDLYVRRRPYIYGASPRKMLIDVSGSVGLTKLIRTSVSEMLETLPD-DFV 289  
 Db 105 NKIDLYVRRRPYIYGASPRKMLIDVSGSVGLTKLIRTSVSEMLETLPD-DFV 289  
 QY 290 NY-ASFSNAQDVS-----CFQHLVQANRKKVYLKA-----VNNIT-----A 327  
 Db 157 NYNVLINSLTETTPAYORIKYVNEKFELETSSKVKKDGSPADILDELFTETELA 216  
 QY 328 KGITDYKKGFSFAFEDLIN--YVNSRANCKRLIMFTGGEEERAEIYAKNKKQKRVF 385  
 Db 217 KSVT---KNDVGFEEFYINTFHDVAVGN-----NLFGRSAKTASLETTKEN--VTS 264  
 QY 386 TFSVGO-HNYDGPQIOMACENKGYEIPISGIRINTOEYLDVLRPMYAGDKAKOV 444  
 Db 265 GSEVGNVYNE---LIVTALQAKAFLLTTCRKLGLADIDYTSIMNHL-----NKEKEE 317  
 QY 445 QMTNYVLDALDELGLVITGTLPEFNTGONENKTNKN-----QIL-----GWCVDVS 493  
 Db 318 FRYNI-----LPTLSNTSPNPAKVKGSDEDAKMIWEAKPGHALIGFEIS 363  
 QY 494 LEDI-----KRLPRF-----TLCPNG-----YF--AIDPNGYLL 523  
 Db 364 NDSITVLKYEAKLKQNVQDKDSLSEYIYGDMDKLCPCDSEQIYTNINIVFNEYVIT 423  
 QY 524 HNNLPKPKQEPYTLDFDLAELENDIKVEIRKMKIDGESGERTFRLVKSODERYIDK 583  
 Db 424 KIDFTKMKKTLREYVTAIFYDSSTG---EIDLNKKV--ESSEAEYRFLSANDGVYMLP 478  
 QY 584 GNRITYT-TPVNGDYSLALVLPYYSFYIKAKIEETITQARSKKMKKDSSETLKPNEF 642  
 Db 479 GVISSETFLTPINGFC-----LQAD--E 498  
 QY 643 ESGTIFAPRDYCNLDKISDNTEFLNFEIDRKTNNPNSCTDLINR-----VLDAAG 698  
 Db 499 NSRLITLCKSYRELILA-----TDSNNEIKLIYPPSG 533  
 QY 699 FTNELVON-----YMSKOKN-----IKGYKARVYVDGITYRYPREAGENV 740  
 Db 534 FISNIVENGSIEDNLEPWNKNNNAVYDHTGVNGTKALYVHDDGISQF---IDKFL 589  
 QY 741 QENPEY-----EDSFYKRSIDNDNYFTAPYFK----- 770  
 Db 590 KPKTEYVYQYVKGKPSILKDENTGYIHEDTNNLEDYQITNKRFTTGTDLKGYLL 649  
 QY 771 ---SGPAGESGINVSKAVEIYIOGKLRKPAVVGKIKIDVNSW 809  
 Db 650 KSONGDEAMGDNFI---LEISPSERKLSPEL---INTNMW 684

## RESULT 14

US-09-815-242-5898

; Sequence 3898, Application US/09815242

; Patent No. US20020061569A1

; GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Karl L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

Query Match 2.88; Score 157.5; DB 10; Length 790;

```

; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 5898
; LENGTH: 1349
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5898

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Query Match      2.7%: Score 152; DB 10; Length 1349;
Best Local Similarity 19.3%; Pred. No. 0.014;
Matches 198; Conservative 124; Mismatches 337; Indels 366; Gaps 48;

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QY 16 SLIISSQEPFSAVITIKSWDKMQEDVTLAKTASGVNQ---LVDIYKYDLYTVEP 72
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 40 TLIFGIGNQAKAEKSTNKE-----LNEATTSASDNQSDKVDQMQLNEDNTKND 90
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 73 NNAQRLVEIAARDIEKLNSKALVRLALEAKVQAAHQWREDFASNEVYIYAKDDL 132
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 91 NQK---EWVSSQNETTSNGK-----LIKESVQST-----TGKRYEVSITAKSD-- 132
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 133 PEKNDEPGSORIKKFEVIDDANFGROIYQHAHAHIPTDIYEGSTIV----- 179
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 133 ---EQASPRSTN-----EDLNTKQIJSNQA---LQDLDQNKSVVAVQPTNENKQVD 180
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 180 -----LN-----ELNMTSALDEVFKKNEEDPSLIM-----QVFGSATGLARYPA 220
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 181 AKTESTTLNVKSDAISKNDIELVDNNSNENNNADILIPKSTAPKRLNTMRILAAVOPS 240
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 221 SPWVON-----SRTPNKIDLYVRRRPVIOGAASPKMDLIVDSGVSGLTFLKILRT 274
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 241 STEAKVNDLITSNTLLVVDADKNNKIYPADYISLKSQITVDKVKSSGYFIITK--- 297
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 275 SVSEMLETISDDFVNVASFN--SNAQDVSCFOHLVQAVNRKKVYLKDVNNTAKGITD 332
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 298 SDTVQYGGINPEDIKNIGIKDPNNGETLATAKH-----DTANNLLTYFTTD 344
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 333 YKGFSEFAFEQOLLNVV-----SRANC-----NK 356
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 345 YVDREN-SVQMGINSIYADADTIPVSKNDVEFNVTIGNTTTKTTANIQFQDYVYVNEKNS 403
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 357 IIMLFYD-----GGEER---AQEITFAKYNKDK---KVRVFTF-----SVQGHNVDRG 397
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 404 IGSAFTEIYSHVGNKKNPEYKOTIYVNSSENLSNAKLKQVAYHSSYPNNIGQINKDVT 463
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 398 PIGMAACE-----NKGIYIEISIGAIRINTOEYIDVLRPM--VLADKRAQV----- 444
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 464 DIRIYVPRKGYTLNKGY-----DVNTEKELTDVINOYLQKLTGYDNNNSAVIDFGNA 513
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 445 -----QWNTN----- 448
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 514 DSAIYVAVNTKFFQYTNSESEFTLYQAMATLSTGKNSVSTGNALGFTNNQSGAGQEVYKIG 573
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 449 --VYLDALIELGIVITGLPFVNT--GQENKNTNLKNOLLGVAGVDSLEDIKRLVPRFT 505
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 574 NYWVEDNKNKGVOELGEKGVAGNTVTVFNNTNTK-----VGEAVTRKEDGSYLIPML- 625
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 506 LCPNGYI--FAIDPNGYVILHNLQPKPK-----SQEPYLDLDELDALENDIVELRN 557
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 626 --ENGDIRVEFSNLPKGYEVT--PSKQGNNEELDSNGLSSIVTVNGKD--NLASLGIYVPK 681
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 558 KMIIDEGEKTFRITVKSQDERYIDKGNRTYTWTVPNGDYSALVILPTYSFYIKAKIE 617
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

```

```

DB 682 YNLCDYWEEDTNKNGIODEDEKGI--SGVTYTLKDENG-----DVL 720
QY 618 ETIQAAKKKKKKMDESEFLKPDNFEESGYFIAPRDYCDLKSIDNTEFLLNFEIDR 677
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 721 KTVTTDADGKKKFTD---LNGNWK---VEFTTPEGTTPTTVYSSGDIE----- 763
QY 678 KTPNPNSCNTDLIN---RVLLDAGFTN---ELVQNTW-----SKQNNIKGV--- 717
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 764 -KDSNGLTGTVINGADNMTLDSGFKTPRYNLGNVWVEDTNKDKGQDSTERGISGVTV 822
QY 718 -----KARFVYTDGIGITRY-----YKKEAGENNQOE----- 742
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 823 LKNEGEVLOTTKDKDKGKTQFTGLENGTYKVEFEPTSGTTPYQVSSGDEIDSGTST 882
QY 743 -----NPETVEDSEFFKRSIDNDNRYFPAFYENKSGPGAYE---SGIMVSKAVEIYIQ 791
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 883 TGVIKDKNDPILDSGFYKPKPYNLGIDYWEPT--NKNQVQDKDEKGISGVTVLKD--N 937
QY 792 GKLLK 796
   :|:|:|
DB 938 DKVLK 942

```

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RESULT 15
US-09-815-242-13137
; Sequence 13137, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyckind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011a
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 13137
; LENGTH: 1349
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-13137

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Query Match      2.7%: Score 152; DB 10; Length 1349;
Best Local Similarity 19.3%; Pred. No. 0.014;
Matches 198; Conservative 124; Mismatches 337; Indels 366; Gaps 48;

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Db 91 NOK-----EMVSSQGNETSNGK-----LIEKESVOST-----TGKKEVEVSTAKSD-- 132

QY 133 PEKNDSEPGSORIKPVEFIDANFGROISYQHAHHIPTDIYEGSTIV----- 179

Db 133 ---EQASPKSTN-----EDINTKOTISNOEA---LOPDIQENKSVVWVQPTNEENKVD 180

QY 180 -----LN-----ELMWTSAIDVEFKKNEEDPSILM-----QVFGSATGLARIYPA 220

Db 181 AKTESTTLNKSDAIKSDETLVNDNSNSNNENNADILLPKSTAPKRLNTRMRIAAYOPS 240

QY 221 SPWVDN-----SRTPNKIDYDVRPRPMYIQGAASPRKMLILVDVSGVSGILFKLIRT 274

Db 241 STEAKNVADLITSNTLLVVDADKNKKIVPADYLSLSQITVDKXSGDYFTIKY--- 297

QY 275 SVSEKLETLSDDDVYVNAFEN--SNAODVSCFOHLVQANVRNKKVYLKDAVNNITAKGTTD 332

Db 298 SDYVOVYGLNPEIDIKNIDIDKPNNGETIATAKH-----DTANNLITYFTD 344

QY 333 YKKGSFAFEQDLNANY-----SRANC-----NK 356

Db 345 YVDREN--SVOMGINSTYMDADTIPVSKNDVEFNVTIGNTTKTANIQYDPDYVNEKNS 403

QY 357 IIMLETTD-----GGER-----AOEIFAKYKNDK---KRVYFTF-----SVGOHNYDRG 397

Db 404 IGSAFETEVSHVGNKENGYKQITIVNPSSENSLTNAKLYQAIHSSYPNNIGQINKDVT 463

QY 398 PIQWMAE-----NKGYEYELPSIGAIRINTQEXYLDVLRPM--VLADKAKOV----- 444

Db 464 DIKTYQVPEKGYTLNKG-----DVNTEKELDVTNQYLOKITYGDNNSAVIDFGNA 513

QY 445 -----OMTN----- 448

Db 514 DSAIVVWVNTKFOYTNSSEPTLVOMATLSTGKNSVSTGNALGFTNNOSGAGQEVYKIG 573

QY 449 --VYIDALEGLVITGLPVENIT--GONENKTNLKNOILLGVMGVDSLEDIKRLTPRFT 505

Db 574 NYWVEDTKNGVQELGEKGVGNVTVYFEDNNTNK-----VEAVTKEDGSLIENL- 625

QY 506 LCPNGY---FAIDPNGYVLLHPNLQPKNPK-----SOEPTVLDPLAELENDIKVEIRN 557

Db 626 --PNGDVRVEFSNLPKGEYEV--PSKOGNNEHIDSNGLSSVITYNGKD--NLSADIGIYKPK 681

QY 558 KMGESGEKTFRTLVKSODERYIDKGNRTYTWTPVNGTDSLALVLPYISFYIKAKIE 617

Db 682 YNLCDYWEEDTNKNGIODDEKGI--SGVYVTLKDENG-----DVL 720

QY 618 ETTQARSKKGMKMDSETLKPDPNEESGYTFIAPRDYCNDLKISDNTEFLANFNEIDR 677

Db 721 KTVTTDADGKXKFTD---LHNGNPK---VEFTTPEGYTPPTVITSGSDIE----- 763

QY 678 KTPNPNSCNDULIN---RVLLDAGFTN---ELVQNTW-----SKOKNIKGV-- 717

Db 764 -KDSNGLTTCVINGADNMGLTSGFYTPKYNLGNVYWEEDTNKDKODSTEGISGVTVT 822

QY 718 -----KAFVYTDGITRY-----YPRKAGENMOE----- 742

Db 823 LKNENGEVLQTKTKDKGKTOFTGLENGTYKVEEFTPSGYTPTOVGSCTDEGIDISNGTST 882

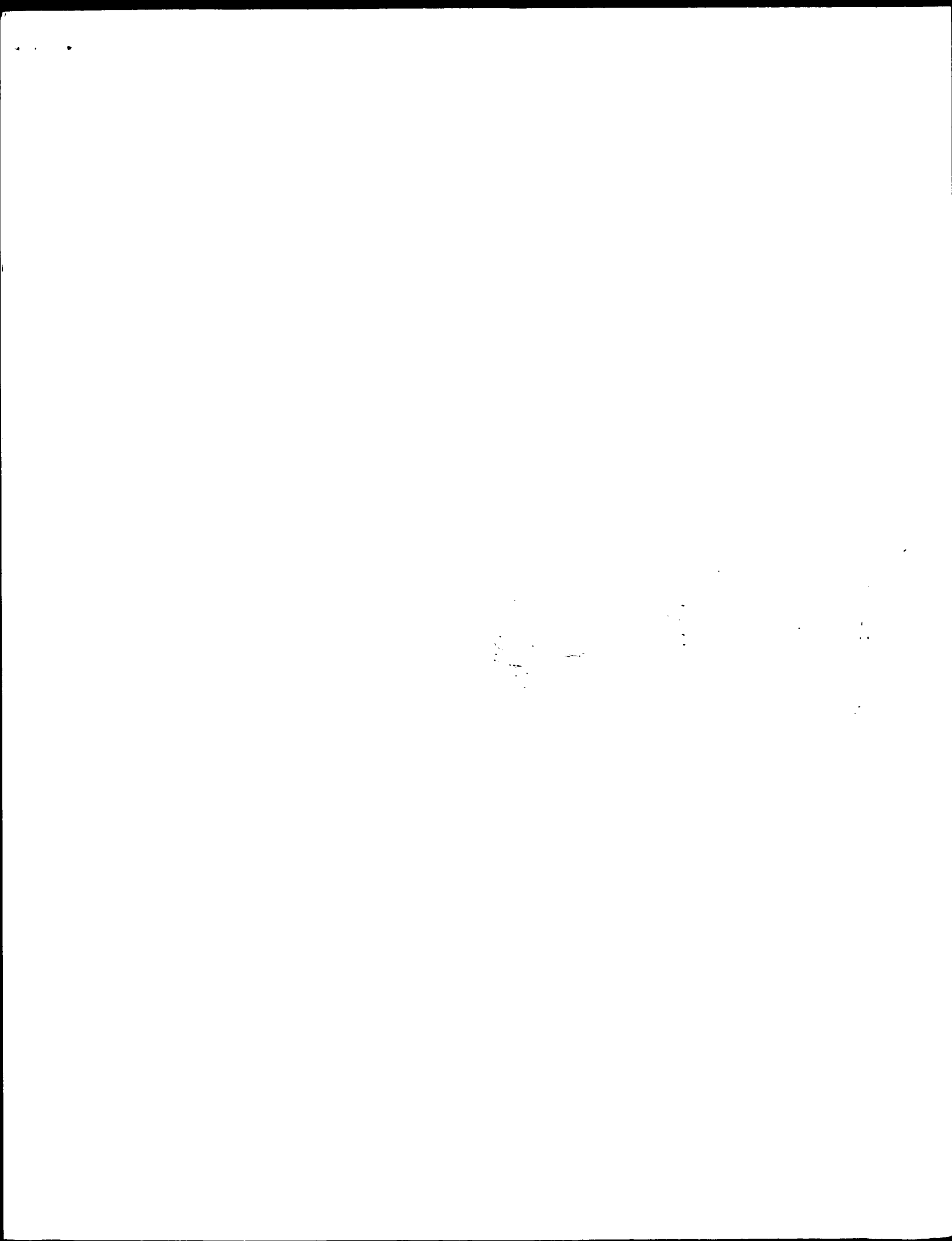
QY 743 -----NPETYEDSFYKRSILDNDNYVFTAPYFNKSGPGAYE-----SGIMWSKAVEIYIQ 791

Db 883 TGVIKDKNDPTIDSGFYKFTYNLGDYWEEDT--NKNGVQDKDEKIGISGVYTLKDE---N 937

QY 792 GKLLK 796

Db 938 DKVLK 942

Search completed: February 10, 2003, 14:48:59  
job time : 11.8601 secs



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Db 61 YEKYODLYVEPNNAQVLEIARADIEKLSNRKALVSLAEKVAQAHOHREDFASN 120
QY 121 EYVYNAKDDLDPEKNDSEPGSORIKPVFIDDANFGROISYQAAVHIPTDIEGSTIVL 180
Db 121 EYVYNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROISYQAAVHIPTDIEGSTIVL 180
QY 181 NELNMTSALDEVEKKNREEDPSLIMOVFGSATGLARYYPASPVWNSRPNKIDLYDVR 240
Db 181 NELNMTSALDEVEKKNREEDPSLIMOVFGSATGLARYYPASPVWNSRPNKIDLYDVR 240
QY 241 RPYIIOGAASPKDMLILVDVSGVSGITLKLRTSVSEMLETSLSDDDFVNVA SFNSNAOD 300
Db 241 RPYIIOGAASPKDMLILVDVSGVSGITLKLRTSVSEMLETSLSDDDFVNVA SFNSNAOD 300
QY 301 VSCFOHLYOANVRNKKVLDVAANNITAKGTDYKKGFSFAEQLLNYSRANCKIIML 360
Db 301 VSCFOHLYOANVRNKKVLDVAANNITAKGTDYKKGFSFAEQLLNYSRANCKIIML 360
QY 361 FTDGGERAOEIFAKYNDKRVFTFSVGOHNYDRGPLOMACENKGYEIPISGAIR 420
Db 361 FTDGGERAOEIFAKYNDKRVFTFSVGOHNYDRGPLOMACENKGYEIPISGAIR 420
QY 421 INTOEYLDVLRPNVLAGDKAKOVMTNYYLDALGLVITGTLPEVFNITGONEKNTMLK 480
Db 421 INTOEYLDVLRPNVLAGDKAKOVMTNYYLDALGLVITGTLPEVFNITGONEKNTMLK 480
QY 481 NOLIIIGWGVNVDLEDIKRLTPRPLCPNGYFAIDPNGVYLLHBNLOPKNPKSOEPTVL 540
Db 481 NOLIIIGWGVNVDLEDIKRLTPRPLCPNGYFAIDPNGVYLLHBNLOPKNPKSOEPTVL 540
QY 541 DELDAELENDIKVEIRNKKMIGESGEKTFRLTVKSODERTYDKGRTYTWVPVNTDLSL 600
Db 541 DELDAELENDIKVEIRNKKMIGESGEKTFRLTVKSODERTYDKGRTYTWVPVNTDLSL 600
QY 601 ALVLEPTYSFYIYKAKIEETITQARSKKMKMDESETLKPDNFEESGTYFIAPRDYCNLDKI 660
Db 601 ALVLEPTYSFYIYKAKIEETITQARSKKMKMDESETLKPDNFEESGTYFIAPRDYCNLDKI 660
QY 661 SUNNTEFLINNEFTDRKTPNPNPCSNADLINRVLLDAGFTMELVONVMSKKNIKGVAR 720
Db 661 SUNNTEFLINNEFTDRKTPNPNPCSNADLINRVLLDAGFTMELVONVMSKKNIKGVAR 720
QY 721 FVYTDGGITRYPKKEAGENMOENPEYTESFYKRSLSLNDNDNTVETAPYNNKSGPGAYESGI 780
Db 721 FVYTDGGITRYPKKEAGENMOENPEYTESFYKRSLSLNDNDNTVETAPYNNKSGPGAYESGI 780
QY 781 MYSKAVEIYIOGKILKPAVVGIKIDVNSMIENFTKTSIRDPACAGPYCDCKRNSDVMCVI 840
Db 781 MYSKAVEIYIOGKILKPAVVGIKIDVNSMIENFTKTSIRDPACAGPYCDCKRNSDVMCVI 840
QY 841 LDDGSEFLMANHDDYTNIGRPFGEIDPSLMRHLVNSVYAFNKSSTYDOSVCEGAPAKQ 900
Db 841 LDDGSEFLMANHDDYTNIGRPFGEIDPSLMRHLVNSVYAFNKSSTYDOSVCEGAPAKQ 900
QY 901 GAGHRSASVPSIADILHIGMATAAAMSIILOQFLSLTFPRLLEAVEHEDEDDFASLSKQ 960
Db 901 GAGHRSASVPSIADILHIGMATAAAMSIILOQFLSLTFPRLLEAVEHEDEDDFASLSKQ 960
QY 961 SCITEQIOTFFPDNDKSKFSVGLDCGNCRIPIHVEKLMNTNLIIFIMVESKGTCPDTRLII 1020
Db 961 SCITEQIOTFFPDNDKSKFSVGLDCGNCRIPIHVEKLMNTNLIIFIMVESKGTCPDTRLII 1020
QY 1021 QABOTSDGPNCDMVKOPRYRKGPDVCPDNNALEDYTDGCVS 1063
Db 1021 QABOTSDGPNCDMVKOPRYRKGPDVCPDNNALEDYTDGCVS 1063

```

RESULT 4  
 US-08-311-363-25  
 : Sequence 25, Application US/08311363  
 : Patent No. 587658  
 : GENERAL INFORMATION:

```

? APPLICANT: Harpold, Michael
? APPLICANT: Ellis, Steven
? APPLICANT: Williams, Mark
? APPLICANT: Feldman, Daniel
? APPLICANT: McCue, Ann
? APPLICANT: Brenner, Robert
? TITLE OF INVENTION: Human Calcium Channel Compositions and
? TITLE OF INVENTION: Methods
? NUMBER OF SEQUENCES: 32
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Brown, Martin, Haller & McClain
? STREET: 1660 Union Street
? CITY: San Diego
? STATE: California
? COUNTRY: USA
? ZIP: 92101-2926
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent in Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/311,363
? FILING DATE:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/745,206
? FILING DATE: 15-AUG-1991
? ATTORNEY/AGENT INFORMATION:
? NAME: Seidman, Stephanie L.,
? REGISTRATION NUMBER: 33,779
? REFERENCE/DOCKET NUMBER: 6362-51506
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (619)238-0999
? TELEFAX: (619)238-0062
? INFORMATION FOR SEQ ID NO: 25:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1091 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-311-363-25

Query Match 97.9%; Score 5532; DB 2; Length 1091;
Best Local Similarity 98.7%; Pired. No. 0;
Matches 1049; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 MAAGCLALTLTLFQSLILIPSSOEPPSAVTIKSWDKMQEDLVTLATASGVNOLVDI 60
Db 1 MAAGCLALTLTLFQSLILIPSSOEPPSAVTIKSWDKMQEDLVTLATASGVNOLVDI 60
QY 61 YEKYODLYVEPNNAQVLEIARADIEKLSNRKALVRLALAEKVAQAHOHREDFASN 120
Db 61 YEKYODLYVEPNNAQVLEIARADIEKLSNRKALVRLALAEKVAQAHOHREDFASN 120
QY 121 EYVYNAKDDLDPEKNDSEPGSORIKPVFIDDANFGROISYQAAVHIPTDIEGSTIVL 180
Db 121 EYVYNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROISYQAAVHIPTDIEGSTIVL 180
QY 181 NELNMTSALDEVEKKNREEDPSLIMOVFGSATGLARYYPASPVWNSRPNKIDLYDVR 240
Db 181 NELNMTSALDEVEKKNREEDPSLIMOVFGSATGLARYYPASPVWNSRPNKIDLYDVR 240
QY 241 RPYIIOGAASPKDMLILVDVSGVSGITLKLRTSVSEMLETSLSDDDFVNVA SFNSNAOD 300
Db 241 RPYIIOGAASPKDMLILVDVSGVSGITLKLRTSVSEMLETSLSDDDFVNVA SFNSNAOD 300
QY 301 VSCFOHLYOANVRNKKVLDVAANNITAKGTDYKKGFSFAEQLLNYSRANCKIIML 360
Db 301 VSCFOHLYOANVRNKKVLDVAANNITAKGTDYKKGFSFAEQLLNYSRANCKIIML 360
QY 361 FTDGGERAOEIFAKYNDKRVFTFSVGOHNYDRGPLOMACENKGYEIPISGAIR 420
Db 361 FTDGGERAOEIFAKYNDKRVFTFSVGOHNYDRGPLOMACENKGYEIPISGAIR 420

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```

QY 61 YEKYODLYVEPNNAQOLVEIARDIEKLISNSKALVRLALEAEKVQAHOQREDFASN 120
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Db 61 YEKYODLYVEPNNAQOLVEIARDIEKLISNSKALVRLALEAEKVQAHOQREDFASN 120
QY 121 EYVYNAKDDLDPEKNDSESGSRIRKPVITDANFGROISYQAAVHIPTDIESTYL 180
   |||||||
Db 121 EYVYNAKDDLDPEKNDSESGSRIRKPVITDANFGROISYQAAVHIPTDIESTYL 180
QY 181 NEIWMTSALDEVEFKKREDEPSSILMOVFSATGLARYPASPVADNSRTPNKIDLVDR 240
   |||||||
Db 181 NEIWMTSALDEVEFKKREDEPSSILMOVFSATGLARYPASPVADNSRTPNKIDLVDR 240
QY 241 RPYWIOGAASPKDMLILVDVSGVSGITLKLITVSSEMLETLSDDEPVNVAFSNMAOD 300
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Db 241 RPYWIOGAASPKDMLILVDVSGVSGITLKLITVSSEMLETLSDDEPVNVAFSNMAOD 300
QY 301 VSCFOHLVQANVNRKVKLDAVNNITAKGTQKKGFSAFEOILLVYNSRANCKNTIML 360
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Db 301 VSCFOHLVQANVNRKVKLDAVNNITAKGTQKKGFSAFEOILLVYNSRANCKNTIML 360
QY 361 FTDGBERAOEIFAKYNDKAVVFVFSVQAHNYDRPIOMMACENKGYEIEPISGAIR 420
   |||||||
Db 361 FTDGBERAOEIFAKYNDKAVVFVFSVQAHNYDRPIOMMACENKGYEIEPISGAIR 420
QY 421 INTQEVLDVIGRPMVLADGAKOVQNTNYLDALEGLVITGTLPVFNITGQNEKNTNLK 480
   |||||||
Db 421 INTQEVLDVIGRPMVLADGAKOVQNTNYLDALEGLVITGTLPVFNITGQNEKNTNLK 480
QY 481 NOILIGVGVDSLEDIKRLTPRTLCPNGYFAIDPNGVLLHPMLQPKNPSCQEPVL 540
   |||||||
Db 481 NOILIGVGVDSLEDIKRLTPRTLCPNGYFAIDPNGVLLHPMLQPKNPSCQEPVL 540
QY 541 DFLDALENDIKYEIRNMKIDSGEKTEFTLVKSODERYIDKNGTYTVPNGDYSL 600
   |||||||
Db 541 DFLDALENDIKYEIRNMKIDSGEKTEFTLVKSODERYIDKNGTYTVPNGDYSL 600
QY 601 ALVLPYISFYIKAKIETITQARSKKGMKDESETLKPDNEESGYTFLAPRDYCNDLKI 660
   |||||||
Db 601 ALVLPYISFYIKAKIETITQARSKKGMKDESETLKPDNEESGYTFLAPRDYCNDLKI 660
QY 661 SDNNTFEILNPFNEIDRKTYPNNSCNDLNRVLLDAGFTNELVQYMWSKQKNIKGVKAR 720
   |||||||
Db 661 SDNNTFEILNPFNEIDRKTYPNNSCNDLNRVLLDAGFTNELVQYMWSKQKNIKGVKAR 720
QY 721 FVYTDGSTRVYPRKEAGENNQENPEYEDSFYKRSIDNDNVYPTADYFNKSGPAGESGI 780
   |||||||
Db 721 FVYTDGSTRVYPRKEAGENNQENPEYEDSFYKRSIDNDNVYPTADYFNKSGPAGESGI 780
QY 781 MYSKAVEITYIQGLKLRPAVVGITIDVNSWTEENTKTSIRDPGAGPVCCDKRNSDVMDCYI 840
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Db 781 MYSKAVEITYIQGLKLRPAVVGITIDVNSWTEENTKTSIRDPGAGPVCCDKRNSDVMDCYI 840
QY 841 LDDGGFLMANHNDYTNOIGRFEGETIDPSLMRLHVNISVYAFNKSVDYOSVCEPGAAPKO 900
   |||||||
Db 841 LDDGGFLMANHNDYTNOIGRFEGETIDPSLMRLHVNISVYAFNKSVDYOSVCEPGAAPKO 900
QY 901 GAGHRSAYVPSIADILITIGMMATPAAMSIIQOFLSLTTPRLLEAVEMEDDDEPTASLSKO 960
   |||||||
Db 901 GAGHRSAYVPSIADILITIGMMATPAAMSIIQOFLSLTTPRLLEAVEMEDDDEPTASLSKO 960
QY 961 SCITTEOTQYFFDNDKSFSSVLDGCGNSRIFFHEKLMNTNLITIMVESKTCPCDTRLILI 1020
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Db 961 SCITTEOTQYFFDNDKSFSSVLDGCGNSRIFFHEKLMNTNLITIMVESKTCPCDTRLILI 1020
QY 1021 QABOTSDGPDPDMVYKQPRYRKGPVOCFDDNNALIEDYTDGGSV 1063
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RESULT 3  
US-08-223-305C-52  
; Sequence 52, Application US/08223305C

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; Patent No. 5851824
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/223,305C
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 52516 (P519739)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1091 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
; US-08-223-305C-52
;
; Query Match 97.9%; Score 5532; DB 2; Length 1091;
; Best Local Similarity 98.7%; Pred. No. 0;
; Matches 1049; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
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Db 1 MAAGCLALTLTLFQSLIGPSSQEPFSAVITIKSWVDKMOEDVTLAKTASGVNQLVDI 60
QY 61 YEKYODLYVEPNNAQOLVEIARDIEKLISNSKALVRLALEAEKVQAHOQREDFASN 120

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 10, 2003, 14:13:55 ; Search time 11.8566 Seconds  
(without alignments)  
2652.785 Million cell updates/sec

Title: US-10-090-827-9

Perfect score: 5650  
Sequence: 1 MAAGCLALTLTLFQSLILG.....NNALEDYDCGSHHHHHH 1069

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents, AA:\*

1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PCrus.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfilest.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5532	97.9	1091	1	US-07-745-206A-25
2	5532	97.9	1091	1	US-08-455-543A-52
3	5532	97.9	1091	2	US-08-223-305C-52
4	5532	97.9	1091	2	US-08-311-363-25
5	5528	97.8	1091	3	US-08-713-118-A
6	5528	97.8	1091	4	US-09-452-007-4
7	5492.5	97.2	1086	1	US-08-455-543A-54
8	5492.5	97.2	1086	2	US-08-223-305C-54
9	5475.5	96.9	1084	1	US-08-455-543A-56
10	5475.5	96.9	1084	2	US-08-223-305C-56
11	5456	96.6	1103	1	US-08-455-543A-53
12	5456	96.6	1103	2	US-08-223-305C-53
13	5436	96.2	1079	1	US-08-455-543A-55
14	5436	96.2	1079	2	US-08-223-305C-55
15	5410.5	95.8	1106	1	US-08-435-675B-5
16	5392.5	95.4	1106	1	US-08-336-257A-8
17	5159.5	91.3	1086	6	5386025-8
18	3025.5	53.5	1145	4	US-09-470-443-2
19	3025.5	53.5	1145	4	US-09-470-443-4
20	3004.5	53.2	1076	4	US-09-470-443-6
21	2563.5	45.4	508	1	US-08-435-675B-6
22	185	3.3	885	3	US-09-074-579-5
23	185	3.3	885	4	US-09-388-774-5
24	164.5	2.9	789	1	US-08-471-033-32
25	164.5	2.9	789	1	US-08-471-044-32
26	164.5	2.9	789	2	US-08-463-483A-32
27	164.5	2.9	789	2	US-08-471-046A-32

28	164.5	2.9	789	2	US-08-470-566B-32	Sequence 32, Appl
29	164.5	2.9	789	2	US-08-838-219B-4	Sequence 4, Appl
30	164.5	2.9	789	2	US-08-469-334-32	Sequence 32, Appl
31	164.5	2.9	789	3	US-09-300-529-32	Sequence 32, Appl
32	164.5	2.9	789	3	US-09-233-336A-4	Sequence 4, Appl
33	164.5	2.9	789	3	US-09-233-336A-4	Sequence 4, Appl
34	164.5	2.9	789	4	US-09-402-036-4	Sequence 4, Appl
35	164.5	2.9	789	4	US-09-904-226-4	Sequence 4, Appl
36	161.5	2.9	746	2	US-08-838-219B-6	Sequence 6, Appl
37	161.5	2.9	746	3	US-09-233-336A-6	Sequence 6, Appl
38	161.5	2.9	746	4	US-09-233-336A-6	Sequence 6, Appl
39	161.5	2.9	746	4	US-09-402-036-6	Sequence 6, Appl
40	161.5	2.9	746	4	US-09-904-226-6	Sequence 6, Appl
41	160.5	2.8	790	4	US-08-960-780-4	Sequence 6, Appl
42	160.5	2.8	790	4	US-09-073-898-4	Sequence 4, Appl
43	160.5	2.8	946	3	US-09-074-579-3	Sequence 3, Appl
44	160.5	2.8	946	4	US-09-388-774-3	Sequence 3, Appl
45	157.5	2.8	789	4	US-08-960-780-6	Sequence 6, Appl

## ALIGNMENTS

RESULT 1  
US-07-745-206A-25  
Sequence 25, Application US/0745206A

Patent No. 5429921

GENERAL INFORMATION:

APPLICANT: Harpold, Michael

APPLICANT: Ellis, Steven

APPLICANT: Williams, Mark

APPLICANT: McCue, Ann

APPLICANT: Feldman, Daniel

TITLE OF INVENTION: Human Calcium Channel Compositions and

TITLE OF INVENTION: Methods

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Fitch, Even, Tabin & Flannery

STREET: 135 S. LaSalle

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/745,206A

FILING DATE: 19910815

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Feder, Scott B

REFERENCE/DOCKET NUMBER: 51504

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-372-7842

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 1091 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

Query Match 97.9%; Score 5532; DB 1; Length 1091;  
Best Local Similarity 98.7%; Pred. No. 0;

Matches 1049; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 MAAGCLALTLTLFQSLILGSSGPEPFAVITKSNVDMKQEDVTLATAGVQVLDI 60  
DB 1 MAAGCLALTLTLFQSLILGSSGPEPFAVITKSNVDMKQEDVTLATAGVQVLDI 60

QY	235	LYDVARRR-----	WYIOGAAS-----	PKOMLLIVDVSGSVGLTEILRT	278
Db	276	MYDVAREEKVEBELFENGYFYHFFAFENDLPKRIILFVIDVSGSMGIGKMKQYEA	AKT		335
QY	279	MLETLSDDEPVNVASFNSNAODVSCFOHLYQAVANVRKKVYLDAVANNITAKG	ITDYKKG-		337
Db	336	ILDDRTEDQFSYVDFFNNVR--TWNRNDLVSA	TQITDAKRYIEKIQPSG	GTINTEALL	393
QY	338	--SFAEQLLVNVSRACNKKIMLEFTG----	GPERAOEI--FAKYKDKKVR	FTFSV	389
Db	394	RAIFLLNRSASINIGMLNPVSVSLIVASQDPTV	VELKLSKLOKRVKONTQDNI	SLEFSIGI	453
QY	350	GOHNYDRGPQIMMACENK-----	YYEII--PSIGAIRINTQOE--	YLD	428
Db	454	G-FQVDYDFELKRLSNENKGIQRIITGNDRTSSQLKFFINQVSTPLLRNVQFNYPPAS	YTD		512
QY	429	VL-----GRPVYLAG--DKAKOVQWNTVYLDAL	ELGIVTGTLLPVPNTIGONE	NK	477

Search completed: February 10, 2003, 14:19:22  
Job time : 14.5046 secs





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QY 487 --VMGVDVSLJEDDKRLTRPFTLCBPGGYFA-----IDPAGVYLLAPLNQ-----PKNP 532

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QY 533 KSOEPTLTDLFAELENDIKVEIRKMKIDGSEGEKTFYLVKSODERYIDKGRNTWTWP 592

Db 517 KKNKMLS-DEIHK-----EWNESYIHSDDNMINKN----- 549

QY 593 VNGTDYSLALVLPYTSFYIAKIEETITQARSKKKKKD-----SELKPDNE 642

Db 550 -----SIIEYIKDKMKNLNLTSSK-KKSTIKRSNPLVOTIKSCLLKQHYIK 596

QY 643 ESGYTFIAPDYCNDDIKISDN-TEFLN-----FNEF-IDRKTNPNSCWTDLIN 693

Db 597 EKREYTYNTNTYCNDDIHNDSTCSSYLLANSEIKOACGYIYIDH-----LCD--INNK 647

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QY 754 RSLDNDNYVTATYAFPKSGPAGVEGIMVSKAVEIIOGKLKPAVYG-----IKIDVN 807

Db 682 NEL-----MGKYSKNEELMGKYSKNEELMGKYSKNEELMGKYSKNEELMGKTIKQOYVDIN 734

QY 808 SWIEPFTKTSIRP-PCAGFPVCDCKRNSDVMCV-----LLDDGFLMANHDYTNQIGRE 862

Db 735 IYHNCNDQNYVDYPCD--YNNCNCNDPYHRELYHNINKNSNFIPEKKNYSNNISEH 791

QY 863 -----FGEIDPSLMRLHLYNIATAF-----NKST 886

Db 792 IKINYPLEFALACHTLSKVNKKIMGDVLELIMFNCDMLINNSFTIKERKKKSV 851

QY 887 DYOSVCPGAPKQAGHGSAAVPSIADILHIGMATTAAMSLIOQFLSLTFPRLLNAV 946

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QY 947 EMEDDFTASLSKOSCTEOTQTFPDNDKS 977

Db 885 -----EFOSRIQMSYIVKST-YGNNDNDNN 909

RESULT 15

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AC P97279;

Db 15-JUL-1998 (Rel. 36, Created)

Db 15-JUL-1998 (Rel. 36, Last sequence update)

Db 15-JUN-2002 (Rel. 41, Last annotation update)

Db Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy chain H2) (HC2).

Db ITH2.

Db Mesocricetus auratus (Golden hamster).

Db Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocricetus.

Db NCBI\_TaxId=10036;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA MEDLINE=97420688; PubMed=9276673;

RX Nakatani T., Suzuki Y., Yamamoto T., Sinochara H.;

RT "Molecular cloning and sequencing of cDNAs encoding three heavy-chain precursors of the inter-alpha-trypsin inhibitor in Syrian hamster: RT implications for the evolution of the inter-alpha-trypsin inhibitor heavy chain family.";

RL J. Biochem. 122:71-82(1997).

RN [2]

RP SEQUENCE OF 55-64; 140-146; 151-156; 424-447; 500-528 AND 577-605,

RP AND SUBUNITS.

RC TISSUE=Plasma;

RX MEDLINE=97018241; PubMed=8864857;

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(INTEINS) FOLLOWED BY PEPTIDE LIGATION.  
 CC -1- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
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 CC or send an email to [license@isb-stb.ch](mailto:license@isb-stb.ch)).  
 CC  
 CC EMBL: Y13030; CAA73475.1; -  
 DR HSP: p56689; ITG0.  
 DR InterPro: IPR002064; DNA\_pol\_B.  
 DR InterPro: IPR003586; Hedgehog\_hntc.  
 DR InterPro: IPR003587; Hedgehog\_hntn.  
 DR InterPro: IPR002203; Intein.  
 DR InterPro: IPR004042; Intein\_endonuc.  
 DR InterPro: IPR004578; Pol2.  
 DR Pfam: PF00136; DNA\_pol\_B; 4.  
 DR Pfam: PF03104; DNA\_pol\_B\_exo; 1.  
 DR PRINTS: PR00379; INTEIN.  
 DR SMART: SM00305; Hntc; 3.  
 DR SMART: SM00486; POLB; 1.  
 DR TIGR: TIGR00592; pol2; 2.  
 DR PROSITE: PS00116; DNA\_POLYMERASE\_B; FALSE\_NEG.  
 DR PROSITE: PS50818; INTEIN\_C\_TER; 3.  
 DR PROSITE: PS50819; INTEIN\_ENDONUCLEASE; 2.  
 DR PROSITE: PS50817; INTEIN\_N\_TER; 3.  
 DR Transferrase: DNA-directed DNA polymerase; DNA replication;  
 DR DNA-binding; Hydrolyase; Endonuclease; Autocatalytic cleavage;  
 DR Protein splicing.  
 FT CHAIN 1 409 DNA POLYMERASE, 1ST PART (POTENTIAL).  
 FT CHAIN 410 769 INTEIN I.  
 FT CHAIN 770 855 DNA POLYMERASE, 2ND PART (POTENTIAL).  
 FT CHAIN 856 1392 INTEIN II.  
 FT CHAIN 1393 1441 DNA POLYMERASE, 3RD PART (POTENTIAL).  
 FT CHAIN 1442 1598 INTEIN III.  
 FT CHAIN 1599 1829 DNA POLYMERASE, 4TH PART (POTENTIAL).  
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 Best Local Similarity 20.8%; Pred. No. 0.13; Indels 284; Gaps 42;  
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 QY 151 DDANGROISTQAAVHIPTD---IYEGSTIV---INELNMTSALDEVFKKREEDPSL 203  
 DB 395 PERGLMENIAYLDFRCH--PADTKVIYKKGKGIYINISVKEGDIILIDG----- 441  
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 DB 442 -WQ---RVKRWKHYEKKLININGLKCTPHNKKVYVTEENDROTRI-----RDSIAKSF 491  
 QY 260 VSGVSGTLKLIPTSVSEMETLSDDFVNVASFSNS----- 297  
 DB 492 LSGAKG---KIITTKL-----FKIAFEKKKPSBEETIKGLSCLIAESTL 537  
 QY 298 -AQVYSCF-----QHLVQANV--RNKKVLKDAV-----NNITAKG----- 329  
 DB 538 LKDIETFDSSRGKKRISHQYRVEITIGENKELLERILITYFDKLGIRPSVKKKKGDINA 597

QY 330 --ITDKGGSFAFOLLINVNSRANCKIIMLFTDGGEERAQETFAKYNKDKVRVPTF 387  
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 QY 388 SVQGHNYDRGPLOMWACENKGY---YVEIPSIGAIRINTQEDLVLGHPVLADGAKOV 444  
 DB 648 -QGTNNKKRIDIVAKLDSLIGPSRYEYKTIENKELTKHILETGD----- 695  
 QY 445 QMTNVLDALEGLVITGTLVFNITGONE-----NKTNLKNQILIGWGVDSLE 495  
 DB 636 -----GLITFQTLVGFISSEKNEALEIAEYRENNRKNNSFYMLSTFEVSE 743  
 QY 496 DIKRLTPFTLCPCNGYFAIDPNGVYLHPMLQPKNPSQSPVTLDFDALENDIVEI 555  
 DB 744 YKGEVYVLTLEGNYYTA---NG-ILFNSLYSIIVTAN-VSPDITLRE----- 789  
 QY 536 RNMIDGESGEKFTFLVKSDERYIDKGNRTYTWTPVNGTYSALVLPYSPFYIKAK 615  
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 QY 616 IERTTQARSKKKKDKSETIKPNEFSG-----TFIAPRDYCNLDKISDNTE 666  
 DB 816 LGEITMROEIKKKK--ATIDPLEKKMLDYORAVKLLANSIIPNEM---LPIENGVEY 870  
 QY 667 FLINNEFIDR-----KTPNPNPCNTDLINVLADAGFTNELVQYWSKOKNIGKARF 721  
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 ID Y103\_SYNT3 STANDARD; PRT; 420 AA.  
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 AC Q55874;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Hypothetical protein s110103.  
 GN SLI0103.  
 OS Synechocystis sp. (strain PCC 6803).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.  
 OX NCBI\_Taxid:1148;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE:96127529; PubMed:8590279;  
 RA Kaneo T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,  
 RA Sugiyama M., Yabata S.;  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb  
 RT region from map positions 648 to 928 of the genome.";  
 RL DNA Res. 2:153-166(1995).  
 CC -1- SIMILARITY: TO E. COLI YEFB.  
 CC -1- SIMILARITY: CONTAINS 1 WMFA DOMAIN.  
 CC  
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 CC or send an email to [license@isb-stb.ch](mailto:license@isb-stb.ch)).  
 CC  
 CC EMBL: D64004; BA10635.1; -  
 DR InterPro: IPR002035; WMF\_A.  
 DR Pfam: PF00092; Wfa; 1.  
 DR SMART: SM00327; WMA; 1.  
 DR PROSITE: PS50234; WMFA; 1.  
 KM Hypothetical protein: Complete proteome.  
 FT DOMAIN 43 215 WMFA.

```

DB 242 LYLKELREDNDIALIYVADSDRIA-----LPSISGSHKAEINAAIDSLDABSTNGAGL 296
QY 338 SFPEDELLWVNSRANCNIIIMLFDTG-----GERRAOEIFAKYKDKKVFVTFSSQ 391
DB 297 ELAYQATK-GRFKIGINR-ILLATDGFENVGIDDKSTLESVWKORREGVLTSTFGVGN 354
QY 392 HNYDRGPIOMWACENKGYEYFISGALININQEVLDVGRPMVL--AGDKAKOVQ---- 445
DB 355 SNNENAMVRIADVGNNGNSYIDTLS-----EAQKVLNENMRQMLITVADKAAQIEFNPA 410
QY 446 WIVNVIDALELGLVITGTLPEVNITGQENKTNLKNQILLGWGVV-SELEI---KRLT 501
DB 411 WTEY---RQIGYE-----KRQLVHEHFNNDVNDVADGIGAGKILT 447
QY 502 PRFTLCNGYFAIDPNGVYLLHPNLQPKPSOE 536
DB 448 LLEFLTLNGOKASIDKLRVA--PDNKLAKSDKTE 480

RESULT 10
ITIH3_MESAU STANDARD: PRT: 886 AA.
AC P97280;
DT 15-JUL-1998 (rel. 36, Created)
DT 15-JUL-1998 (rel. 36, Last sequence update)
DT 16-OCT-2001 (rel. 40, Last annotation update)
DE Inter-alpha-trypsin inhibitor heavy chain H3 precursor (ITI heavy
chain H3) (HC3).
GN ITIH3.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OY NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=97420688; PubMed=927673;
RA Nakatani T., Suzuki Y., Yamamoto T., Sinohara H.;
RT "Inter-alpha-trypsin inhibitor and its related proteins in Syrian
hamster urine and plasma."
RT Implications for the evolution of the inter-alpha-trypsin inhibitor
heavy chain family."
RT J. Biochem. 122:71-82(1997).
RN [2]
RP SEQUENCE OF 31-50; 446-472 AND 504-523, AND SUBUNITS.
RC TISSUE=Plasma;
RX MEDLINE=97018241; PubMed=864857;
RA Yamamoto T., Yamamoto K., Sinohara H.;
RT "Inter-alpha-trypsin inhibitor and its related proteins in Syrian
hamster urine and plasma."
RT J. Biochem. 120:145-152(1996).
CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
SIMILARITY).
CC -1- SUBUNIT: I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2
AND BIKUNIN. INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
BIKUNIN. AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.
CC -1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.
CC -1- SIMILARITY: CONTAINS 1 WFPA DOMAIN.
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CC or send an email to license@isb-sib.ch).
CC -----
DB EMBL; D89287; BAA13940.1; .
DR InterPro; IPR002035; WFPA.
DR Pfam; PF00092; vwa; 1.
DR SMART; SM00327; vwa; 1.
DR PROSITE; PS0234; WFPA; 1.
KW Serine protease inhibitor; Repeat; Signal; Multigene family;
KX Glycoprotein.
FT SIGNAL 1 18
FT PROPEP 19 30
FT CHAIN 31 646
FT PROPEP 647 886
FT DOMAIN 279 439
FT CARBOHYD 88 88
FT CARBOHYD 577 577
FT BINDING 646 646
SQ SEQUENCE 886 AA; 99018 MW; AC0594C6852575B8 CRC64;

Query Match 3.08; Score 166; DB 1; Length 886;
Best Local Similarity 23.28; Pred. No. 0.025;
Matches 66; Conservative 57; Mismatches 111; Indels 51; Gaps 11;

QY 202 SLIMOVFSATGLARYPASPVPVNSRT-PNKID-----LYDVRR-PMYIOGA-- 248
DB 208 SALTFSFGSKGHVSFKS---LDQKSCPTCTBSLNGDPTIYDVNRKSPGVQVYNG 264
QY 249 -----ASPKDMLIVDVGSVSGTLKRLTIRVSEMLETISDDFVNVASFNS 296
DB 265 YVHFEPAGLGVPEVKNIVFVIDISGSMAGRIQOTRVALLKIIDDKODDYLIFFST 324
QY 297 NADVSCFOHLYQAVNRKKVYKADAVNNTAKGIDTYKKGSFAFEQLN-----YNSRA 352
DB 325 GV--TTKMSLVQAPPALEARTVRSISDQGMNINDGLRGLTMDARREOHTVPER 382
QY 353 NCNKTIMLFTDS-----GERRAOEIFAKYKDKKVFVTFSSVQ-OHNYDRGPIOMWACENK 407
DB 383 STSIITML-TDGDANTGESRPEKIOENVRKAIEGFPLYNIGFNLMVNFLEMALENH 441
QY 408 GYVEIPISGALRINTQEVLDVGRPMVLADGKAKOVQNTVNYLD 452
DB 442 GVARRIYEDSDANLQDGFYEYEVANPLL-----TWVEYE 475

RESULT 11
DPOL_THEST STANDARD: PRT: 1829 AA.
AC O33845;
DT 15-DEC-1998 (rel. 37, Created)
DT 15-DEC-1998 (rel. 37, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE DNA polymerase (EC 2.7.7.7).
GN POL.
OS Thermococcus sp. (strain TY).
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Thermococcus.
OY NCBI_TaxID=110163;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98094267; PubMed=9434178;
RA Niehaus F., Frey B., Antiklian G.;
RT "Cloning and characterisation of a thermostable alpha-DNA polymerase
from the hyperthermophilic archaeon Thermococcus sp. Ty."
RT Gene 204:153-158(1997).
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
+ (DNA)(N).
CC -1- PTM: THIS PROTEIN UNDERGOES A PROTEIN SELF SPLICING THAT INVOLVES
A POST-TRANSLATIONAL EXCISION OF THE THREE INTERVENING REGION

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FT SIGNAL 1 21 POTENTIAL.
FT PROPEP 22 33 BY SIMILARITY.
FT CHAIN 34 647 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN
FT PROPEP 648 887 BY SIMILARITY.
FT DOMAIN 282 442 WFPA.
FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 580 580 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT BINDING 647 647 CHONDROITIN 4-SULFATE, CROSS-LINK SITE
FT SEQUENCE 887 AA: 99097 MW: 3890FF96D514096 CRC64:

Query Match 3.4%; Score 183.5; DB 1; Length 887;
Best Local Similarity 18.4%; Pred. No. 0.0023;
Matches 172; Conservative 139; Mismatches 353; Indels 271; Gaps 37;

QY 27 PPSAATIKSMVMDKQEDVTLAKTASGVNQLDIYEKQODVLTPEPNNARQVLEIADI 86
DB 101 YGSGYKEKVAQKQYKAVSOKTAG---LVKASGRKLEKFTVSVNAAGSKVIFELTY 156
QY 87 EKLSNRKALVRLALEAKVQAHOQRED---FASNEVYVYNAKDDLDPEKNDSEPSQ 143
DB 157 EELL-KRNGKXYEMLYKQPKQLVHFELDAHIFEPQISMUDA----- 199
QY 144 RIKPEIDANFROISTOHAHVHPTDIESTIVLNLMTSALDEVEFKKNEEDPSL 203
DB 200 -----DASF-----ITNDL-LGSAITKSF----- 217
QY 204 LMQVGSATGLARYYPASPVVNSRT-PNKID-----LYDVRRRP----- 244
DB 218 -----SGKKGVSPKPSIDQKSCPTCDLSLNGDFTIYVYVNRSPGVQVLCGYF 269
QY 245 I-----QG-ASPKMLLVVDSGSGITLKITFSVSEMLETISDDDFVAVASFSNSA 298
DB 270 VHEFAPQGVPPVPRKNIAVIVDVSMSGRKIQOTREALKILDDKEDYINLIFSTGV 329
QY 299 QVSGFOHLYOANVNNKVKYLKAVNNITAKGTDYKGFSAFEGLLNYSNRAN----- 353
DB 330 ---TTKDHLYKATPANLEAFYKNIIDRSKTNINDLGLTEML---NAREDHLYPE 384
QY 334 -CNKIMLETDG---GEERQELFAKYNKDKKVFETFSVG-QHNYDRGFIOMACENK 407
DB 385 RSTSLVLMITDQDANTGSRPEKIQENVRNAIRGFPLYNLFGNNLNYNLESLALENH 444
QY 408 GYVYIPISIGAIRINTQYELVIGRPVLAQKAKQVOWTVNYDALELGLVITGLPVE 467
DB 445 GFARIVEDSDASIQLOGFEEVAVNPLD---TWLELEYPENA-----IL 485
QY 468 NITGONENKTNLKNQILIGVGVVDSLEDIKRIPRFTLCPNGVYFAIDPVGYLHNPL 527
DB 486 DLTRSYHFYDGSSEIYVAGLVDRNVN-----FKADVGHGALN--- 526
QY 528 QPKNKSGEPTLDFLALENDIKVELIRNMIDEGSEKTF-----RTLVKSQDERYI 581
DB 527 ---DLTFEEYDMKEMDAALK-----EGQYIFGDYIERLMAVLITIEQLLEKKNRQD 576
QY 582 DKGRNTYVWTVNGTDSLAL-LVLPITYSFYIAKIEFTTQARSKKGGKADSET---L 636
DB 577 EKENIT-----AEALEISLKYHFTPLTSMVYTKPEDNEDDTALADKPGEALISASTYL 631
QY 637 KPDNFESGYTFIAPRDYCNCLKISDNNTFELNF-----NEFDIKRTNNPNSCNTDLNRY 693
DB 632 TSQGSHPSPYV-----DGDPHFTIYVPGKNDITCINIDEKPEYVSLIQDP 679
QY 694 LLDAQFTNELVONTWSKQNKIKYKARFVYTDGITRYVREAGENNQENPEYEDSFYK 753
DB 680 VTGIAVIGQIT-----GEKGNASSRTGKT----- 704
QY 754 RSLDNVNVFTAPYFNKSGPARYESGLIMKAVAVIYIGKILKAVVYIGIIVNSWLENF 813
DB 705 -----TFGKIGLIANAMDFRIEYTERKIIIGN-----GDALSTFSWLDYV 744
QY 814 TKTSIRDPGAPVDCRKNSDVMDCVILDDG-GFLLMAN-----HDDYTNQIGAFPG 864

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DB 745 TVTQ-----TGLSVTINKKMNV---VSPEDGISYIVYLVHQQVKKHPVHDFLG-----FY 792
QY 865 EIDPSLNRHLNIVSVAFNKSQYQSV-CEFGAAP 898
DB 793 VVDSHRMSAQTHGLGQFFQFDEKVFVDVRCGSP 827

RESULT 9
YFBK_ECOLI
ID YFBK_ECOLI STANDARD; PRT; 575 AA.
AC P/6481;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein yfbk.
GN YFBK OR B2270.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
CC - SIMILARITY: TO SYNECHOCYSTIS PCC 6803 SLI0103.
CC - SIMILARITY: CONTAINS 1 WFPA DOMAIN.
CC
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DR EMBL: AE000317; AAC75330.1; -.
DR EcoGene; EGI4095; yfbk.
DR InterPro; IPR002035; WFPA_A.
DR Pfam; PF00092; vwa; 1.
DR SMART; SM00327; vwa; 1.
DR PROSITE; PS0234; WFPA; 1.
KM Hypothetical protein; Complete proteome.
FT DOMAIN 216 394 WFPA.
SQ SEQUENCE 575 AA: 63634 MW: 7B6A1A7A2BE11 CRC64:

Query Match 3.1%; Score 168.5; DB 1; Length 575;
Best Local Similarity 21.6%; Pred. No. 0.0096;
Matches 111; Conservative 94; Mismatches 205; Indels 105; Gaps 24;

QY 71 EPNARQVLEIARIDEKILSNRSKALVRLALEAKVQAHOQREDFAENEYVYVYNAKD 130
DB 22 QPKNKSGEPTLDFLALENDIKVELIRNMIDEGSEKTF-----RTLVKSQDERYI 581
QY 131 LDPEKND-----SEGSORIKVFTIDANFGQISYQHA---VHLPDI 172
DB 76 LQGRLEAPFTFAAKAKAKATHIANPSTARYQOF---DQNPQVQVQNPPLATFSLDVDS 132
QY 173 YEGSTIVLE-----LWMTSALDEVEFKKNEEDPSLIMOVFGSATGLARY 218
DB 133 YANVRFLNQGILPPDAVAVEIVYFSPDMDI---KDKQSIIPASKPIPFAMRYELA--- 187
QY 219 PASPVVNSRTPNKIDLVVRRRPVYIGGAASPKMLLVVDSGSGITLKITRTSVS 277
DB 188 PA-PW-NEQRTILKVLIDAKDKRSELPAS---NLVFLIDISGKMSIDERLPLQSSIK 241
QY 278 EMLETLISDDDFVAVASFSNSADVSCFOHLYOANVNNITAKGTDYKKG 337

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X70393; CAA49843.1; -
DR MGD; MGI:96620; Itih3.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00927; VWA; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS00334; VWFA; 1.
KW Serine protease inhibitor; Repeat; Signal; Multigene family;
KW Glycoprotein.
FT SIGNAL 1 18 POTENTIAL.
FT PROPEP 19 30 BY SIMILARITY.
FT CHAIN 31 646 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN
FT H3.
FT PROPEP 647 886 BY SIMILARITY.
FT DOMAIN 279 439 VWFA.
FT CARBOHYD 88 88 N-LINKED (GLCNAc...) (POTENTIAL).
FT CARBOHYD 577 577 N-LINKED (GLCNAc...) (POTENTIAL).
FT BINDING 646 646 CHONDROITIN 4-SULFATE, CROSS-LINK SITE
FT (BY SIMILARITY).
SQ SEQUENCE 886 AA; 98977 MW; 1595308CF5030A CRC64;
Query Match 3.6%; Score 196.5; DB 1; Length 886;
Best Local Similarity 20.5%; Pred No. 0.00038;
Matches 189; Conservative 142; Mismatches 349; Indels 243; Gaps 46;
QY 45 VTLAKTASGVNOLVDYERKODLYVEPNARQVEIARDEKILSNKSKALVALALEA 104
DB 78 VELPKAFATNTFTLT-----DGVTY-PEGVKE-KEVAQKQEKAVSQGKTGL----- 124
QY 105 EKVQAAHOREDE-----ASNEVYVYAKADDPEKNDSPGSGORIKPVFIDANGR 157
DB 125 --VKASGRLEKFTVSVNVAASGKVFELTYELLKRNKGYEMYLKVP-----K 173
QY 158 QISYQHAAYHPTDIYEGSTVILNELNMTSALDEYFKKREEDPSILMOVFSGA-----T 212
DB 174 QV-VRH--FEIDAHIFEPQGI-----SMLD-----AASPTINDLSGALSATKFS 215
QY 213 GLARYRPAWPWNSRT-PNKID-----LYVRRRP-----WYI-----QG- 247
DB 216 GKGVHSEKPSLDQORSCPTCTDLSLNGDFTLYDVNRESPGNVQIVNGYEHFAPQGL 275
QY 248 AASPKDMLLVDSVSGSLTLKLRTSVSEMLETLSDDPFNVAASESMNADVSCFQ-H 306
DB 276 PVVPRNIVYVIDVSGSMGRKIQQTRREALKLLDVKEDDYINFTLFTST--DVITWMDH 332
QY 307 LVQAVNRKKVYLKDAVNNITAKGIDYRKGSFAFEQLLNVSHPAN-----CNKIML 360
DB 333 LVQATPAMLEKKEFTVKNHDSMTNINDGLKIGEML--NKAREDTVPERSITIIIM 389
QY 361 FLDG-----GEBAQEIFAKYKN--DKKRVVTFVSQGNINYDRGPIOMACENKGYEIP 414
DB 390 LDDGANTGESPEKIQENVRNAGKPLNLFPG--NNLWYNFLETLALEHNGIARILY 448
QY 415 SIGAIRINTOEYLDVIGRPVYLAGDKARQVOMTNYVLDALFGLVITGLTFVFNITGNE 474
DB 449 EDSQANLQLOGFYEYVAPLL-----TIVEYVYPRNA-----TLDLTRNSY 489
QY 475 NKTNIKNOILGVGVDSVLEDIRLPRTLCNGYFAIDPNGVYLLHPNLOPKNKS 534
DB 490 PHEYDSEIIVAGRLVDRNMDN-----FKADVGHGLN-----DLTE 527
QY 535 QEPVTLDELDELNDIKVELRNKMIQESGEK--TFPTLYKSDDERYIDKGNFTYWP 592
DB 528 TEEVDMEEDALK-----EGYIFGDYIERLMAVLTITBOLLKRNKNAAGDEKENT- 579

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QY 593 VNGTDYSIA--LVLPYSFYIKAKIEETITQASKKCKMDSFT-----LKPNFEESG 645
DB 580 AEALDLSLKHYHVPYLTSMVYTKPEDNEDQISADNMGEEAFLETWMSFLTQOSSQSP 639
QY 646 YTFIAPRDYCDNLKISDNTEFLNFNEFDIKRTPNPNSCWTDLINRYLDAGFTNELVQ 705
DB 640 YYYV-----DQDPHFIIQI-----PGKNDISCFNIDEKRGVTLILQ 676
QY 706 NWSKQKNIKGVKAFVYTTDGTIRVYRKKEAGEMWQENPEYTEDSFKRSILDNDNYFTA 765
DB 677 D-----PVT--GIT-VTGQIIIGD-----KRS--NASSRTGK 702
QY 766 PFNKSQPGAYESGIMVSKAVEIYIOGKLKPAVYGIKIDVNSIENFTKTSINDPCAGP 825
DB 703 TYFGKLGITNAMMPDRVEVTEKILG-----TGAELSTFSWLDVYVYTIQ-----TGL 750
QY 826 VCDCKRNSDWDVCYLLDDG-GFLMAN-----HDDYTNQIGRFGEIDPSLMRLVN 876
DB 751 SVTIRKKKNV--VSFGDISFVILLHQWKKHPHVDLGL-----FYVDSHRMSQTH 803
QY 877 ISVYAFNKSVDYQSY-CEPGAAP 898
DB 804 GLIGCFQFPDFKVPVGIKPGSDP 826
RESULT 7
ID ITH3_HUMAN STANDARD; PRT; 885 AA.
AC Q06033; 099085;
DC 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DI 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inter-alpha-trypsin inhibitor heavy chain H3 precursor (Itr heavy
DE chain H3) (Serum-derived hyaluronan-associated protein) (SHAP).
GN ITH3
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93215656; PubMed=7681778;
RA Bourguignon J., Dalaria-Mehrpour M., Thiberville L., Bost F.,
RA Sesboue R., Martin J.P.;
RT "Human pre-alpha-trypsin inhibitor-precursor heavy chain. cDNA and
RT deduced amino-acid sequence."
RL Eur. J. Biochem. 212:771-776(1993).
RN [2]
RP SEQUENCE OF 341-885 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89137072; PubMed=2465147;
RA Dalaria-Mehrpour M., Bourguignon J., Sesboue R., Mattei M.-G.,
RA Passage E., Saller J.P., Martin J.P.;
RT "Human plasma inter-alpha-trypsin inhibitor is encoded by four genes
RT on three chromosomes."
RL Eur. J. Biochem. 179:147-154(1989).
RN [3]
RP SEQUENCE OF 30-49; 463-477 AND 497-515.
RX MEDLINE=89380192; PubMed=2476436;
RA Engchild J.J., Thøgersen I.B., Pizzo S.V., Salvesen G.;
RT "Analysis of inter-alpha-trypsin inhibitor and a novel trypsin
RT inhibitor, pre-alpha-trypsin inhibitor, from human plasma."
RL J. Biol. Chem. 264:15975-15981(1989).
RN [4]
RP SEQUENCE OF 631-647, AND CROSS-LINKAGE SITE TO BIKUNIN.
RX MEDLINE=91093267; PubMed=1898736;
RA Engchild J.J., Salvesen G., Hetta S.A., Thøgersen I.B.,
RA Rutherford S., Pizzo S.V.;
RT "Chondroitin 4-sulfate covalently cross-links the chains of the
RT human blood protein pre-alpha-inhibitor."
RL J. Biol. Chem. 266:747-751(1991).
CC FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A

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OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabditoidea;  
OC Rhabdilitidae; Pelodetrinae; Caenorhabditis.  
ON NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Bristol N2;  
RX MEDLINE-PubMed-94150718; PubMed-7906398;  
RA Milson R., Annsough R., Anderson K., Baynes C., Berts M.,  
RA Bonfield J., Button G., Connell M., Copsey T., Cooper J., Coulson A.,  
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,  
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,  
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,  
RA Lathwell P., Lightning T., Lloyd C., Mortimore B., O'Callaghan M.,  
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showgreen R.,  
RA Sims M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden R.,  
RA Sulston J., Thierry-Mieg J., Thomas K., Vaubin M., Vaughan K.,  
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,  
RA Wohldman P.;  
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
RL elegans".  
RL Nature 368:32-38(1994)  
CC -1- SIMILARITY: TO CALCITUM CHANNEL ALPHA-2B SUBUNIT.  
CC -1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.  
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DR DR EMBL: LI4433; AAA27969.1; -.  
DR PTR: S44617; S44617.  
DR Wormpep: CS0C3.11; CE00117.  
DR InterPro: IPR004010; Cache.  
DR InterPro: IPR002035; VWF\_A.  
DR Pfam: PF00092; Vwa; 1.  
DR Pfam: PF00743; Cache; 1.  
DR SMART: SM00337; VMA; 1.  
DR PROSITE: PS0234; VWFA; 1.  
RW Ionic channel; Ion transport; Voltage-gated channel; Calcium channel;  
KW Glycoprotein.  
FT FT 250 435 VWFA.  
FT CARBOHD 100 100 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHD 140 140 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHD 146 146 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHD 302 302 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHD 476 476 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHD 514 514 N-LINKED (GLCNAC . .) (POTENTIAL).  
SQ SEQUENCE 734 AA; 85034 MW; CCFBYGCBDEAB7IF CRC64;  
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Query Match		11.2%;	Score 611;	DB 1;	Length 734;
Best Local Similarity	26.58%;	Pred.	No. 5.6e-29;		
Matches 179;	Conservative 127;	Mismatches 261;	Indels 108;	Gaps 19;	

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47 LAKTASGVNOLVDIYEKODLYTPVNNARLOVEIAARDIEKLNSRKAL--VRLLAEA 104
   : : : : : : | : | : | : | : | : | : | : | : | : | : | : |||
Db 36 MKETRSKISHETILLKNQTEKVLVEEEOFPRALRKSKHRIEDYLVYRSOFAIKAKISLEA 95
      : : : : : : : : : : : : : : : : : : : : : : : : : : : |||
Oy 105 EKVOAHOWREDPASNEVVYYNAKDLDPEK-NDSEPGSORIKP-----VEIDANF-G 156
     : : : : : : : : : : : : | : | : | : | : | : | : | : | : |||
Db 96 RSVRSDSTVNDSPOSFSFIEMSAKGNGDQTIIYESNHHLCKRLKVNETKSFNLQNANFEY 155
     : : : : : : : : : : : : | : | : | : | : | : | : | : | : |||
Oy 157 ROISQHAHVHPDIYEGSTIVLMELMNTSLADVEFKNRREDDSSLIHQVGSGATGLAR 216
     : : : : : : : : : : : : : : : : : : : : : : : : : : : |||
Db 156 LPTSSVSVAVHLPPLDYDNEDLKRDIM-SOLIDAVYRTNRETDLAQLCSCSEAGYMR 214
     : : : : : : : : : : : : : : : : : : : : : : : : : : : |||
Oy 217 YYPASPFW-DNSRTFNKKIDYLTVRRPPYIQCAAPSKMDILDVDSGGVGTLLKIPTS 275
||| : : : : : : : : : : | : | : | : : | : : : : : : : : : : : :
Db 215 YYPASPWFNDG--DEHIDLFDCAHTIEWYTINATNSKNVLLMLDMSGMSLGORYEVAKQT 272 ,

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OY      VSEMIETLISDDPFNVNVSFNNA----ODVSCFOHLVOAVNRKMKVLKDVA>NNNTIAGITD    3320
        ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      273 TEALLETLSHNDYINIMTFSKNTFTLLDGCNTOTGLDATRKALKLRKKMDTYOSEKAE    3322
OY      333 YKKGFSFEQOLLNYN-----VSRANCKITMFTDGGEEBAOEIFAKYKKDKRVYETF   387
        . : : : | : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      333 YEKAFLPLAFSVLLIDINNCGDNNGACENVMILITTDAPAKAYKIFPMYNADKKRVYETF   3920
OY      388 SVSGOHNDRCGFIOMWACKENGKYEYEISIGAIRINTGEYL-----DYLGPRMVLAGDAKQ   4430
Db      393 LVGDEAIDFNEVREMACNNRGIYMHVANAMADVDEKIHHYIRMSRYVGRIHKESQLS--   4500
OY      444 VQMTNVVLDALDELGL--VTGTLPVPFNITGONEKTN-----                     4780
        ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      451 -MMTGVRHERLYDRPREIFAEPVPIITNQSFVNKKMASRRKIRLOKSEARSMPVTVSY       5090
OY      479 --LKNOILLGYMGVDYSLEDIKRLTPRTLCPNQIYYAIDPNGVLLHPMLQPRNP-----  5320
        : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      510 PYIVNETFMFGAAVANIPLTEVAOKSHPANIGSKSYFPMLOONGVMVHPOLRPIDPTKY     5650
OY      533 KSQEPVTLDFLD-----ALEENDIKEIRNKMTIGE 5635
        | : : : | : : : : : : : : : : : : : : : : : : : : : : : :
Db      570 HKONTNNMDLLELEVGVGNQNRSSOKSOASVDLYCESGANAAECVDDLRAVRKMIIICD    6290
OY      584 SGEKTFRLLVKSQDERY---IDK---GNRTYTWPVANGTDYSLALVPLYTSFYIAKI    6160
        : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      630 NSD-----VOLDLVLTATELDRVYPOTNTYVEACINHANFVLGLAVAGDDRYVVK-    6820
OY      617 EETIQARSKKKGMK 631
        | : : : | : : : : : : : : : : : : : : : : : : : : : : : :
Db      683 -----QRKTYDGCRVK 692

RESULT 6
ITH3_MOUSE
ID ITH3 MOUSE STANDARD; PRT; 886 AA.
NC 061704:
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inter-alpha-trypsin inhibitor heavy chain H3 precursor (ITI heavy
chain H3).
GN ITIH3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6N; TISSUE=Liver;
RX MEDLINE=95194326; Pubmed=7534067;
RA Chan P., Ristler J.-U., Raquezuez G., Salter J.-P.;
RT "The three heavy-chain precursors for the inter-alpha-inhibitor
family in mouse: new members of the multicopier alpha protein group
with differential transcription in liver and brain.";
RL Biochem. J. 306:505-512(1995).
CC -! FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
SIMILARITY).
CC -! SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
BICUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2
AND BIKUNIN. INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
BIKUNIN, AND PR-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.
CC -! TISSUE SPECIFICITY: EXPRESSED IN BOTH LIVER AND BRAIN.
CC -! PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
4-SULFATE BRIDGE TO THEIR C-TERMINAL ASPARTATE (BY
SIMILARITY).
CC -! SIMILARITY: BELONGS TO THE ITIH FAMILY.
CC -! SIMILARITY: CONTAINS 1 VWFA DOMAIN.
```

Db	215	YTPAASFWMDNO--DEHLDLPDCRTEWYINSATNSKRVLLIMLDMSSGMIGOREYVAKOT	272
Qy	276	VSEMLLETISDDPEFVWVASENSA---QDVSCFOHLVQAVNPKYVLDAVNNITAKGTTD	333
Db	273	TEALLETISHNDYENIMFESKNTFLDLOCNGTNGLQATMKNKALKLRKMDTYSSEKAE	333
Qy	333	YKKGSPFPEOLLNTN-----VSRANCKITMLTDDGEEPAOEIFAKYNNKDKRVVTFE	387
Db	333	YEKALPIAFSVYLLDINNCGDNNRGCACNVLMITDGCAPNAKKIFPMYVNDKRVRYTFE	392
Qy	388	SVGQHNRYDRCGLIOWACENCKGYEYIEPISGIRINTOEYU---DVGRLPVLAGDKAKQ	444
Db	393	LVGDALIDFENYREACNNRRTGMVHANMADYDEKIHHTIRMSRVYGRATKESQLS-	450
Qy	444	VQMTNVYLDALIELG--VITGTLDPVNTIGONENKTN-----	478
Db	451	WMVGVRERERLYPRPELFAEPVPIITNOSFVANNKMSRRKIRLOKSEARSMEFTVTSY	508
Qy	479	--LNKQILLGWDVSLIEDIKRLPRTTLCPNQYFAIDPNGVYLLHPNLQPNP----	533
Db	510	PVIYVETMGAANAIVIPLTEVAOKSHPANIGSKSTFFMLDONGVMVHPOLRPIDEPTKY	566
Qy	533	KSQEPVTLDFLD-----AELENDIKVEIRKIMIDGE	563
Db	570	HKQVNNMDLLELEVGQNVNRSSQKSAQVADLVCESGANYAEVVDLRRAVRKMITCD	623
Qy	584	SGEKTFRILVASODERY---IDK---GNKRYTTPVANGDYSIALVLPYSEYIYAKI	616
Db	630	NSD-----VOQDLVYATELLIDVYPTQNTYVACELNHANFVGLGVAAGDDYRV---	679
Qy	617	EETITQASKKGGKMKDSETLKPDNEESGYEFIAPRDYC--NDKISDNTTE--FLNFNE	673
Db	680	-----YKQKQYVDGVRVMDMGQRKMLHNMRYCYCLNDTDHMSKEAPEIYAQQ	731
Qy	674	FIDR-KTPPNNSCTDLINRYLVDAGFTNELVONTMSKQKNIG--VKARFVYTDGKIT	729
Db	732	MSDGGKAPLLCEYRNRLVEKLLIDMEATSNLIDS--WTOFNFKNMNLINHLAFATPSGMI	790
Qy	730	RYVP-----KEAGNMOE-----NPETEDSPFKRS----	755
Db	791	RYVNLTLDDYVIDPYMSIFEPHIGHLSIEIAQSYNHFTDLNRKSTDRTYRRARMK	850
Qy	756	-----LDNDNYFTAPYFNKSGPAGESGLIMSKAVE--IYIOGKLLKPAVYGIKIDVNS	808
Db	851	DTIMEFVSNNSKIYKSETOQLTGLENNLTMLOAKRATY-----LDKRAVLG-----S	900
Qy	809	WIENFTTSISDPCAGVQCDCKRRSDVMDVYIIDGGSEFLMANHDVT-----NQI	859
Db	901	GFE-FAIDHYVDYIAEH--GCPASDDKWKCVLIDENAHVFFSOMNDISTYDYLVGSKHI	957
Qy	860	GRPFGEIDPSLMRLHVNISYAFNKS-----DYQVSCERPGARPKOGAHRSAUYPSIA	913
Db	958	SOYQEGGLNRIQORAM--ALLVEKREYTKLYTDNQNAVCAEKVYVTTSGRKLRRPPIFR	101
Qy	914	DILHIGMATAAAMSSIIQVLLSLTFPRLLLEAVEMEDDTASLSKOS-----CITEQTOY	969
Db	1015	FLMOTFENMWRLASOISGGFLIMLPNIQTEA-----YTASFHGTDVYPPKQSSPFY	106
Qy	970	FFPDNDSKFSGV--LDCGN-----CSRIFHEKIMLNTLFIYV-ESKGQCP	1014
Db	1068	FSNMDGNRGTHTLVGNNSERCRCKNNAKCSYKMEASFVDGINTLVYVWITQKASENC	1126
RESULT 5			
UN36_CAEEL			
ID	UN36_CAEEL	STANDARD:	PRT; 734 AA.
AC	P34374;		
DT	01-FEB-1994 (Rel. 28, Created)		
DT	01-FEB-1994 (Rel. 28, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Protein unc-36.		
DN	UNC-36 OR UNC-72 OR C50C3.11.		

RP SEQUENCE OF 961-975, 992-1000 AND 1033-1050.  
 RA MEDLINE-9036635; Pubmed-2168391;  
 RX de Jongh K.S., Warner C., Caterall W.A.;  
 RT "Subunits of purified calcium channels. Alpha 2 and delta are encoded  
 by the same gene."  
 RL J. Biol. Chem. 265:14738-14741(1990).  
 CC -1- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN  
 EXCITATION-CONTRACTION COUPLING.  
 CC -1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:  
 ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS  
 HETERODIMERS THAT ARE DISULFIDE-LINKED.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE  
 SPLICING.  
 CC -1- TISSUE SPECIFICITY: SKELETAL MUSCLE.  
 CC -1- PFM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM  
 A PRECURSOR FORM.  
 CC -1- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.  
 CC -1- SIMILARITY: CONTAINS 1 VFMA DOMAIN.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: M21948; AAA81562.1; -  
 DR PIR: S10579; CHRA2.  
 DR InterPro: IPR004010; Cache.  
 DR InterPro: IPR002035; VFMA\_A.  
 DR Pfam: PF00092; vma; 1.  
 DR Pfam: PF02743; Cache; 1.  
 DR SMART: SM00327; VMA; 1.  
 DR PROSITE: PS0234; VFMA; 1.  
 DR Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;  
 KW Calcium channel; Glycoprotein; Phosphorylation; Signal;  
 KM Alternative splicing.  
 FT SIGNAL 1 26  
 FT CHAIN 27 960  
 FT TRANSMEM 961 1106  
 FT TRANSMEM 448 471  
 FT TRANSMEM 921 945  
 FT TRANSMEM 1082 1101  
 FT DOMAIN 255 432  
 FT CARBOHYD 94 94  
 FT CARBOHYD 138 138  
 FT CARBOHYD 186 186  
 FT CARBOHYD 326 326  
 FT CARBOHYD 350 350  
 FT CARBOHYD 477 477  
 FT CARBOHYD 606 606  
 FT CARBOHYD 615 615  
 FT CARBOHYD 678 678  
 FT CARBOHYD 784 784  
 FT CARBOHYD 827 827  
 FT CARBOHYD 891 891  
 FT CARBOHYD 898 898  
 FT CARBOHYD 988 988  
 FT CARBOHYD 1001 1001  
 FT MOD\_RES 503 503  
 FT MOD\_RES 848 848  
 FT MOD\_RES 1106 1106  
 FT SEQUENCE 1106 AA; 125042 MW; B00DE7F3C877B618 CRC64;

Query Match 96.5%; Score 5253.5; DB 1; Length 1106;  
 Best Local Similarity 95.4%; Pred. No. 1,6e-305;  
 Matches 1009; Conservative 11; Mismatches 9; Indels 29; Gaps 4;

OY 1 MAAGCLALFTLFGS--LLIGPSQEPFSAVTIKSWDKQEDLVLTAKTASGVNOLV 58  
 DB 1 MAAGRPALMTILMQAMLILIGPSSEBPFAVTIKSWDKQEDLVLTAKTASGVNOLV 60

OY 59 DIYEKODLYTEBPNNAQLOVEIAARDIEKLISNRKALVRLALAEKVOAAHOMREDA 118  
 DB 61 DIYEKODLYTEBPNNAQLOVEIAARDIEKLISNRKALVRLALAEKVOAAHOMREDA 120  
 OY 119 SNEVYVYNAADDDLPENDEBPSQRKPYFIDANFGRISTQHAANIPDIDYGSST 178  
 DB 121 SNEVYVYNAADDDLPENDEBPSQRKPYFIDANFGRISTQHAANIPDIDYGSST 180  
 OY 179 VLNELMTASLDEYFKKREDEPSILMOVGSATGLARYPAAPWPNDSRTPKIDLYOV 238  
 DB 181 VLNELMTASLDEYFKKREDEPSILMOVGSATGLARYPAAPWPNDSRTPKIDLYOV 240  
 OY 239 RRRPWYIOGAASPRKMLILVDGSGVSGTLKILRTSVSEMLETSLDDDFVNVASPNNA 298  
 DB 241 RRRPWYIOGAASPRKMLILVDGSGVSGTLKILRTSVSEMLETSLDDDFVNVASPNNA 300  
 OY 299 ODVSCFQHLVQANVRNKKVLAADVNNITAGTIDYKKGFSFAEQLLNNVSAKCNKII 358  
 DB 301 ODVSCFQHLVQANVRNKKVLAADVNNITAGTIDYKKGFSFAEQLLNNVSAKCNKII 360  
 OY 359 MLFTDGEERAQELIFAKYKKNKRVFTFSVGOHNDRGPLOMACENKGYEIPISGA 418  
 DB 361 MLFTDGEERAQELIFAKYKKNKRVFTFSVGOHNDRGPLOMACENKGYEIPISGA 420  
 OY 419 IRIWQYLDVIGRPVYLAGDKAKOVQWNTVYLDALGLVITGTLPVNITGQENKTN 478  
 DB 421 IRIWQYLDVIGRPVYLAGDKAKOVQWNTVYLDALGLVITGTLPVNITGQENKTN 480  
 OY 479 LKNOILIGVGVGVSLIEDIRLTPRTFLCPNGYFPALDPNGYVLLPNIQPK----- 530  
 DB 481 LKNOILIGVGVGVSLIEDIRLTPRTFLCPNGYFPALDPNGYVLLPNIQPKIGVIGPT 540  
 OY 531 -----NPKSOEPTLDELDALENDIKEYELRNKIDSESEKFTRTLVKSODER 579  
 DB 541 INLRKRPNVQNRKSGPQPVYLDLDELDALENDIKEYELRNKIDSESEKFTRTLVKSODER 600  
 OY 580 YIDKGNRTYWTVPVNGTDY-SLALVLPYTSFYIKAKIEETITQARSKKMKMSETLKP 638  
 DB 601 YIDKGNRTYWTVPVNGTDYSLALVLPYTSFYIKAKIEETITQAR-----SETLKP 653  
 OY 639 DNFESGYTAPADYCNDKISDNNTFELNNEFIDRTPNPSCNTDLINRYLLDAG 698  
 DB 654 DNFESGYTAPADYCNDKISDNNTFELNNEFIDRTPNPSCNTDLINRYLLDAG 713  
 OY 699 FTNELVQNYMSKONIKGVARFVTDGITYRYPRKAGENMOENETEDSFYKRSIDN 758  
 DB 714 FTNELVQNYMSKONIKGVARFVTDGITYRYPRKAGENMOENETEDSFYKRSIDN 773  
 OY 759 DNYFTAPYFNKSGPGAYESGIWAKAVEIYIOGKLKPAVVGIKIDVNSWLENPTKTSI 818  
 DB 774 DNYFTAPYFNKSGPGAYESGIWAKAVEIYIOGKLKPAVVGIKIDVNSWLENPTKTSI 833  
 OY 819 RDPACAGVCCCKRSDVMDCVIILDDGFLMANHDDYTNOIGFEEIDPSILRHLVNTS 878  
 DB 834 RDPACAGVCCCKRSDVMDCVIILDDGFLMANHDDYTNOIGFEEIDPSILRHLVNTS 893  
 OY 879 VYAFNKSVDYQVCEPAGAPKQAGHRSAYVPSIADILHIGWATAAANSIIQOFLLSLT 938  
 DB 894 VYAFNKSVDYQVCEPAGAPKQAGHRSAYVPSIADILHIGWATAAANSIIQOFLLSLT 953  
 OY 939 FPRILEAVEHEDDFTASLSKQSCITEQIYFPDNDKSFSGVLDGCGNSRIFHYEKLNN 998  
 DB 954 FPRILEAVEHEDDFTASLSKQSCITEQIYFPDNDKSFSGVLDGCGNSRIFHYEKLNN 1013  
 OY 999 TNLIFIVESKGTCPDTRILLIOAEOTSDGPDPCDMVK 1036  
 DB 1014 TNLIFIVESKGTCPDTRILLIOAEOTSDGPDPCDMVK 1051

RESULT 4  
 YLJ9 CAEL  
 ID YLJ9 CAEL STANDARD; PRT; 1205 AA.  
 AC P34372;

DR InterPro: IPR004010; Cache.  
 DR Pfam: PF00092; vwa; 1.  
 DR Pfam: PF02743; Cache; 1.  
 DR SMART: SM00327; vwa; 1.  
 DR PROSITE: PS02324; vwa; 1.  
 DR Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;  
 KW Calcium channel; Glycoprotein; Phosphorylation; Signal;  
 KW Alternative splicing.  
 FT CHAIN 1 24  
 FT CHAIN 25 944  
 FT CHAIN 945 1091  
 FT TRANSMEM 445 468  
 FT TRANSMEM 906 930  
 FT TRANSMEM 1067 1086  
 FT DOMAIN 252 429  
 FT CARBOHYD 92 92  
 FT CARBOHYD 136 136  
 FT CARBOHYD 184 184  
 FT CARBOHYD 323 323  
 FT CARBOHYD 347 347  
 FT CARBOHYD 474 474  
 FT CARBOHYD 584 584  
 FT CARBOHYD 593 593  
 FT CARBOHYD 663 663  
 FT CARBOHYD 769 769  
 FT CARBOHYD 812 812  
 FT CARBOHYD 876 876  
 FT CARBOHYD 883 883  
 FT CARBOHYD 973 973  
 FT CARBOHYD 986 986  
 FT MOD.RES 500 500  
 FT MOD.RES 833 833  
 FT SEQUENCE 1091 AA: 123822 MM: 7054907D9D343B34 CRC64;  
 Query Match 96.7%; Score 5268; DB 1; Length 1091;  
 Best Local Similarity 96.2%; Pred. No. 2; le-306;  
 Matches 998; Conservative 23; Mismatches 14; Indels 2; Gaps 2;

QY 1 MAAGCLLATLTLLFOSLTLGSSOEPSPSAVTIKSWDKMOEDLVTLATASGVNDLVI 60  
 Db 1 MAAGCLLATLTLLFOSLTLGSSOEPSPSAVTIKSWDKMOEDLVTLATASGVNDLVI 60  
 QY 61 YEKYODLYTEPNNAQVLEIARDIEKLSNRKALVRLALEAEVQAQHQREDFASN 120  
 Db 61 YEKYODLYTEPNNAQVLEIARDIEKLSNRKALVRLALEAEVQAQHQREDFASN 120  
 QY 121 EYVYNAKDDLDPEKNDSEPGSRIRKPVITDANFGROISYQHAAYHPTDIYEGSTIVL 180  
 Db 121 EYVYNAKDDLDPEKNDSEPGSRIRKPVITDANFGROISYQHAAYHPTDIYEGSTIVL 180  
 QY 181 NELNMTSALDEVFKKRNREDEPSLTLQVFGSATGLARYYPASPVNDSSRTNPKIDLVDR 240  
 Db 181 NELNMTSALDEVFKKRNREDEPSLTLQVFGSATGLARYYPASPVNDSSRTNPKIDLVDR 240  
 QY 241 RPYVIGGASPKDMLTLVDVSGVSGLLTKLIRTSYSEMLETLSDDDPFNVASFNSNAD 300  
 Db 241 RPYVIGGASPKDMLTLVDVSGVSGLLTKLIRTSYSEMLETLSDDDPFNVASFNSNAD 300  
 QY 301 VSCFOHLYOANVANKKVLKDAVNNITAKGTTDYKGFSTAFEOOLLVYNSRANCKIIML 360  
 Db 301 VSCFOHLYOANVANKKVLKDAVNNITAKGTTDYKGFSTAFEOOLLVYNSRANCKIIML 360  
 QY 361 FTGGEERAOEIRAKYNNKKVAVFPEVSGOHYDGRPIOMACENKGYVEIPISGAIR 420  
 Db 361 FTGGEERAOEIRAKYNNKKVAVFPEVSGOHYDGRPIOMACENKGYVEIPISGAIR 420  
 QY 421 INTQEVLDVIGRPMVLADGKAKOVQNTNYLADLELGLVYTGTLPEVNTTQGENENTNKL 480  
 Db 421 INTQEVLDVIGRPMVLADGKAKOVQNTNYLADLELGLVYTGTLPEVNTTQGENENTNKL 480  
 QY 481 NOLILGVNGVDVSLIEDIRLIPRFTLCGNGYFFALDPNGVYLLHPNLIQPKNPKSQEPVTL 540  
 Db 481 NOLILGVNGVDVSLIEDIRLIPRFTLCGNGYFFALDPNGVYLLHPNLIQPKNPKSQEPVTL 540  
 QY 541 DFLDALENDIKVETIRNMKMGESGEKTEFRLVYSQDERYIDKGNRTYTWTPVNGTQYS- 599  
 Db 541 DFLDALENDIKVETIRNMKMGESGEKTEFRLVYSQDERYIDKGNRTYTWTPVNGTQYS- 599  
 QY 600 IALVPTYSFYIKAKIEETITQARSKGKKMKDSETLKPDNFESGYYFIRAPRYCNDLK 659  
 Db 600 IALVPTYSFYIKAKIEETITQARSKGKKMKDSETLKPDNFESGYYFIRAPRYCNDLK 659  
 QY 660 ISDNTEPELLNNEFDIRKTPNNSCNTDLINRVLADAGFTNEIYQNTWSKOKNIKGYKA 719  
 Db 660 ISDNTEPELLNNEFDIRKTPNNSCNTDLINRVLADAGFTNEIYQNTWSKOKNIKGYKA 719  
 QY 720 RPYVVDGTTTRYPKAEENNOENPEYEDSPYKSLNDNDVYFAPYFNKSGGAYESG 779  
 Db 720 RPYVVDGTTTRYPKAEENNOENPEYEDSPYKSLNDNDVYFAPYFNKSGGAYESG 779  
 QY 780 IMVSAVEIYIOGKLKPAVYCIKIDVNSWIEENFTKTSIRPCAGPYCDCKRNSDVMDCV 839  
 Db 780 IMVSAVEIYIOGKLKPAVYCIKIDVNSWIEENFTKTSIRPCAGPYCDCKRNSDVMDCV 839  
 QY 840 IIDDGFLMANHNDYTNQIGRFGESIDPSLMRHLVNISVYAFNKSYDYGVCEPGAAPK 899  
 Db 840 IIDDGFLMANHNDYTNQIGRFGESIDPSLMRHLVNISVYAFNKSYDYGVCEPGAAPK 899  
 QY 900 OGAGRSRVAVPSITDILIGWATATAASTIIOQPLSTIFRLLAEVMEEDDTFASISK 959  
 Db 900 OGAGRSRVAVPSITDILIGWATATAASTIIOQPLSTIFRLLAEVMEEDDTFASISK 959  
 QY 960 OSCITEOTQYFEDNDSKFSFVGLDCGNSRIFFHEKLANLMLIFPMVSKTCQCDTRL 1019  
 Db 960 OSCITEOTQYFEDNDSKFSFVGLDCGNSRIFFHEKLANLMLIFPMVSKTCQCDTRL 1019  
 QY 1020 IQAEGTSDGPDPCDMVK 1036  
 Db 1020 IQAEGTSDGPDPCDMVK 1036

RESULT 3  
 C1C2\_RABIT STANDARD; PRT; 1106 AA.  
 AC P13806;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta  
 DE subunits precursor.  
 GN CACNA2D1 OR CACNA2A OR CCHL2A.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxId=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88336904; PubMed=2458626;  
 RA Ellis S.B., Williams M.E., Ways N.R., Brenner R., Sharp A.H.,  
 RA Leung A.T., Campbell K.P., McKenna E., Koch W.J., Hui A.,  
 RA Schwartz A., Halperin M.M.;  
 RT "Sequence and expression of mRNAs encoding the alpha 1 and alpha 2  
 RT subunits of a dihydropyridine-sensitive calcium channel.";  
 RL Science 241:1661-1664(1988).  
 RN [2]  
 RP SEQUENCE OF 961-973.  
 RX MEDLINE=91131638; PubMed=1847144;  
 RA Jay S.D., Sharp A.H., Kahl S.D., Vedvick T.S., Harpold M.M.,  
 RA Campbell K.P.;  
 RT "Structural characterization of the dihydropyridine-sensitive calcium  
 RT channel alpha 2-subunit and the associated delta peptides.";  
 RL J. Biol. Chem. 266:3287-3293(1991).  
 RN [3]

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FT FT CHAIN 945 1091 (BY SIMILARITY)
FT FT TRANSMEM 446 469 L-TYPE CALCIUM CHANNEL DELTA SUBUNIT (BY
FT FT TRANSMEM 906 930 POTENTIAL)
FT FT TRANSMEM 1067 1086 POTENTIAL.
FT FT DOMAIN 253 430 POTENTIAL.
FT FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT FT CARBOHYD 324 324 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT FT CARBOHYD 348 348 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT FT CARBOHYD 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT FT CARBOHYD 585 585 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT FT CARBOHYD 663 663 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT FT CARBOHYD 769 769 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT FT CARBOHYD 876 876 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT FT CARBOHYD 973 973 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT FT CARBOHYD 986 986 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT FT MOD_RES 501 501 PHOSPHORYLATION (BY PKA) (BY SIMILARITY)
FT FT MOD_RES 833 833 PHOSPHORYLATION (BY PKA) (BY SIMILARITY)
SQ SEQUENCE 1091 AA; 123183 MW; 2E4E13EE29A47837 CRC64;

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Query Match 98.8%; Score 5380; DB 1; Length 1091;
Best Local Similarity 98.7%; Pred. No. 4.4e-313;
Matches 1023; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

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QY 1 MAAGCLLALTLTLFOSLLGSSOEPFSAVTIKSWYCKMODIVTLAKTAGVNOYDI 60
DB 1 MAAGCLLALTLTLFOSLLGSSOEPFSAVTIKSWYCKMODIVTLAKTAGVNOYDI 60
QY 61 YEKYODLYVEBPNNARQVLEIARDIEKLNSRKALYALAEAKVQAQHWREDFASN 120
DB 61 YEKYODLYVEBPNNARQVLEIARDIEKLNSRKALYALAEAKVQAQHWREDFASN 120
QY 121 EYVYNAKDDLPKNDSPGSOIRKPVITDANGROISYQAAHVHPTDIEGSTIVL 180
DB 121 EYVYNAKDDLPKNDSPGSOIRKPVITDANGROISYQAAHVHPTDIEGSTIVL 180
QY 181 NELNMTSALDEYFKKRNREDEPSLLMQVFSATGATLARYYPASPMVNSRTPNKIDYDVR 240
DB 181 NELNMTSALDEYFKKRNREDEPSLLMQVFSATGATLARYYPASPMVNSRTPNKIDYDVR 240
QY 241 RFWYIOGAASPKDMLILDVSGSVGLTLKLRISVSEMLETLSDDFEVNVAFSNSNAD 300
DB 241 RFWYIOGAASPKDMLILDVSGSVGLTLKLRISVSEMLETLSDDFEVNVAFSNSNAD 300
QY 301 VSCPOHIVQANVRNKKVLLKDAVNNNTAGTIDYKKGFSAPFQOLLNVNVRANCKIIML 360
DB 301 VSCPOHIVQANVRNKKVLLKDAVNNNTAGTIDYKKGFSAPFQOLLNVNVRANCKIIML 360
QY 361 FTDGGEERAQELFAKYNKDKKRVETFSVGOHNDYRGPIONWACENKGYEYIPSIGAIR 420
DB 361 FTDGGEERAQELFAKYNKDKKRVETFSVGOHNDYRGPIONWACENKGYEYIPSIGAIR 420
QY 421 INTQYELVLYGPRVYLADGKAKOVQWNTVYDALELGLVITGTLPEVFNITGQFEKKTMLK 480
DB 421 INTQYELVLYGPRVYLADGKAKOVQWNTVYDALELGLVITGTLPEVFNITGQFEKKTMLK 480
QY 481 NOLILGVGVDSIEDIKRLPRFLCPNGYFAFDIPNGYVLLHNPLOPKPKSGSEPTVL 540
DB 481 NOLILGVGVDSIEDIKRLPRFLCPNGYFAFDIPNGYVLLHNPLOPKPKSGSEPTVL 540
QY 541 DELDALENDIKVEIRNKMIDGSEGEKTFRTLVKSODERYIDKGNRTYTTWTPVNGTDSL 600
DB 541 DELDALENDIKVEIRNKMIDGSEGEKTFRTLVKSODERYIDKGNRTYTTWTPVNGTDSL 600
QY 601 ALVPTYSFYIKAKIETITQARSKKKKMDSETLAKDNFEESGYFIADRYCNDIKI 660
DB 601 ALVPTYSFYIKAKIETITQARSKKKKMDSETLAKDNFEESGYFIADRYCNDIKI 660

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QY 661 SDNTEFLNENEFIDRKTTPNPNPSCNTDLINRVLLDAGFTNELVQNYKSKOKNIKGYKAR 720
DB 661 SDNTEFLNENEFIDRKTTPNPNPSCNTDLINRVLLDAGFTNELVQNYKSKOKNIKGYKAR 720
QY 721 FVYTGIGITRYVPKAGENWOENPETYDSFYKNSLNDNVTFTAPYFNKSGPAYESGI 780
DB 721 FVYTGIGITRYVPKAGENWOENPETYDSFYKNSLNDNVTFTAPYFNKSGPAYESGI 780
QY 781 MYSKAVEIYIGKILKPRVVGKIDVNSWIENTFTKTSIRDCACAPYCDCKRNSVIMCVI 840
DB 781 MYSKAVEIYIGKILKPRVVGKIDVNSWIENTFTKTSIRDCACAPYCDCKRNSVIMCVI 840
QY 841 IDDGFEFLMANHDDYTNOIGRFFGEIDPSLRHVNISVYAFNKSQYOSVCEPAAPO 900
DB 841 IDDGFEFLMANHDDYTNOIGRFFGEIDPSLRHVNISVYAFNKSQYOSVCEPAAPO 900
QY 901 GAGHSATVPSTADTLIHGMWATAAAMSILOOFTLSLTFPRLBAVEMEDDDFTASLSKO 960
DB 901 GAGHSATVPSTADTLIHGMWATAAAMSILOOFTLSLTFPRLBAVEMEDDDFTASLSKO 960
QY 961 SCITEQYFFDNDKSKSFSGVLDGNCRIHVRKIMNTNLIPTWVSKGTCPCDTRILLI 1020
DB 961 SCITEQYFFDNDKSKSFSGVLDGNCRIHVRKIMNTNLIPTWVSKGTCPCDTRILLI 1020
QY 1021 QAEQTSIDGPDPCDMVK 1036
DB 1021 QAEQTSIDGPDPCDMVK 1036

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RESULT 2
CIC2_RAT STANDARD; PRT; 1091 AA.
AC P54290;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Dlyndropyridine-sensitive L-type, calcium channel alpha-2/delta
DE subunits precursor.
GN CACNA2D1 OR CACNL2A OR CCHL2A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92228762; PubMed=1314383;
RA Kim H.L., Kim H., Lee P., King R.G., Chin H.;
RT "Rat brain expresses an alternatively spliced form of the
RT dlyndropyridine-sensitive L-type calcium channel alpha 2 subunit.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:3251-3255(1992).
CI -1- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN
CI EXCITATION-CONTRACTION COUPLING.
CC -1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:
CC ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS
CC HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM
CC A PRECURSOR FORM (BY SIMILARITY).
CC -1- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.
CC -1- SIMILARITY: CONTAINS 1 WFMA DOMAIN.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC DR EMBL; M66621; AAAA1088.1;

```

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 10, 2003, 14:13:50 : Search time 9.50459 Seconds  
(without alignments)  
4520.920 Million cell updates/sec

Title: US-10-090-827-7

Perfect score: 5446

Sequence: 1 MAAGCLIANITLTLFQSLILIG.....RLTIQAEQTSDDPCDVK 1036

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt-40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5380	98.8	1091	CIC2_HUMAN	P54289 homo sapien
2	5268	96.7	1091	CIC2_RAT	P54290 ratus norv
3	5253.5	96.5	1106	CIC2_RABIT	P13806 oryctolagus
4	739.5	13.6	1205	YLJ9_CAEEL	P34374 caenorhabd
5	611	11.2	734	UN36_CAEEL	P34374 caenorhabd
6	196.5	3.6	886	ITR3_MOUSE	P61704 mus musculu
7	185	3.4	885	ITR3_HUMAN	P06033 homo sapien
8	183.5	3.4	887	ITR3_RAT	P06416 ratus norv
9	168.5	3.1	575	YFER_ECOLI	P76481 escherichia
10	162	3.0	886	ITR3_MESAU	P97280 mesocricetu
11	166	3.0	1829	DPOL_THERST	P03845 thermococcu
12	160.5	2.9	420	Y103_SYNY3	P05874 synchocyst
13	155.5	2.9	946	ITR2_HUMAN	P19823 homo sapien
14	155	2.8	1956	ATX1_PLAFA	P04856 plasmodium
15	153	2.8	946	ITR2_MESAU	P97279 mesocricetu
16	149.5	2.7	654	MCPC_BACSU	P54576 bacillus su
17	149.5	2.7	921	ITR4_PIG	P79263 sus scrofa
18	147	2.7	1087	XYNX_CLOTM	P38335 clostridium
19	144.5	2.7	929	CALC_NOTVI	P01424 notophthalm
20	144	2.6	930	ITR4_HUMAN	P14624 h inter-alp
21	143.5	2.6	935	ITR2_PIG	P02668 sus scrofa
22	142	2.6	964	DPOL_CBBPV	P09715 choristoneu
23	142	2.6	3063	CALC_HUMAN	P09715 homo sapien
24	141.5	2.6	946	ITR2_MOUSE	P061703 mus musculu
25	141	2.6	1290	BXCI_CLOBO	P18640 clostridium
26	140.5	2.6	764	PAG_BACAN	P13423 bacillus an
27	140	2.6	1180	C4AA_BACTI	P16480 bacillus th
28	138.5	2.5	382	YLJ9_CAEEL	P34373 caenorhabd
29	137.5	2.5	862	MUTS_BORBU	P05177 borrelia bu
30	137	2.5	3305	APLP_MANSE	P025490 manduca sex
31	136	2.5	687	YEPG_SCHPO	P013773 schizosacch
32	134	2.5	1251	RBP2_PLAIVB	P007799 plasmodium
33	133	2.4	1169	SMC_METUA	P059037 methanococc

## ALIGNMENTS

RESULT 1	ID	CIC2_HUMAN	STANDARD	PRT: 1091 AA.
AC	P54289:			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta			
DE	subunits precursor.			
GN	CACNA2D1 OR CACNA2A OR CCHL2A.			
OC	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.			
OX	NCBI_TaxID=9606;			
RM	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92110010; PubMed=1309651;			
RA	Williams M.E., Feldman D.H., McCue A.F., Brenner R.,			
RA	Veilleux G., Ellis S.B., Harpold M.W.,			
RT	"Structure and functional expression of alpha 1, alpha 2, and beta			
RT	subunits of a novel human neuronal calcium channel subtype.";			
RT	Neuron 8:71-84(1992).			
RL	FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN			
CC	EXCITATION-CONTRACTION COUPLING			
CC	- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:			
CC	ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS			
CC	HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).			
CC	- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	- TISSUE SPECIFICITY: CENTRAL NERVOUS SYSTEM, SKELETAL MUSCLE AND			
CC	AORTA TISSUES.			
CC	- PFM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM			
CC	A PRECURSOR FORM (BY SIMILARITY).			
CC	- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.			
CC	- SIMILARITY: CONTAINS 1 VWFA DOMAIN.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	EMBL: M76559; AA051903.1; -			
CC	Genew: HGNC:1399; CACNA2D1.			
CC	MIM: 114204; -			
CC	InterPro: IPR004010; Cache.			
CC	InterPro: IPR002035; VWFA.			
CC	DR pfam: PF00092; vwa; 1.			
CC	DR pfam: PF02743; Cache; 1.			
CC	DR SMART: SM00327; vwa; 1.			
CC	DR PROSITE: PS00334; VWFA; 1.			
CC	KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;			
CC	calcium channel; Glycoprotein; Phosphorylation; signal.			
CC	SIGNAL			
CC	FT CHAIN 25 944 L-TYPE CALCIUM CHANNEL, ALPHA-2 SUBUNIT			



Query Match 98.6%; Score 5526; DB 14; Length 1091;  
 Best Local Similarity 98.6%; Pred. No. 0;  
 Matches 1048; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 MAGCLLALTLTLFQSLIGPSSQEPSPAVTIKSWDKMQEDVTLAKTAGVNOVDI 60  
 1 MAAGCLLALTLTLFQSLIGPSSQEPSPAVTIKSWDKMQEDVTLAKTAGVNOVDI 60  
 DB 61 YEKYQDLTYVERPNNAQOLVEIARDIEKLNSKALVRLALFAEKVQAHOHREDFASN 120  
 QY 61 YEKYQDLTYVERPNNAQOLVEIARDIEKLNSKALVRLALFAEKVQAHOHREDFASN 120  
 DB 61 YEKYQDLTYVERPNNAQOLVEIARDIEKLNSKALVRLALFAEKVQAHOHREDFASN 120  
 QY 121 EYVYNAKDDLDPEKNDSESGRIKPFVIEDANFGROISYQHAAYHPTDIYEGSTIVL 180  
 DB 121 EYVYNAKDDLDPEKNDSESGRIKPFVIEDANFGROISYQHAAYHPTDIYEGSTIVL 180  
 QY 181 NELNMTSALDEVPKKNREDDPSLLMOVFGSAGTGLARYPASPVWDSRTPNKIDLYVR 240  
 DB 181 NELNMTSALDEVPKKNREDDPSLLMOVFGSAGTGLARYPASPVWDSRTPNKIDLYVR 240  
 QY 241 RPYWIGGAASPKDMLILYDSSVSGITLKITVSSEMETLSDDDFVNVASFNSNAD 300  
 DB 241 RPYWIGGAASPKDMLILYDSSVSGITLKITVSSEMETLSDDDFVNVASFNSNAD 300  
 QY 301 VSCFOHLVQANVRNKKVLDVANNITAKGIDYKKGFSFAEQLLNVNVRANCKNIIML 360  
 DB 301 VSCFOHLVQANVRNKKVLDVANNITAKGIDYKKGFSFAEQLLNVNVRANCKNIIML 360  
 QY 361 FTBGGERRAOEITAKYKDKKRVFTSVQOHYDGRPIOMMACENKGYEETPSIGAIR 420  
 DB 361 FTBGGERRAOEITAKYKDKKRVFTSVQOHYDGRPIOMMACENKGYEETPSIGAIR 420  
 QY 421 INFOEYLDVGRPVNLAGDRAKOVMTNVYLDLLEGLVTTGTLPEVNTIGONENKTNLK 480  
 DB 421 INFOEYLDVGRPVNLAGDRAKOVMTNVYLDLLEGLVTTGTLPEVNTIGONENKTNLK 480  
 QY 481 NQILLGVAGVDSLEDIKRLTPRETLCPNGYFAIDPNGYVLLHPNLOPKNPKSOEPTVL 540  
 DB 481 NQILLGVAGVDSLEDIKRLTPRETLCPNGYFAIDPNGYVLLHPNLOPKNPKSOEPTVL 540  
 QY 541 DFLDAELENDIKVIRKMKIDGESGEKFTPIVKSODERYIDKGNRTYTWTPVNGTDYSL 600  
 DB 541 DFLDAELENDIKVIRKMKIDGESGEKFTPIVKSODERYIDKGNRTYTWTPVNGTDYSL 600  
 QY 601 ALVLPYSEFYIKAKIETITQARSKKGMKDSSETLKPDNFEESGYTFIAPRDYCNLDKI 660  
 DB 601 ALVLPYSEFYIKAKIETITQARSKKGMKDSSETLKPDNFEESGYTFIAPRDYCNLDKI 660  
 QY 661 SDNNTPELLNENEFIDRKTPNPNPSCNTDLINRVLLDAGFTNEIVONTWSKOKNIKGVKAR 720  
 DB 661 SDNNTPELLNENEFIDRKTPNPNPSCNTDLINRVLLDAGFTNEIVONTWSKOKNIKGVKAR 720  
 QY 721 FVWVDGGITRYPRKAGENQENPETEDSFYKRSINDNYPVFTAPYFNKSGPGAYESGI 780  
 DB 721 FVWVDGGITRYPRKAGENQENPETEDSFYKRSINDNYPVFTAPYFNKSGPGAYESGI 780  
 QY 781 MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPACAPVDCCKRNSDVMDCVI 840  
 DB 781 MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPACAPVDCCKRNSDVMDCVI 840  
 QY 841 LDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNISVYAFNKSVDYQSVCEPGAAPKQ 900  
 DB 841 LDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNISVYAFNKSVDYQSVCEPGAAPKQ 900  
 QY 901 GAGHSAYVPSIADLIHIGMATAAAMSIILOPILSLTFPRLLAEVEMEDDDFTASLSKQ 960  
 DB 901 GAGHSAYVPSIADLIHIGMATAAAMSIILOPILSLTFPRLLAEVEMEDDDFTASLSKQ 960  
 QY 961 SCITEQTOYFFDNDKSKFSFVLDGNCRSRIFHVEKIMNTNLIIFWVESKGTCPDTRLLI 1020  
 DB 961 SCITEQTOYFFDNDKSKFSFVLDGNCRSRIFHVEKIMNTNLIIFWVESKGTCPDTRLLI 1020  
 QY 1021 QAEQTSDEGPCDMVKQPRYRKGPVCFDNNALBDYTDGCGVS 1063

DB 1021 QAEQTSDEGPCDMVKQPRYRKGPVCFDNNALBDYTDGCGVS 1063  
 Search completed: February 10, 2003, 14:18:10  
 Job time : 39.4969 secs



CC and omega-conotoxin GVIA toxin sensitive potassium-stimulated  
 CC calcium uptake, indicating that the proteins expressed by the  
 CC clones are capable of forming a functioning calcium channel.  
 CC Nucleic acids encoding the 3 subunits, as well as vectors, host  
 CC cells and methods of isolating nucleic acids encoding related  
 CC calcium channels are disclosed. Fusion proteins incorporating the  
 CC subunit proteins, antibodies, and assays for identifying agents  
 CC that modulate calcium channel activity are also provided. Such  
 CC agents can be used to treat certain central nervous system  
 CC disorders by altering calcium channel activity. Methods of  
 CC diagnosing diseases associated with particular calcium channels,  
 CC such as Lambert-Eaton syndrome, are disclosed.

XX Sequence 1091 AA:

Query Match 98.7%; Score 5528; DB 19; Length 1091;  
 Best Local Similarity 98.6%; Pred. No. 0;  
 Matches 1048; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLTLPSSLSSEPPSAVTIKSVWDKMODLVTLAKTAGVNLVDI 60  
 DB 1 MAAGCLLALTLTLPSSLSSEPPSAVTIKSVWDKMODLVTLAKTAGVNLVDI 60  
 QY 61 YEKQDLYTEPNNAQVLEIARDIEKLISNSKALVLAELAEKVQAHHQWREDFASN 120  
 DB 61 YEKQDLYTEPNNAQVLEIARDIEKLISNSKALVLAELAEKVQAHHQWREDFASN 120  
 QY 121 EYVYVNAKDLDPKNDSESGSRIKPVFIIDANPFRQISYQAAHPTDYEESTYL 180  
 DB 121 EYVYVNAKDLDPKNDSESGSRIKPVFIIDANPFRQISYQAAHPTDYEESTYL 180  
 QY 121 EYVYVNAKDLDPKNDSESGSRIKPVFIIDANPFRQISYQAAHPTDYEESTYL 180  
 DB 121 EYVYVNAKDLDPKNDSESGSRIKPVFIIDANPFRQISYQAAHPTDYEESTYL 180  
 QY 181 NELNMTSALDEVEFKKNEEDPSILMOYFSGATGLARYYPASPVWDSRTPNKIDLYDVR 240  
 DB 181 NELNMTSALDEVEFKKNEEDPSILMOYFSGATGLARYYPASPVWDSRTPNKIDLYDVR 240  
 QY 241 RPWTIOGAASPKDMLLVDSVSGVGLTKLITVSSEMETISDDDFVNASFNSNAD 300  
 DB 241 RPWTIOGAASPKDMLLVDSVSGVGLTKLITVSSEMETISDDDFVNASFNSNAD 300  
 QY 301 VSCFOHLYQAVNRKVKYLKAVNNITAKGTDYKGFSPFEBOLLVYNSRANCKNIML 360  
 DB 301 VSCFOHLYQAVNRKVKYLKAVNNITAKGTDYKGFSPFEBOLLVYNSRANCKNIML 360  
 QY 301 VSCFOHLYQAVNRKVKYLKAVNNITAKGTDYKGFSPFEBOLLVYNSRANCKNIML 360  
 DB 301 VSCFOHLYQAVNRKVKYLKAVNNITAKGTDYKGFSPFEBOLLVYNSRANCKNIML 360  
 QY 361 FTDSGEERAQEFIAKYNKDKKRVFTEPSVGOHNYDRGPIDMACENKGYEIEPSIGAIR 420  
 DB 361 FTDSGEERAQEFIAKYNKDKKRVFTEPSVGOHNYDRGPIDMACENKGYEIEPSIGAIR 420  
 QY 361 FTDSGEERAQEFIAKYNKDKKRVFTEPSVGOHNYDRGPIDMACENKGYEIEPSIGAIR 420  
 DB 361 FTDSGEERAQEFIAKYNKDKKRVFTEPSVGOHNYDRGPIDMACENKGYEIEPSIGAIR 420  
 QY 421 INTQETLDVIGRPVYLAGDKRAKQVQWNTNYLDLELGLVITGLPVPFNITGQENKTNLK 480  
 DB 421 INTQETLDVIGRPVYLAGDKRAKQVQWNTNYLDLELGLVITGLPVPFNITGQENKTNLK 480  
 QY 421 INTQETLDVIGRPVYLAGDKRAKQVQWNTNYLDLELGLVITGLPVPFNITGQENKTNLK 480  
 DB 421 INTQETLDVIGRPVYLAGDKRAKQVQWNTNYLDLELGLVITGLPVPFNITGQENKTNLK 480  
 QY 481 NOLIGVGVDSLEDIRLPRTILCPNGYFAIDPNGVVLHPNLQPKNPSOEPRVL 540  
 DB 481 NOLIGVGVDSLEDIRLPRTILCPNGYFAIDPNGVVLHPNLQPKNPSOEPRVL 540  
 QY 481 NOLIGVGVDSLEDIRLPRTILCPNGYFAIDPNGVVLHPNLQPKNPSOEPRVL 540  
 DB 481 NOLIGVGVDSLEDIRLPRTILCPNGYFAIDPNGVVLHPNLQPKNPSOEPRVL 540  
 QY 541 DFLDAELNDIKVEIRNKMIDEGSEKTFRTLVKSQDERITDKGNRTYTTPANGDYSL 600  
 DB 541 DFLDAELNDIKVEIRNKMIDEGSEKTFRTLVKSQDERITDKGNRTYTTPANGDYSL 600  
 QY 541 DFLDAELNDIKVEIRNKMIDEGSEKTFRTLVKSQDERITDKGNRTYTTPANGDYSL 600  
 DB 541 DFLDAELNDIKVEIRNKMIDEGSEKTFRTLVKSQDERITDKGNRTYTTPANGDYSL 600  
 QY 601 ALVLTYSFYIKAKIEETITQARSKKGMDSLETKPDPNFEESGYFFIAPROVCNDLKI 660  
 DB 601 ALVLTYSFYIKAKIEETITQARSKKGMDSLETKPDPNFEESGYFFIAPROVCNDLKI 660  
 QY 601 ALVLTYSFYIKAKIEETITQARSKKGMDSLETKPDPNFEESGYFFIAPROVCNDLKI 660  
 DB 601 ALVLTYSFYIKAKIEETITQARSKKGMDSLETKPDPNFEESGYFFIAPROVCNDLKI 660  
 QY 661 SDNNTFFLNFNEFIDRTKTPNNPSCNDLIRVLLDAGFTNELVQVNTWSKOKNITGVKAR 720  
 DB 661 SDNNTFFLNFNEFIDRTKTPNNPSCNDLIRVLLDAGFTNELVQVNTWSKOKNITGVKAR 720  
 QY 661 SDNNTFFLNFNEFIDRTKTPNNPSCNDLIRVLLDAGFTNELVQVNTWSKOKNITGVKAR 720  
 DB 661 SDNNTFFLNFNEFIDRTKTPNNPSCNDLIRVLLDAGFTNELVQVNTWSKOKNITGVKAR 720  
 QY 721 FVYTDGIGITRVYKRAGENWOENPETYEDSPYKSLDNDNVFAPFNKSGPAYSIGI 780  
 DB 721 FVYTDGIGITRVYKRAGENWOENPETYEDSPYKSLDNDNVFAPFNKSGPAYSIGI 780  
 QY 721 FVYTDGIGITRVYKRAGENWOENPETYEDSPYKSLDNDNVFAPFNKSGPAYSIGI 780  
 DB 721 FVYTDGIGITRVYKRAGENWOENPETYEDSPYKSLDNDNVFAPFNKSGPAYSIGI 780  
 QY 781 MYSKAVEIYIQGKLLKPAVVGIKIDVNSMIENFTKTSIRDCAGPVDCCKNSDVMDCVI 840  
 DB 781 MYSKAVEIYIQGKLLKPAVVGIKIDVNSMIENFTKTSIRDCAGPVDCCKNSDVMDCVI 840

DB 781 MYSKAVEIYIQGKLLKPAVVGIKIDVNSMIENFTKTSIRDCAGPVDCCKNSDVMDCVI 840  
 QY 841 LDDGFFLMAHNDVDTNOIGRFFGEIDPSILMRHLNIVSYAFNKSVDYQSCGEPGAAPK 900  
 DB 841 LDDGFFLMAHNDVDTNOIGRFFGEIDPSILMRHLNIVSYAFNKSVDYQSCGEPGAAPK 900  
 QY 901 GAGHRSAVYPSVADILQIGMATAAAMSTLQOFLSLTFPRILLEAVEMEDDFTASLSKQ 960  
 DB 901 GAGHRSAVYPSVADILQIGMATAAAMSTLQOFLSLTFPRILLEAVEMEDDFTASLSKQ 960  
 QY 961 SCITTEQTOYFFNDSDSKSFSGVLDCCGNSRIFRGEKLMNTNLIIFIMVESKGNPCDTRLII 1020  
 DB 961 SCITTEQTOYFFNDSDSKSFSGVLDCCGNSRIFRGEKLMNTNLIIFIMVESKGNPCDTRLII 1020  
 QY 1021 QABOTSDGPPCDMVKOPRYRKGPDPVCPDNALLEDYTDGCGVS 1063  
 DB 1021 QABOTSDGPPCDMVKOPRYRKGPDPVCPDNALLEDYTDGCGVS 1063

# RESULT 15

AA33553  
 ID AAR33553 standard; Protein; 1091 AA.

AC AAR33553:

DT 30-JUN-1993 (first entry)

DE Sequence of the alpha 2 human calcium channel subunit.

KW Human calcium channel subunit; diagnosis; agonist; antagonist;  
 KW Lambert Eaton syndrome.

OS Homo sapiens.

PN WC9304083-A.

PD 04-MAR-1993.

PF 14-AUG-1992; 92MO-US06903.

PR 15-AUG-1991; 91US-0745206.

PR 10-APR-1992; 92US-0868354.

PA (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.

PI Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF,  
 PI Williams ME;

PS WPI: 1993-093936/11.

DR N-PSDB: AAQ37821.

PT DNA encoding specific human calcium channel sub-units - used for  
 PT identifying calcium channel agonists and antagonists and  
 PT diagnosing Lambert Eaton syndrome

PS Disclosure: Page 134-138; 150pp; English.

CC DNA encoding a human neuronal calcium channel alpha 2 subunit was  
 CC isolated from a human genomic DNA library probed under low and high  
 CC stringency conditions with a fragment of DNA encoding the rabbit  
 CC skeletal muscle calcium channel alpha 2 subunit. The fragment  
 CC included nucleotides having a sequence corresponding to the  
 CC nucleotide sequence between nucleotides 43 and 272 inclusive of  
 CC rabbit back skeletal muscle calcium channel alpha 2 subunit cDNA.  
 CC PCR analysis identified splice variants of the human calcium alpha  
 CC 2 subunit transcript. In particularly preferred embodiments, the  
 CC DNA encoding the alpha 2 subunit is produced by alternative  
 CC processing of a primary transcript that includes DNA encoding the  
 CC amino acids set forth in AAR33553 and the DNA of AAQ37823 inserted  
 CC between nucleotides 1624 and 1625 of AAQ37821.

SQ Sequence 1091 AA:

XX WPI: 2001-257902/26.  
 DR N-PSDB; AAF57563.  
 XX Competitive binding assay for screening ligands which bind a cerebral  
 PT cortical voltage-dependent calcium channel alpha2delta-1 subunit,  
 PT where the ligands identified are useful for treating disorders of the  
 PT nervous system, including pain -  
 XX  
 PS Claim 7; Page 139-142; 158pp; English.  
 XX  
 CC The invention relates to a new method for screening ligands which bind a  
 CC cerebral cortical voltage-dependent calcium channel alpha2delta subunit,  
 CC preferably alpha2delta-1 subunit. The method comprises contacting a  
 CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of  
 CC interest and a labelled compound which binds the subunit, followed by  
 CC measuring the level of binding of the labelled compound to alpha2delta-1  
 CC subunit. The method is useful for screening ligands, preferably  
 CC biologically active products that modulate a nervous system function,  
 CC which bind a cerebral cortical voltage-dependent calcium channel  
 CC alpha2delta-1 subunit. The ligands identified by the method are useful  
 CC for treating disorders of the nervous system, including pain, epilepsy  
 CC and anxiety. The present sequence represents a porcine calcium channel  
 CC alpha2delta subunit.  
 CC  
 SQ Sequence 1091 AA;

Query Match 98.8%; Score 5532; DB 22; Length 1091;  
 Best Local Similarity 98.7%; Pred. No. 0;  
 Matches 1049; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLFLFOSLLIGPSSOEPPSAVITKSWDKMEDVLTAKTAGSYNOVLVI 60  
 DB 1 MAAGCLLALTLFLFOSLLIGPSSOEPPSAVITKSWDKMEDVLTAKTAGSYNOVLVI 60  
 QY 61 YEKYODLYTVEPNNAKQLEIARDIEKLNSRKALRYLAEKYOAAHOMREDFASN 120  
 DB 61 YEKYODLYTVEPNNAKQLEIARDIEKLNSRKALRYLAEKYOAAHOMREDFASN 120  
 QY 121 EYVYVNAKDLDPEKNDESPGSRKPYFIDANFGROISTOHAHVPIDIEGSTITVL 180  
 DB 121 EYVYVNAKDLDPEKNDESPGSRKPYFIDANFGROISTOHAHVPIDIEGSTITVL 180  
 QY 121 EYVYVNAKDLDPEKNDESPGSRKPYFIDANFGROISTOHAHVPIDIEGSTITVL 180  
 DB 121 EYVYVNAKDLDPEKNDESPGSRKPYFIDANFGROISTOHAHVPIDIEGSTITVL 180  
 QY 181 NELNMTSALDEYFKKNEDEPSLLMOYFSGATGLARYPPSPWDSNRTNKTIDLYVRR 240  
 DB 181 NELNMTSALDEYFKKNEDEPSLLMOYFSGATGLARYPPSPWDSNRTNKTIDLYVRR 240  
 QY 241 RPWTYOGAASPRKDMILVDVSGVSGTLKILRTSVSEMLETSLDDDFVNVASFNSAOD 300  
 DB 241 RPWTYOGAASPRKDMILVDVSGVSGTLKILRTSVSEMLETSLDDDFVNVASFNSAOD 300  
 QY 301 VSCFOHLVQAVNRKKVYLKADAVNNITAKGITDYKKGFSFAFEOLNANNRANCKNTIMC 360  
 DB 301 VSCFOHLVQAVNRKKVYLKADAVNNITAKGITDYKKGFSFAFEOLNANNRANCKNTIMC 360  
 QY 301 VSCFOHLVQAVNRKKVYLKADAVNNITAKGITDYKKGFSFAFEOLNANNRANCKNTIMC 360  
 DB 301 VSCFOHLVQAVNRKKVYLKADAVNNITAKGITDYKKGFSFAFEOLNANNRANCKNTIMC 360  
 QY 361 FTDGGEERAQEIFAKYKNDKRVFTFVSQOHNYDRPIQMACENKGGYETEPISGAILR 420  
 DB 361 FTDGGEERAQEIFAKYKNDKRVFTFVSQOHNYDRPIQMACENKGGYETEPISGAILR 420  
 QY 421 INFOYLDVGRPVYLAGDAKAOYQNTNYLDLLEGLVITGTLPEVFNITGONENKTNLK 480  
 DB 421 INFOYLDVGRPVYLAGDAKAOYQNTNYLDLLEGLVITGTLPEVFNITGONENKTNLK 480  
 QY 481 NQTLIGVGVDSLEDIKRLTPRTTLCPNGYPAIDPNCVILHPLMQKNKRSQEPVYL 540  
 DB 481 NQTLIGVGVDSLEDIKRLTPRTTLCPNGYPAIDPNCVILHPLMQKNKRSQEPVYL 540  
 QY 541 DFLDAELNDIKVEIRKMKIDSGEGKTEFTLVKSODERYIDKGNFTYWTVPVNGTDSL 600  
 DB 541 DFLDAELNDIKVEIRKMKIDSGEGKTEFTLVKSODERYIDKGNFTYWTVPVNGTDSL 600  
 QY 601 ALVLPYTSFYIKAKIETITQARSKKGGKKOSETLAKPNFEESGYTTPAPDYCNDIKI 660  
 DB 601 ALVLPYTSFYIKAKIETITQARSKKGGKKOSETLAKPNFEESGYTTPAPDYCNDIKI 660

DB 601 ALVLPYTSFYIKAKIETITQARSKKGGKKOSETLAKPNFEESGYTTPAPDYCNDIKI 660  
 QY 661 SDNNTFEFLNFEPIIDKTPNNPSCNTDLINRYLDAGFTNELYONYSKOKINIGYKAR 720  
 DB 661 SDNNTFEFLNFEPIIDKTPNNPSCNTDLINRYLDAGFTNELYONYSKOKINIGYKAR 720  
 QY 721 FVYTDGGITRVYKKEGEMWQENPEYEDSFYKRSIDNDNYFTAPYRNKSGPAYESGI 780  
 DB 721 FVYTDGGITRVYKKEGEMWQENPEYEDSFYKRSIDNDNYFTAPYRNKSGPAYESGI 780  
 QY 781 MYSKAVEIYIOGKLPAVAVGIKIDVNSWIEFPTKSTRIDPCAGVYCDCKNSDMCVI 840  
 DB 781 MYSKAVEIYIOGKLPAVAVGIKIDVNSWIEFPTKSTRIDPCAGVYCDCKNSDMCVI 840  
 QY 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNSVYAFNKSVDYQSCBGAAPKQ 900  
 DB 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNSVYAFNKSVDYQSCBGAAPKQ 900  
 QY 901 GAGHRSAVYPSIADILHIGMWTAAAMSTIQFLSLTFPRLLEAVEMEDDFTASLSKQ 960  
 DB 901 GAGHRSAVYPSIADILHIGMWTAAAMSTIQFLSLTFPRLLEAVEMEDDFTASLSKQ 960  
 QY 961 SCITTEQTYEFFNDKSKSPSGVLDGCGNSRIFHVEKLMNTNLIPTMYESKGTCPDTRLLI 1020  
 DB 961 SCITTEQTYEFFNDKSKSPSGVLDGCGNSRIFHVEKLMNTNLIPTMYESKGTCPDTRLLI 1020  
 QY 1021 QAEQTSDEGPDPCDMYKQRRYKRGPDVCPDNALBEDYTDGCGVS 1063  
 DB 1021 QAEQTSDEGPDPCDMYKQRRYKRGPDVCPDNALBEDYTDGCGVS 1063

RESULT 14  
 AAM37879  
 ID AAM37879 standard; Protein: 1091 AA.

AC AAM37879;  
 XX  
 DT 28-AUG-1998 (first entry)

DE Human calcium channel  $\alpha 2 \delta$  subunit.

KM Calcium channel; human; central nervous system disorder;  
 KM Lambert-Eaton syndrome; diagnosis; therapy.

OS Homo sapiens.

PN MO981131-A2.

PD 19-MAR-1998.

PE 11-SEP-1997; 97WO-US16146.

PR 16-SEP-1996; 96US-0713118.

PA (AMHP) AMERICAN HOME PROD CORP.

P1 Chen ARS, Franco R, Shuey DJ;

DR WPI: 1998-207325/18.  
 DR N-PSDB; AAV29060.

PT DNA encoding human neuronal calcium channel subunit(s) - useful for  
 PT diagnosis of and treatment of central nervous system disorders, e.g.  
 PT Lambert-Eaton syndrome  
 PS Disclosure; Fig 2; 89pp; English.  
 XX This polypeptide comprises the  $\alpha 2 \delta$  subunit of the human neuronal  
 CC calcium channel. cDNA clones (see AAV29059-61) encoding the  $\alpha 1 \beta$   
 CC subunit (see AAM37879), the  $\alpha 2 \delta$  subunit and a  $\beta 3$  subunit (see AAM37880)  
 CC have been isolated. These have been inserted into expression  
 CC vectors and are stably expressed in transformed cell lines. The  
 CC transformed cells show omega-conotoxin GVIA binding activity.

PN W0200119870-A2.  
 XX  
 PD 22-MAR-2001.  
 XX  
 PF 18-SEP-2000; 2000WO-EP09137.  
 XX  
 PR 16-SEP-1999; 9905-0397550.  
 XX  
 PA (WARN) WARNER LAMBERT CO.  
 XX  
 PI Brown JP, Bertelli F;  
 DR WPI: 2001-235262/24.  
 XX N-PSDB; AAS01426.  
 XX  
 PT Calcium channel alpha2delta subunits, useful in e.g. SPA assays,  
 PT Flashplate assays, Nickel Flashplate assays, Filter binding assays or  
 PT Wheat Germ Lectin Flashplate assays -  
 XX  
 PS Claim 30; Page 141-144; 160pp; English.  
 CC  
 CC The present sequence represents human secreted calcium channel  
 CC alpha2delta subunit #15 which is soluble and retains the functional  
 CC characteristics of the full length or wild type alpha2delta subunit  
 CC (AAU01025) from which it is derived. The invention relates to truncated  
 CC alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins  
 CC which retain their affinity for radioactively labelled gabapentin. The  
 CC alpha2delta subunit is 1 of the components of the heteromultimeric  
 CC voltage-dependent calcium channel (VDCC) complexes present in neuronal  
 CC and non-neuronal tissues including heart and skeletal muscle. Numerous  
 CC soluble forms of the human calcium channel alpha2delta subunits  
 CC (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the  
 CC porcine calcium channel alpha2delta subunits (AAU01027-AAU01031) are  
 CC described. The secreted soluble alpha2delta subunit may be used in assays.  
 CC e.g. scintillation proximity assay (SPA), flashplate, nickel flashplate,  
 CC filter binding or wheat germ lectin flashplate assays to detect or  
 CC measure the binding or interaction of a ligand (e.g. gabapentin,  
 CC L-Norleucine, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Isoleucine,  
 CC L-Valine, Spermine and/or L-phenylalanine) of a calcium channel  
 CC alpha2delta subunit.  
 CC  
 SO Sequence 1091 AA:  
 Query Match 98.8%; Score 5532; DB 22; Length 1091;  
 Best Local Similarity 98.7%; Pred. No. 0;  
 Matches 1049; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Db 361 FTDGGEERAQELFNKYNKKRVFRFSVGHNTERGEIOMACENKGYEIPISGAIR 420  
 QY 421 INFOEYLDVLRPNVLADGKAKOVOMTNYVLDALDELGLVITGTLTPVENITGONENKTNLK 480  
 Db 421 INFOEYLDVLRPNVLADGKAKOVOMTNYVLDALDELGLVITGTLTPVENITGONENKTNLK 480  
 QY 481 NOLILGVGVDSLEDIRLPPRTLCPNGYFFAIDPNGVYLLHPNLQPKNPKSQEPVTL 540  
 Db 481 NOLILGVGVDSLEDIRLPPRTLCPNGYFFAIDPNGVYLLHPNLQPKNPKSQEPVTL 540  
 QY 541 DFLDALENDIKVEIRKMKIDGSESEKTEPRLLYKSQDRLYIDKGRRTYTPVNGTYSL 600  
 Db 541 DFLDALENDIKVEIRKMKIDGSESEKTEPRLLYKSQDRLYIDKGRRTYTPVNGTYSL 600  
 QY 601 ALVLPYSPFYTKAKIEETITQARSKKMKDSEFLKPDNEESGYTFIAPRDYCNLDKI 660  
 Db 601 ALVLPYSPFYTKAKIEETITQARSKKMKDSEFLKPDNEESGYTFIAPRDYCNLDKI 660  
 QY 661 SDNTEEFLLNFEFIDRKTNNPSCNTDLINRVLLDAGFTNELVONWYSKOKNIKGVAR 720  
 Db 661 SDNTEEFLLNFEFIDRKTNNPSCNTDLINRVLLDAGFTNELVONWYSKOKNIKGVAR 720  
 QY 721 FVYTOGCTIRVYPRKAGENWMOENPEYEDSEFKRSLLDNDYVETAPYFNKSGPAYESGI 780  
 Db 721 FVYTOGCTIRVYPRKAGENWMOENPEYEDSEFKRSLLDNDYVETAPYFNKSGPAYESGI 780  
 QY 781 MYSKAVEIYIOGKLKPAVVGKIDVNSWIENFTKTSIRDPGAGVCDCKRNSDVMCVI 840  
 Db 781 MYSKAVEIYIOGKLKPAVVGKIDVNSWIENFTKTSIRDPGAGVCDCKRNSDVMCVI 840  
 QY 841 LDDGGLMANHDDYTNQIGREFGEIDPSLMRLNYSYAFNKSYDYQSVCEPAAAKQ 900  
 Db 841 LDDGGLMANHDDYTNQIGREFGEIDPSLMRLNYSYAFNKSYDYQSVCEPAAAKQ 900  
 QY 901 GAGHRSAVYPSIADILHIGMWTAAAMSLIOQFLSLFPPRLLEAVEMEDDFTASLSKO 960  
 Db 901 GAGHRSAVYPSIADILHIGMWTAAAMSLIOQFLSLFPPRLLEAVEMEDDFTASLSKO 960  
 QY 961 SCITTEOTGYFFDNDKSFSGVLDCCGNSRIFFHEKIMLNTNLFIWVESKGTGCTPTRLII 1020  
 Db 961 SCITTEOTGYFFDNDKSFSGVLDCCGNSRIFFHEKIMLNTNLFIWVESKGTGCTPTRLII 1020  
 QY 1021 QAEOTSDGPPCDMVKOPRYRKGPDYCFDNNALIEDYTDGCGVS 1063  
 Db 1021 QAEOTSDGPPCDMVKOPRYRKGPDYCFDNNALIEDYTDGCGVS 1063

RESULT 13  
 AAB62259  
 ID AAB62259 standard; protein; 1091 AA.  
 XX  
 AC AAB62259;  
 XX  
 DT 11-JUN-2001 (first entry)  
 XX  
 DE Porcine calcium channel alpha2delta subunit.  
 KW Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;  
 KW nervous system disorder; pain; epilepsy; anxiety; pig.  
 OS Sus scrofa.  
 XX  
 PN W0200120336-A2.  
 XX  
 PD 22-MAR-2001.  
 XX  
 PF 18-SEP-2000; 2000WO-EP09136.  
 XX  
 PR 16-SEP-1999; 9905-0397549.  
 XX  
 PA (WARN) WARNER LAMBERT CO.  
 XX  
 PI Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;

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XX  US6096514-A.
PN
XX
PD  01-AUG-2000.
XX
PE  25-MAY-1995; 9505-0450562.
XX
PR  04-APR-1988; 88US-0176689.
PR  02-FEB-1990; 90US-0482384.
PR  08-NOV-1990; 90US-0603751.
PR  30-NOV-1990; 90US-0620250.
PR  15-AUG-1991; 91US-0745206.
PR  10-APR-1992; 92US-0868354.
PR  13-JUL-1992; 92US-0914231.
PR  11-AUG-1993; 93US-0105536.
PR  05-NOV-1993; 93US-0149097.
PR  07-FEB-1994; 94US-0193078.
PR  04-APR-1994; 94US-0223305.
PR  11-AUG-1994; 94US-0290012.
PR  23-SEP-1994; 94US-0311363.
PR  28-SEP-1994; 94US-0314083.
PR  07-NOV-1994; 94US-0336257.
PR  13-MAR-1995; 95US-0404950.
XX
PA  (SIBI-) SIBIA NEUROSCIENCES INC.
XX
PI  Ellis SB, Williams ME, McCue AF, Harpold MM.
XX
DR  MPI: 2000-548330/50.
XX  N-PSDB: AAA71707.
XX
PT  Human calcium channel beta subunit polynucleotides, useful for
PT  producing recombinant eukaryotic cells and for diagnosing Lambert Eaton
PT  Syndrome -
XX
PS  Example IV; Column 135-144; 153pp; English.
XX
CC  This invention describes a novel isolated DNA molecule (I) comprising a
CC  sequence encoding a beta3-1 subunit of a human calcium channel.
CC  Nucleic acid probes comprising 14-30 contiguous nucleotides of
CC  beta3 subunit encoding DNA are useful for isolation and cloning of
CC  calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that
CC  express heterologous calcium channel are useful for identifying
CC  agonists and antagonists of calcium channel activity in humans. Human
CC  calcium channel subunit or eukaryotic cells expressing the channel are
CC  useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This
CC  sequence represents the human calcium channel alpha-2 subunit which is
CC  described in the method of the invention.
XX
SQ  Sequence 1091 AA;
Query Match 98.8%; Score 5532; DB 21; Length 1091;
Best Local Similarity 98.7%; Freq. No. 0;
Matches 1049; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
QY  1 MAAGCLATLTLFOSLIGPSQEPSPSAVTIKSWVKMOEDVTLAKTASGVNOLVDI 60
DB  1 MAAGCLATLTLFOSLIGPSSEPFPSATIKSWDKMEDVTLAKTASGVNOLVDI 60
QY  61 YEKYODLTYVEPNNAKQLVEIAARDIEKLSNRKALVRLALEAKVQAAHQWREDFASN 120
DB  61 YEKYODLTYVEPNNAKQLVEIAARDIEKLSNRKALVRLALEAKVQAAHQWREDFASN 120
QY  121 EYVYINAKDDLDPEKNSEPSQRIKPYFIDANFGRKISQHAHVIPTDIYEGSTIVL 180
DB  121 EYVYINAKDDLDPEKNSEPSQRIKPYFIDANFGRKISQHAHVIPTDIYEGSTIVL 180
QY  181 NEIMNTSALDEVEFKKREDEPSILMOYVGSATGLARYVPASPWVNSRTPKIDLYVRR 240
DB  181 NEIMNTSALDEVEFKKREDEPSILMOYVGSATGLARYVPASPWVNSRTPKIDLYVRR 240
QY  241 RPWTIOGAASPKDMLLDVSGSVSGLTLKLIRTSVSEMLETLSDDDFVNVAFSNSAOD 300

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DB  241 RPWTIOGAASPKDMLLDVSGSVSGLTLKLIRTSVSEMLETLSDDDFVNVAFSNSAOD 300
QY  301 VSCFOHLYOANVRNKKVYLKDAVNNITKAGITDYKKGFSEFAFOLLNVAHRANCKITML 360
DB  301 VSCFOHLYOANVRNKKVYLKDAVNNITKAGITDYKKGFSEFAFOLLNVAHRANCKITML 360
QY  361 FPDGGEERAQELFEPAKYNNKDKKRVFTSPVSGHNDRGPLOMAGENKGYEIPISGAIR 420
DB  361 FPDGGEERAQELFEPAKYNNKDKKRVFTSPVSGHNDRGPLOMAGENKGYEIPISGAIR 420
QY  421 INTQYELVYLGPRPVLAADKAKOVQWIVNYIDALELGIVITGTLVPVNTITQNEKNTLK 480
DB  421 INTQYELVYLGPRPVLAADKAKOVQWIVNYIDALELGIVITGTLVPVNTITQNEKNTLK 480
QY  481 NQILGVAGVDSLEDIKRLTPRETLCPNGYFFAIDPAGYVLLHPNLOPKPKSOEPTVL 540
DB  481 NQILGVAGVDSLEDIKRLTPRETLCPNGYFFAIDPAGYVLLHPNLOPKPKSOEPTVL 540
QY  541 DFLDAELNDIKVEIRNKMIDEGSEKTRFLVKSQDERYIDKGNKRYTWTVPNGTDSL 600
DB  541 DFLDAELNDIKVEIRNKMIDEGSEKTRFLVKSQDERYIDKGNKRYTWTVPNGTDSL 600
QY  601 ALVLPYSFYIYKAKIETITQARSKKGMKDSSTLKPDPNEEGTFFIAPROYCNDLKI 660
DB  601 ALVLPYSFYIYKAKIETITQARSKKGMKDSSTLKPDPNEEGTFFIAPROYCNDLKI 660
QY  661 SDNNTFELNFEFIDRKTPNNPSCNTDLINRVLLDAGTFTELQYONTWSKOKNKGKAR 720
DB  661 SDNNTFELNFEFIDRKTPNNPSCNTDLINRVLLDAGTFTELQYONTWSKOKNKGKAR 720
QY  721 FVYVDGCTIRYPRVAGEENMOENPEYEDSFYKRSKLDNDNVFTAPYPMKSGPAYESGI 780
DB  721 FVYVDGCTIRYPRVAGEENMOENPEYEDSFYKRSKLDNDNVFTAPYPMKSGPAYESGI 780
QY  781 MYSRAVEYIYOGKILKPAVVGKIDVNSMTENFTKTSIRPQAGPVDCRNSVMDCVI 840
DB  781 MYSRAVEYIYOGKILKPAVVGKIDVNSMTENFTKTSIRPQAGPVDCRNSVMDCVI 840
QY  841 LDDGFFLMAHNDYTNQIGFEGEIDPSLMRHLVINSYAFNKSXYDSVCEBGAAPK 900
DB  841 LDDGFFLMAHNDYTNQIGFEGEIDPSLMRHLVINSYAFNKSXYDSVCEBGAAPK 900
QY  901 GAGHRSAYVSADIILITIGMWTAAANSIIQOFLSLTFPRLLFAVEMEDDFTASLSK 960
DB  901 GAGHRSAYVSADIILITIGMWTAAANSIIQOFLSLTFPRLLFAVEMEDDFTASLSK 960
QY  961 SCITEQYVFPDNDKSFSGVLDGNCSTRIFHEKLMNTLIFIMWESKGTCCDTRLLI 1020
DB  961 SCITEQYVFPDNDKSFSGVLDGNCSTRIFHEKLMNTLIFIMWESKGTCCDTRLLI 1020
QY  1021 QAEQTSDDGPPCDMVKQPRYRKGPVCFDNNALDEYTDGCGVS 1063
DB  1021 QAEQTSDDGPPCDMVKQPRYRKGPVCFDNNALDEYTDGCGVS 1063
RESULT 12
AAU01035 standard; Protein; 1091 AA.
AAU01035;
04-JUL-2001 (first entry)
Human secreted soluble alpha2delta calcium channel subunit #15 protein.
Human: secreted calcium channel alpha2delta subunit; alpha2delta-2;
alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VCC;
gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;
filter binding assay; wheat germ lectin flashplate assay.
Homo sapiens.

```

AC AAM63145;  
 XX 12-OCT-1998 (first entry)  
 XX Human calcium channel alpha-2 subunit.  
 DE  
 XX Alpha-2 subunit; human; calcium channel; assay; detection;  
 KM characterisation; Lambert Eaton Syndrome; LES; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX US5792846-A.  
 XX 11-AUG-1998.  
 PD 31-MAY-1995; 95US-0455543.  
 XX  
 PF 04-APR-1994; 94US-0223305.  
 PR 04-APR-1988; 88US-0176899.  
 PR 04-APR-1983; 89US-0603751.  
 PR 20-FEB-1990; 89WO-0501408.  
 PR 30-NOV-1990; 90US-0482384.  
 PR 15-AUG-1991; 91US-0745206.  
 PR 31-MAY-1995; 95US-0455543.  
 XX  
 PA (SIBI-) SIBIA NEUROSCIENCES INC.  
 PI Brenner R, Ellis SB, Feldman DH, Harpold MM, McQue AF;  
 PI Williams ME;  
 XX WPT: 1998-456192/39.  
 DR N-PSDB: AAA42689.  
 XX  
 PT DNA encoding human calcium channel alpha 1b subunit protein -  
 PT useful for recombinant production of the channel for screening of  
 PT its modulators, and diagnosis of Lambert Eaton Syndrome  
 XX  
 PS Claim 4; Columns 283-288; 166pp; English.  
 XX  
 CC The present sequence represents the alpha-2 subunit of a human calcium  
 CC channel. Calcium channels are membrane-spanning, multi-subunit proteins  
 CC that allow controlled entry of calcium ions into cells. This leads  
 CC to depolarisation events required for muscle contraction. The recombinant  
 CC subunit, when expressed with nucleic acids encoding the complete calcium  
 CC channel, can be used in assays for the detection and characterisation of  
 CC compounds that modulate the channel. The DNA encoding the subunits can  
 CC be alternatively spliced when transcribed, giving more than one form of  
 CC the protein from the same transcript, each having slightly different  
 CC properties. In addition, the reactivity of the alpha 1 subunit with IgG  
 CC molecules from the serum of an individual with Lambert Eaton Syndrome  
 CC (LES) can be used as a diagnostic for the disease.  
 CC  
 CC Sequence 1091 AA;  
 SQ  
 Query Match 98.8%; Score 5532; DB 19; Length 1091;  
 Best Local Similarity 98.7%; Pred. No. 0;  
 Matches 1049; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Db 181 NELMNTSALDEVFKKNEDEPSLLMOVGSATGLARYYPASPMVDNSRPNKIDLYDVR 240  
 Qy 241 RPWYIOGAASPKDMLILVDVSGSVSGTLKILRTVSSEMETLSDDDFVAVASFNNAOD 300  
 Db 241 RPWYIOGAASPKDMLILVDVSGSVSGTLKILRTVSSEMETLSDDDFVAVASFNNAOD 300  
 Qy 301 VSCFOHLVQAVNRNKKVYLKADAVNNITAKGJTDYKKGFSFAFEOLLNYSRANCKIIML 360  
 Db 301 VSCFOHLVQAVNRNKKVYLKADAVNNITAKGJTDYKKGFSFAFEOLLNYSRANCKIIML 360  
 Qy 361 FTDCGEERAOEIFAKYKDKKVRVFTSVGOHNDRPQIOMMACEKNGYYEELPSIGAIR 420  
 Db 361 FTDCGEERAOEIFAKYKDKKVRVFTSVGOHNDRPQIOMMACEKNGYYEELPSIGAIR 420  
 Qy 421 INFOEYLDVIGRPVNLGDKAKQVQMTNVYLDALDELGLVTGTLPVNNITGONENKTNLK 480  
 Db 421 INFOEYLDVIGRPVNLGDKAKQVQMTNVYLDALDELGLVTGTLPVNNITGONENKTNLK 480  
 Qy 481 NQILGVKGVDSVLEDIKRLTPRTLCPNGYEALIDPNGVYLLHPNLQPRNKSQEPVTL 540  
 Db 481 NQILGVKGVDSVLEDIKRLTPRTLCPNGYEALIDPNGVYLLHPNLQPRNKSQEPVTL 540  
 Qy 541 DELDAELENQIKVRLRNKMDIGESGEKTFRTLVKSQDERYIDGKNRTYTTPVNGTDSL 600  
 Db 541 DELDAELENQIKVRLRNKMDIGESGEKTFRTLVKSQDERYIDGKNRTYTTPVNGTDSL 600  
 Qy 601 ALVLPYTSFYIKAKIETITQARSKKGMKDSFTLKPDPNEESGYFTIAPROYCNDLKI 660  
 Db 601 ALVLPYTSFYIKAKIETITQARSKKGMKDSFTLKPDPNEESGYFTIAPROYCNDLKI 660  
 Qy 661 SDNTEFLNPNNEFIDKTPNPNPCNTDLINRVLLDAGFTNELVQYNSKOKNIKGVKAR 720  
 Db 661 SDNTEFLNPNNEFIDKTPNPNPCNTDLINRVLLDAGFTNELVQYNSKOKNIKGVKAR 720  
 Qy 721 FVVVDGGITRYPKEAGENMOENPEYEDSPYKSLNDNDVYFTAPFNKSGGAEESGI 780  
 Db 721 FVVVDGGITRYPKEAGENMOENPEYEDSPYKSLNDNDVYFTAPFNKSGGAEESGI 780  
 Qy 781 MYSKAVEIYIOGKLLKPAVVGIRIDVNSWIENFTKTSIRPDCAGPYCDCKRNSDVMCVI 840  
 Db 781 MYSKAVEIYIOGKLLKPAVVGIRIDVNSWIENFTKTSIRPDCAGPYCDCKRNSDVMCVI 840  
 Qy 841 LDDGFFLMAHNDYTNQIGRFESEIDPSLMRHLVNIYSVAFNKSTYDGVCEGAPKQ 900  
 Db 841 LDDGFFLMAHNDYTNQIGRFESEIDPSLMRHLVNIYSVAFNKSTYDGVCEGAPKQ 900  
 Qy 901 GAGRSATVPISADILHIGWMTAAWSIIQOFLSLTFRLLAEVEMEDDFTASLSKQ 960  
 Db 901 GAGRSATVPISADILHIGWMTAAWSIIQOFLSLTFRLLAEVEMEDDFTASLSKQ 960  
 Qy 961 SCITEQOYFFPDNDKSFSGVLDGNCRSRIFFHVKLMNTNLIIFIMBSKGTCPDTRLI 1020  
 Db 961 SCITEQOYFFPDNDKSFSGVLDGNCRSRIFFHVKLMNTNLIIFIMBSKGTCPDTRLI 1020  
 Qy 1021 QAEOTSDGPDPCDMVKQPRRKSGPVCFNNALEDYIDCGSV 1063  
 Db 1021 QAEOTSDGPDPCDMVKQPRRKSGPVCFNNALEDYIDCGSV 1063  
 RESULT 11  
 AAB10576  
 ID AAB10576 standard; Protein: 1091 AA.  
 XX AAB10576;  
 AC  
 XX  
 DT 22-DEC-2000 (first entry)  
 DE Human calcium channel alpha-2 subunit protein.  
 XX  
 DE Human; calcium channel; calcium channel subunit; diagnosis;  
 KM Lambert Eaton Syndrome; calcium channel subunit alpha-2.  
 XX  
 OS Homo sapiens.

Db 961 SCITEQYFFNDKSKFSVLDGNCSTRLEPHEKLMNTVLIFLWESKGTCCDTRLII 1020  
 QY 1021 QAEQTSDDPDCDMVKQPRYRKGPVCFDNNALJEDYDCCGVS 1063  
 1021 QAEQTSDDPDCDMVKQPRYRKGPVCFDNNALJEDYDCCGVS 1063

## RESULT 9

AA71011  
 ID AAR71011 standard; Protein: 1091 AA.

XX  
 AC AAR71011;

DT 01-DEC-1995 (first entry)

XX Human neuronal calcium channel subunit alpha 2b.

KW Calcium channel subunit; antagonist; agonist; diagnosis;  
 Lambert Eaton Syndrome.

OS Homo sapiens.

XX W09504822-A.

PN 16-FEB-1995.

XX 11-AUG-1994; 94MO-0509230.

XX 11-AUG-1993; 93US-0105536.

PR 05-NOV-1993; 93US-0149097.

XX (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.

PI Ellis SB, Gillespie A, Harpold KM, McCue AF, Williams ME;

DR WPI; 1995-090900/12.

XX N-PSDB; AA084664.

PT DNA encoding human calcium channel sub-unit(s) - used for

XX developing prods. for studying calcium channels, e.g. for

PS obtaining agonists and antagonists

XX Disclosure; Page 166-171; 285pp; English.

XX Human neuronal alpha 2 coding sequence (AA084664) transcript is

CC differentially processed in skeletal muscle, aorta, and CNS in

CC the region corresp. to nt 1595-1942 of AA084664 in each of the

CC tissues. Five alternatively spliced variant transcripts that differ

CC in the presence or absence of one to three different portions of

CC this region. There are three sequences involved (see AA084664 FT

CC and AA084665 FT), sequence 1, sequence 2 and sequence 3. The five

CC alpha 2 encoding transcripts from the different tissues include

CC different combinations of the three sequences, except for one of

CC the alpha 2 transcripts expressed in aorta which lacks all three

CC sequences. The five alpha 2 forms identified are (1) a form that

CC lacks sequence 3 called alpha 2a, expressed in skeletal muscle

CC (2) one that lacks sequence 1 called alpha 2b, expressed in CNS

CC (3) one that lacks sequences 1 and 2 called alpha 2c, expressed in

CC aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,

CC expressed in aorta and (5) one that lacks sequences 1 and 3

CC called alpha 2e.

XX Sequence 1091 AA;

XX

Query Match 98.8%; Score 5532; DB 16; Length 1091;

Best Local Similarity 98.7%; Pred. No. 0;

Matches 1049; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 MAAGCLATLTTLTFLFOSLLIGSSOEPPSPASVTIKSWDKQEDLVTLAKTASGVNOLVDI 60

Db 1 MAAGCLATLTTLTFLFOSLLIGSSOEPPSPASVTIKSWDKQEDLVTLAKTASGVNOLVDI 60

XX

RESULT 10

AA63145

ID AAM63145 standard; Protein: 1091 AA.

XX

QY 61 YEKYODLYVEBNNAKQVLEIARDEIKLSNRKALVRLALEAKVOAAHQWREDFASN 120

Db 61 YEKYODLYVEBNNAKQVLEIARDEIKLSNRKALVRLALEAKVOAAHQWREDFASN 120

QY 121 EYVYNAKDDLDPEKNDSPGSGRIKPVFIDANGRGQISYQAAVHPTDIYESTIVL 180

Db 121 EYVYNAKDDLDPEKNDSPGSGRIKPVFIDANGRGQISYQAAVHPTDIYESTIVL 180

QY 121 EYVYNAKDDLDPEKNDSPGSGRIKPVFIDANGRGQISYQAAVHPTDIYESTIVL 180

Db 121 EYVYNAKDDLDPEKNDSPGSGRIKPVFIDANGRGQISYQAAVHPTDIYESTIVL 180

QY 181 NELNMTSALDEVEKKNREEDPSILMQVFGSATGLARYYPASPMVNSRTPNKIDLYDVR 240

Db 181 NELNMTSALDEVEKKNREEDPSILMQVFGSATGLARYYPASPMVNSRTPNKIDLYDVR 240

QY 241 RPWYIQAASPKDMLILDVSGSVSGLTCLKIRISVSEMLETLSDDDFVNAVSFNSNAQD 300

Db 241 RPWYIQAASPKDMLILDVSGSVSGLTCLKIRISVSEMLETLSDDDFVNAVSFNSNAQD 300

QY 241 RPWYIQAASPKDMLILDVSGSVSGLTCLKIRISVSEMLETLSDDDFVNAVSFNSNAQD 300

Db 241 RPWYIQAASPKDMLILDVSGSVSGLTCLKIRISVSEMLETLSDDDFVNAVSFNSNAQD 300

QY 301 VSCFOHLVQANRNKVKLDAVNNITAGINDYKKGFSFAEQLLNINVSANCKIIML 360

Db 301 VSCFOHLVQANRNKVKLDAVNNITAGINDYKKGFSFAEQLLNINVSANCKIIML 360

QY 361 FTDGGERAOEITFAKYNKDKKVRVFTFSVGOHNDRCPTIOMMACENKGYEIPISGAIR 420

Db 361 FTDGGERAOEITFAKYNKDKKVRVFTFSVGOHNDRCPTIOMMACENKGYEIPISGAIR 420

QY 421 INTQYLDVLAGRPVLAGDKAKQVQWTVNYLDALGLVITGTLPEVNIQONENKTMLK 480

Db 421 INTQYLDVLAGRPVLAGDKAKQVQWTVNYLDALGLVITGTLPEVNIQONENKTMLK 480

QY 481 NOLLIQVGVGVDSLEDIRKLPRLCPNGYFALDPNGYVLLHPNLOPKPKSQEPYTL 540

Db 481 NOLLIQVGVGVDSLEDIRKLPRLCPNGYFALDPNGYVLLHPNLOPKPKSQEPYTL 540

QY 541 DELDALENDIKVEIRNKKMIDEGSEKTEFRLVKSQDERYIDKGRITWTVPVNGTDSL 600

Db 541 DELDALENDIKVEIRNKKMIDEGSEKTEFRLVKSQDERYIDKGRITWTVPVNGTDSL 600

QY 601 ALVLPYSPYTYTKAKIEETIQAASKKGMKDEFLKPDNFEESGYTIAIDRYCNDIKI 660

Db 601 ALVLPYSPYTYTKAKIEETIQAASKKGMKDEFLKPDNFEESGYTIAIDRYCNDIKI 660

QY 661 SUNNTEFLNTEFIDRKTPNNPSCNADLINVVLDAQFTNLYONYSKOKNIKGVAR 720

Db 661 SUNNTEFLNTEFIDRKTPNNPSCNADLINVVLDAQFTNLYONYSKOKNIKGVAR 720

QY 721 FVYTDGGITRYVPKEAGENWQENPETYEDSFYKSLDNDNYFTAPYNNKSGPAYESGI 780

Db 721 FVYTDGGITRYVPKEAGENWQENPETYEDSFYKSLDNDNYFTAPYNNKSGPAYESGI 780

QY 781 MYSKAVEIYIOGKLLKPAVAVGIKIDVNSWIENFTKTSIRDPACGVCDCCKRNSDVMCVI 840

Db 781 MYSKAVEIYIOGKLLKPAVAVGIKIDVNSWIENFTKTSIRDPACGVCDCCKRNSDVMCVI 840

QY 841 LDDGGFLMANHDDTNOIGRFGFIDPSIMHVLNIVYAFNKSVDYDQSCGEPGAAPKQ 900

Db 841 LDDGGFLMANHDDTNOIGRFGFIDPSIMHVLNIVYAFNKSVDYDQSCGEPGAAPKQ 900

QY 901 GAGHSAYVPSIADILIGWATAAAMSILQFLSTLTPRLLAEVEMEDDFTASLSKQ 960

Db 901 GAGHSAYVPSIADILIGWATAAAMSILQFLSTLTPRLLAEVEMEDDFTASLSKQ 960

QY 961 SCITEQYFFNDKSKFSVLDGNCSTRLEPHEKLMNTVLIFLWESKGTCCDTRLII 1020

Db 961 SCITEQYFFNDKSKFSVLDGNCSTRLEPHEKLMNTVLIFLWESKGTCCDTRLII 1020

QY 1021 QAEQTSDDPDCDMVKQPRYRKGPVCFDNNALJEDYDCCGVS 1063

Db 1021 QAEQTSDDPDCDMVKQPRYRKGPVCFDNNALJEDYDCCGVS 1063

XX

DB 721 FVYTDGITRYVPEKAGENNQENPEYEDSFYRSIDNDNYVTATPYFNKSGCAIESGI 780  
 QY 781 MYSKAVEITYIOGKILKPAVVGKIDVNSWJENFTKTSIRDPACGAVCDCKRNSDVMDCVI 840  
 DB 781 MYSKAVEITYIOGKILKPAVVGKIDVNSWJENFTKTSIRDPACGAVCDCKRNSDVMDCVI 840  
 QY 841 LDDGGFLMANHDDYTNQIGRFGEIDPSLMRLVNSVYAFNKSVDYOSVCEPGAAPQ 900  
 DB 841 LDDGGFLMANHDDYTNQIGRFGEIDPSLMRLVNSVYAFNKSVDYOSVCEPGAAPQ 900  
 QY 901 GAGHRSAYVPSIADLIHIGWATAAAMSILOQFLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
 DB 901 GAGHRSAYVPSIADLIHIGWATAAAMSILOQFLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
 QY 961 SCITEGTQYFFDNDKSFSGVLDGNCSTRIFHEVEKLMNTNLIPIVWESKGTGCTDRLLI 1020  
 DB 961 SCITEGTQYFFDNDKSFSGVLDGNCSTRIFHEVEKLMNTNLIPIVWESKGTGCTDRLLI 1020  
 QY 1021 QABOTSDGPPDCMVKOPRRYRKGPDYCFDNNALDGYTDCGGVS 1063  
 DB 1021 QABOTSDGPPDCMVKOPRRYRKGPDYCFDNNALDGYTDCGGVS 1063

## RESULT 8

AAB62258 standard; Protein; 1063 AA.

AAB62258;

11-JUN-2001 (first entry)

Porcine calcium channel alpha2delta subunit.

Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex; nervous system disorder; pain; epilepsy; anxiety; pig.

Sus scrofa.

MO200120336-A2.

22-MAR-2001.

18-SEP-2000; 2000MO-EP09136.

16-SEP-1999; 9905-0397549.

(WARN) WARNER LAMBERT CO.

Bertelli F, Brown JP, Dissanayake V, Suman-Chanuan N, Gee NS;

WPI: 2001-257902/26.

N-PSDB: AAF57562.

Competitive binding assay for screening ligands which bind a cerebral cortical voltage-dependent calcium channel alpha2-delta-1 subunit, where the ligands identified are useful for treating disorders of the nervous system, including pain.

Claim 8: Page 135-139; 158pp; English.

The invention relates to a new method for screening ligands which bind a cerebral cortical voltage-dependent calcium channel alpha2delta subunit, preferably alpha2delta-1 subunit. The method comprises contacting a secreted soluble recombinant alpha2delta-1 subunit with a ligand of interest and a labelled compound which binds the subunit, followed by measuring the level of binding of the labelled compound to alpha2delta-1 subunit. The method is useful for screening ligands, preferably biologically active products that modulate a nervous system function, which bind a cerebral cortical voltage-dependent calcium channel alpha2delta-1 subunit. The ligands identified by the method are useful for treating disorders of the nervous system, including pain, epilepsy and anxiety. The present sequence represents a porcine calcium channel

CC alpha2delta subunit.  
 XX Sequence 1063 AA;

Query Match 98.8%; Score 5532; DB 22; Length 1063;  
 Best Local Similarity 98.7%; Pred. No. 0;  
 Matches 1049; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 MAAGCLLATLTTLFQSLILGSPSSQEPFSAVYIKSWDKMEDVTLAKTASGVNQLVDI 60  
 DB 1 MAAGCLLATLTTLFQSLILGSPSSQEPFSAVYIKSWDKMEDVTLAKTASGVNQLVDI 60  
 QY 61 YEKYODLTYVEPNNAKQVEIAARDIEKLSNRKALVRLALBAEKVOAHOQMBDEFSN 120  
 DB 61 YEKYODLTYVEPNNAKQVEIAARDIEKLSNRKALVRLALBAEKVOAHOQMBDEFSN 120  
 QY 121 EYVYVNAKDLDLPEKNDSEPGSQRIRKPFIDANGROISTOHAAPHIPTYIGGSTVYL 180  
 DB 121 EYVYVNAKDLDLPEKNDSEPGSQRIRKPFIDANGROISTOHAAPHIPTYIGGSTVYL 180  
 QY 181 NELNMTSALDEVFKKRNREDEPSLWQVFSATGLARYPASPWYDNRTPKIDLYDVR 240  
 DB 181 NELNMTSALDEVFKKRNREDEPSLWQVFSATGLARYPASPWYDNRTPKIDLYDVR 240  
 QY 241 RPWYIOGAASPKDMLILVDVSGVSGTLKLIPTSVSEMLETSLDDDFVNVASFNSNAQD 300  
 DB 241 RPWYIOGAASPKDMLILVDVSGVSGTLKLIPTSVSEMLETSLDDDFVNVASFNSNAQD 300  
 QY 301 VSCFOHLVOANRKNKVLKDAVNNITAKGIDYKGFSEAFEOILNTVNSRANCKITML 360  
 DB 301 VSCFOHLVOANRKNKVLKDAVNNITAKGIDYKGFSEAFEOILNTVNSRANCKITML 360  
 QY 361 FTDGGEERAQELIFAKYKNDKRVFTFSVGOHNDRGSIQMMACENKGYEIPISGAIK 420  
 DB 361 FTDGGEERAQELIFAKYKNDKRVFTFSVGOHNDRGSIQMMACENKGYEIPISGAIK 420  
 QY 421 INTQFELYLGRPWVLADGKAKQVOMTVNYLDALBLGVITGTLPEVNTIGONENKTNL 480  
 DB 421 INTQFELYLGRPWVLADGKAKQVOMTVNYLDALBLGVITGTLPEVNTIGONENKTNL 480  
 QY 481 NOLILGVAGVDVSLIEDIRLTPRFTLCNGYFPATIDPGVYLLHPNLOPKRPSQEPVTL 540  
 DB 481 NOLILGVAGVDVSLIEDIRLTPRFTLCNGYFPATIDPGVYLLHPNLOPKRPSQEPVTL 540  
 QY 541 DELDAELENDIKVELIRNMIDGESSEKTFRTLVNSODERYIDKGNRTYTWTVPVGTDSL 600  
 DB 541 DELDAELENDIKVELIRNMIDGESSEKTFRTLVNSODERYIDKGNRTYTWTVPVGTDSL 600  
 QY 601 ALVLPYTFYIYIKAKIETITQASKKKMKDSEFLKPDNFEESGYTFIAPRDYCNLDKI 660  
 DB 601 ALVLPYTFYIYIKAKIETITQASKKKMKDSEFLKPDNFEESGYTFIAPRDYCNLDKI 660  
 QY 661 SDNTEFLNFEFIDRKTPNNPSCNTDILIRVLLDGFTELVONTWSOKNKIKGYKAR 720  
 DB 661 SDNTEFLNFEFIDRKTPNNPSCNTDILIRVLLDGFTELVONTWSOKNKIKGYKAR 720  
 QY 721 FVYTDGITRYVPEKAGENNQENPEYEDSFYKRSIDNDNYVTATPYFNKSGCAIESGI 780  
 DB 721 FVYTDGITRYVPEKAGENNQENPEYEDSFYKRSIDNDNYVTATPYFNKSGCAIESGI 780  
 QY 781 MYSKAVEITYIOGKILKPAVVGKIDVNSWJENFTKTSIRDPACGAVCDCKRNSDVMDCVI 840  
 DB 781 MYSKAVEITYIOGKILKPAVVGKIDVNSWJENFTKTSIRDPACGAVCDCKRNSDVMDCVI 840  
 QY 841 LDDGGFLMANHDDYTNQIGRFGEIDPSLMRLVNSVYAFNKSVDYOSVCEPGAAPQ 900  
 DB 841 LDDGGFLMANHDDYTNQIGRFGEIDPSLMRLVNSVYAFNKSVDYOSVCEPGAAPQ 900  
 QY 901 GAGHRSAYVPSIADLIHIGWATAAAMSILOQFLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
 DB 901 GAGHRSAYVPSIADLIHIGWATAAAMSILOQFLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
 QY 961 SCITEGTQYFFDNDKSFSGVLDGNCSTRIFHEVEKLMNTNLIPIVWESKGTGCTDRLLI 1020

QY 601 ALVLPYSEFYIAKIEETITQARSKKGMKDSITLKPDPNEESGYTFIAPROYCNDLKI 660  
 DB 601 ALVLPYSEFYIAKIEETITQARSKKGMKDSITLKPDPNEESGYTFIAPROYCNDLKI 660  
 QY 661 SDNTEFLNENFIDRKTPNNPSCNTDLINRYLLDAGFTNELVQNTWSKOKINIGVKAR 720  
 DB 661 SDNTEFLNENFIDRKTPNNPSCNTDLINRYLLDAGFTNELVQNTWSKOKINIGVKAR 720  
 QY 721 FVVTGIGITRVYPRKAGEENMOENPEYEDSEFYKRSLLDNNDNVYTFAPYFNKSGPAYESGI 780  
 DB 721 FVVTGIGITRVYPRKAGEENMOENPEYEDSEFYKRSLLDNNDNVYTFAPYFNKSGPAYESGI 780  
 QY 781 MVSRAVEIYIGKILKRAVYVGIKIDVNSWIFNFTKTSIRDPACAPVDCCKRNSVMCVI 840  
 DB 781 MVSRAVEIYIGKILKRAVYVGIKIDVNSWIFNFTKTSIRDPACAPVDCCKRNSVMCVI 840  
 QY 841 LDDGGLMANHDDYTNQIGRFGEIDPSLNRHLVNSIYVAFNKSYYQSCVCEGAAPKQ 900  
 DB 841 LDDGGLMANHDDYTNQIGRFGEIDPSLNRHLVNSIYVAFNKSYYQSCVCEGAAPKQ 900  
 QY 901 GAGHRSAYVPSIADILHIGMWATAAWSIIQOFLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
 DB 901 GAGHRSAYVPSIADILHIGMWATAAWSIIQOFLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
 QY 961 SCITEGQYQYFPNDNSKSSVGLDCGNCSTRFHVKKLMTNLIIFTMVSCKGTCPCDTRILLI 1020  
 DB 961 SCITEGQYQYFPNDNSKSSVGLDCGNCSTRFHVKKLMTNLIIFTMVSCKGTCPCDTRILLI 1020  
 QY 1021 QAEQTSDDGPCDPMVKOPRYRKGPVCFDNNALDIEDYDCGVS 1063  
 DB 1021 QAEQTSDDGPCDPMVKOPRYRKGPVCFDNNALDIEDYDCGVS 1063

RESULT 7  
 AAD01034  
 ID AAD01034 standard; Protein; 1063 AA.

XX AAD01034;

XX 04-JUL-2001 (first entry)

XX Human secreted soluble alpha2delta calcium channel subunit #14 protein.

XX Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;

KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;

KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;

KW filter binding assay; wheat germ lectin flashplate assay.

XX Homo sapiens.

XX WO200119870-A2.

XX 22-MAR-2001.

XX 18-SEP-2000; 2000WO-EP09137.

XX 16-SEP-1999; 99US-0397550.

XX (WARN) WARNER LAMBERT CO.

XX Brown JP, Bertelli F;

XX WPI: 2001-235262/24.

XX N-PSDB; AAS01425.

XX Calcium channel alpha2delta subunits, useful in e.g. SPA assays,

XX Flashplate assays, Nickel Flashplate assays, Filter binding assays or

XX Wheat Germ Lectin Flashplate assays -

XX Claim 31; Page 137-140; 160pp; English.

CC The present sequence represents human secreted calcium channel

CC alpha2delta subunit #14 which is soluble and retains the functional

CC characteristics of the full length or wild type alpha2delta subunit  
 CC (AA001025) from which it is derived. The invention relates to truncated  
 CC alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins  
 CC which retain their affinity for radioactively labeled gabapentin. The  
 CC alpha2delta subunit is 1 of the components of the heteromultimeric  
 CC voltage-dependent calcium channel (VDCC) complexes present in neuronal  
 CC and non-neuronal tissues including heart and skeletal muscle. Numerous  
 CC soluble forms of the human calcium channel alpha2delta subunits  
 CC (AA001014-AA001024 and AA001032-AA001038) and 5 soluble forms of the  
 CC porcine calcium channel alpha2delta subunits (AA001027-AA001031) are  
 CC described. The secreted soluble alpha2delta subunit may be used in assays  
 CC e.g. scintillation proximity assay (SPA), flashplate, nickel flashplate,  
 CC filter binding or wheat germ lectin flashplate assays to detect or  
 CC measure the binding or interaction of a ligand (e.g. gabapentin,  
 CC L-Norleucine, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Isoleucine,  
 CC L-Valine, Spermine and/or L-Phenylalanine) of a calcium channel  
 CC alpha2delta subunit.

SQ Sequence 1063 AA;

Query Match

Best Local Similarity 98.8%; Score 5532; DB 22; Length 1063;

Matches 1049; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 MAAGCLLATLTLPQSLIGPSSQEPFSAVITKSWVDMKQEDVTLAKTAGVQMDYDI 60

DB 1 MAAGCLLATLTLPQSLIGPSSQEPFSAVITKSWVDMKQEDVTLAKTAGVQMDYDI 60

QY 61 YERYQDLYTEPNNAQVLEIAARDIEKLSNRKALVRLAEVQVAAHQRDEFSN 120

DB 61 YERYQDLYTEPNNAQVLEIAARDIEKLSNRKALVRLAEVQVAAHQRDEFSN 120

QY 121 EYVYNAKDDLPDEKNDSEPGSORIKPVEIDANFGROIISYOHAAVHIPTDIESTIYL 180

DB 121 EYVYNAKDDLPDEKNDSEPGSORIKPVEIDANFGROIISYOHAAVHIPTDIESTIYL 180

QY 181 NELNWTSAIDVYKKNREDPSILMWQVFSAGLAKYYPASVWDSRTPNKIDLYDVR 240

DB 181 NELNWTSAIDVYKKNREDPSILMWQVFSAGLAKYYPASVWDSRTPNKIDLYDVR 240

QY 241 RPYVIGGAASPKDMLILVYVSGVSGLTLLRTSVSEMLETLSDDDFNVASFSNMAD 300

DB 241 RPYVIGGAASPKDMLILVYVSGVSGLTLLRTSVSEMLETLSDDDFNVASFSNMAD 300

QY 301 VSCFOHLYOANVANKVLDVANNITAKGIDYKKGSFAFQDLNLYNSRANCKIIML 360

DB 301 VSCFOHLYOANVANKVLDVANNITAKGIDYKKGSFAFQDLNLYNSRANCKIIML 360

QY 361 FTDGGERAEIETPAKYNKOKKAVFTFSVGOHNYDRPIQWACENKGYIETPSIGAIR 420

DB 361 FTDGGERAEIETPAKYNKOKKAVFTFSVGOHNYDRPIQWACENKGYIETPSIGAIR 420

QY 421 INFOEYLDVYGRPMVLAGKAKOVONTNYLDALDELGLVITGLPVPENTTGNENKTNLK 480

DB 421 INFOEYLDVYGRPMVLAGKAKOVONTNYLDALDELGLVITGLPVPENTTGNENKTNLK 480

QY 481 NQILIGMVDVSLIEDIKRLTPRTLCPNGYFAIDPNQYVLLHPNLQPKNSQSEPYTL 540

DB 481 NQILIGMVDVSLIEDIKRLTPRTLCPNGYFAIDPNQYVLLHPNLQPKNSQSEPYTL 540

QY 541 DFIDAELENDIKVETIRNKAKIDGESGKTRITLVKSODEYIKGNRTYTWTPVNGDYSL 600

DB 541 DFIDAELENDIKVETIRNKAKIDGESGKTRITLVKSODEYIKGNRTYTWTPVNGDYSL 600

QY 601 ALVLPYSEFYIAKIEETITQARSKKGMKDSITLKPDPNEESGYTFIAPROYCNDLKI 660

DB 601 ALVLPYSEFYIAKIEETITQARSKKGMKDSITLKPDPNEESGYTFIAPROYCNDLKI 660

QY 661 SDNTEFLNENFIDRKTPNNPSCNTDLINRYLLDAGFTNELVQNTWSKOKINIGVKAR 720

DB 661 SDNTEFLNENFIDRKTPNNPSCNTDLINRYLLDAGFTNELVQNTWSKOKINIGVKAR 720

QY 721 FVVTGIGITRVYPRKAGEENMOENPEYEDSEFYKRSLLDNNDNVYTFAPYFNKSGPAYESGI 780



QY 361 FTGGERAEIIFAKYNNKKKVVFTESVGOHNYDRGPOMMACENKGYEELPSIGAIR 420  
 DB 361 FTGGERAEIIFAKYNNKKKVVFTESVGOHNYDRGPOMMACENKGYEELPSIGAIR 420  
 QY 421 INTQEVLDVIGRPMVLADGKAKOVNTNYLDALDELGLVITGTLPEVNTIGONENKTNLK 480  
 DB 421 INTQEVLDVIGRPMVLADGKAKOVNTNYLDALDELGLVITGTLPEVNTIGONENKTNLK 480  
 QY 481 NQILICVGVDSLEDIKRLPREFTLCPNGYFFAIDPNGYVLLHPNLQPKNKSQEPVTL 540  
 DB 481 NQILICVGVDSLEDIKRLPREFTLCPNGYFFAIDPNGYVLLHPNLQPKNKSQEPVTL 540  
 QY 541 DFLDALENDIKVEIRNKKMIDGSEGEKTRTLVKSODERYIDKGNRTYTWTVPVNGTDSL 600  
 DB 541 DFLDALENDIKVEIRNKKMIDGSEGEKTRTLVKSODERYIDKGNRTYTWTVPVNGTDSL 600  
 QY 601 ALVLPYSEFYIKAKIEETITQARSKKGMKDETLKPNFESGTYTPIAPDYCNDLKI 660  
 DB 601 ALVLPYSEFYIKAKIEETITQARSKKGMKDETLKPNFESGTYTPIAPDYCNDLKI 660  
 QY 661 SDNTEFLNLFNEFIDRKTPNNPSCNTDLINRYLDAGFTNELVONYSKOKNKGVAR 720  
 DB 661 SDNTEFLNLFNEFIDRKTPNNPSCNTDLINRYLDAGFTNELVONYSKOKNKGVAR 720  
 QY 721 FVYTDGITRVPYKKEAGEMOENPETEYDSFYKRSIDNNTYFAPYENKSGPAVEGI 780  
 DB 721 FVYTDGITRVPYKKEAGEMOENPETEYDSFYKRSIDNNTYFAPYENKSGPAVEGI 780  
 QY 781 MYSKAVEIYIOGRLKPAVVGIKIDVNSWIEFTKTSIDPCGAPGCDCKRNSDVWDCYI 840  
 DB 781 MYSKAVEIYIOGRLKPAVVGIKIDVNSWIEFTKTSIDPCGAPGCDCKRNSDVWDCYI 840  
 QY 841 LDGCGFLMANHDDYNOJGRFFGELIDPSLMRLVNI SYAENKSYDYOVCPEGAAPKQ 900  
 DB 841 LDGCGFLMANHDDYNOJGRFFGELIDPSLMRLVNI SYAENKSYDYOVCPEGAAPKQ 900  
 QY 901 GAGHRAYVPSIADILHIGMWTAAAMSTIIOQFLSLTPRLLEAVEMEDDDFTASLSKQ 960  
 DB 901 GAGHRAYVPSIADILHIGMWTAAAMSTIIOQFLSLTPRLLEAVEMEDDDFTASLSKQ 960  
 QY 961 SCITTEJOYFFENDSKSFSGVLDCCGNSRI FHYEKLMNTNLI FIVESKGTCPDTRLI 1020  
 DB 961 SCITTEJOYFFENDSKSFSGVLDCCGNSRI FHYEKLMNTNLI FIVESKGTCPDTRLI 1020  
 QY 1021 QAQOTSDGDPDCMVKQPRYRKGPVYCFDNNALDEYTDCCGVS 1063  
 DB 1021 QAQOTSDGDPDCMVKQPRYRKGPVYCFDNNALDEYTDCCGVS 1063

## RESULT 6

AAB62251

ID AAB62251 standard; Protein: 1091 AA.

AC AAB62251:

DT 11-JUN-2001 (first entry)

DE Porcine calcium channel subunit alpha2delta-1.

KM Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;

XX nervous system disorder; pain; epilepsy; anxiety; pig.

OS Sus scrofa.

PN WO200120336-A2.

PD 22-MAR-2001.

PF 18-SEP-2000; 2000WO-EP09136.

PR 16-SEP-1999; 99US-0397549.

PA (WARN ) WARNER LAMBERT CO.

XX Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;  
 PI WPI: 2001-257902/26.  
 DR N-PSDB; AAF57556.  
 XX Competitive binding assay for screening ligands which bind a cerebral  
 PT cortical voltage-dependent calcium channel alpha2delta-1 subunit,  
 PT where the ligands identified are useful for treating disorders of the  
 PT nervous system, including pain -  
 PS Claim 7; Page 109-112; 158pp; English.  
 XX The invention relates to a new method for screening ligands which bind a  
 CC cerebral cortical voltage-dependent calcium channel alpha2delta subunit,  
 CC preferably alpha2delta-1 subunit. The method comprises contacting a  
 CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of  
 CC interest and a labelled compound which binds the subunit, followed by  
 CC measuring the level of binding of the labelled compound to alpha2delta-1  
 CC subunit. The method is useful for screening ligands, preferably  
 CC biologically active products that modulate a nervous system function,  
 CC which bind a cerebral cortical voltage-dependent calcium channel  
 CC alpha2delta-1 subunit. The ligands identified by the method are useful  
 CC for treating disorders of the nervous system, including pain, epilepsy  
 CC and anxiety. The present sequence represents a porcine calcium channel  
 CC subunit alpha2delta-1.  
 CC  
 XX  
 .50 Sequence 1091 AA;  
 Query Match 100.0%; Score 5602; DB 22; Length 1091;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAAGCLALTLTLTQSLIGPSQEPFSAVTITSWDKMEDLVTLAKTASGVNQLVDI 60  
 DB 1 MAAGCLALTLTLTQSLIGPSQEPFSAVTITSWDKMEDLVTLAKTASGVNQLVDI 60  
 QY 61 YEKYODLYTVEPNNAKQVETIARDIEKLSNRKALVRLALEKYOAAHOMREDFASN 120  
 DB 61 YEKYODLYTVEPNNAKQVETIARDIEKLSNRKALVRLALEKYOAAHOMREDFASN 120  
 QY 121 EYVYVNAKDDLDPEKNDESPSORIKPFIDDPNGRQISQHAHVHPIDYIGSTIVL 180  
 DB 121 EYVYVNAKDDLDPEKNDESPSORIKPFIDDPNGRQISQHAHVHPIDYIGSTIVL 180  
 QY 181 NELNMTSALDEVFKKRNREDPSLLMOVFGSATGLARYYPASPVWDSNRTPKIDLYVRR 240  
 DB 181 NELNMTSALDEVFKKRNREDPSLLMOVFGSATGLARYYPASPVWDSNRTPKIDLYVRR 240  
 QY 241 RPYVIOGAASPRKMLILVDVSGSVSGTLKILRTSVSEMLETTSDDDFVNVASFNSAOD 300  
 DB 241 RPYVIOGAASPRKMLILVDVSGSVSGTLKILRTSVSEMLETTSDDDFVNVASFNSAOD 300  
 QY 301 VSCFOHLVQAVNRKKNVYLKDAVNNITAKGIDYKKGFSFAEQLNNTVSRANCKITIML 360  
 DB 301 VSCFOHLVQAVNRKKNVYLKDAVNNITAKGIDYKKGFSFAEQLNNTVSRANCKITIML 360  
 QY 361 FTGGERAEIIFAKYNNKKKVVFTESVGOHNYDRGPOMMACENKGYEELPSIGAIR 420  
 DB 361 FTGGERAEIIFAKYNNKKKVVFTESVGOHNYDRGPOMMACENKGYEELPSIGAIR 420  
 QY 421 INTQEVLDVIGRPMVLADGKAKOVNTNYLDALDELGLVITGTLPEVNTIGONENKTNLK 480  
 DB 421 INTQEVLDVIGRPMVLADGKAKOVNTNYLDALDELGLVITGTLPEVNTIGONENKTNLK 480  
 QY 481 NQILICVGVDSLEDIKRLPREFTLCPNGYFFAIDPNGYVLLHPNLQPKNKSQEPVTL 540  
 DB 481 NQILICVGVDSLEDIKRLPREFTLCPNGYFFAIDPNGYVLLHPNLQPKNKSQEPVTL 540  
 QY 541 DFLDALENDIKVEIRNKKMIDGSEGEKTRTLVKSODERYIDKGNRTYTWTVPVNGTDSL 600  
 DB 541 DFLDALENDIKVEIRNKKMIDGSEGEKTRTLVKSODERYIDKGNRTYTWTVPVNGTDSL 600

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Db 181 NELNMTSALDEVEFKKREDEPSLLMOVFGSATGLARYYPASPMWDNSRTPNKIDLYDVR 240
OY 241 RPYWIOGAASPKDMLILVDVSGVSGTLTKIRTSVSEMLETLSDDDPVVAVASFNSAOD 300
Db 241 RPYWIOGAASPKDMLILVDVSGVSGTLTKIRTSVSEMLETLSDDDPVVAVASFNSAOD 300
OY 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGTTDYKKGFSFAEQLLNYSRANCKNIIML 360
Db 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGTTDYKKGFSFAEQLLNYSRANCKNIIML 360
OY 361 PFTGGERRAEIIRAKYKDKKVVFTFVSGOHNYDRGP IOWMACENKGYEELPSIGAIR 420
Db 361 PFTGGERRAEIIRAKYKDKKVVFTFVSGOHNYDRGP IOWMACENKGYEELPSIGAIR 420
OY 421 INFOEYLDVGRPMVLADGAKOVMTNVLDLDELGLVTGTLPEVNITGONENKTNLK 480
Db 421 INFOEYLDVGRPMVLADGAKOVMTNVLDLDELGLVTGTLPEVNITGONENKTNLK 480
OY 481 NOLILGVMGVDSLEDIKRLTPRTLCPNGYEPAIDPNGVLLHPNLOPKNPSQEPVTL 540
Db 481 NOLILGVMGVDSLEDIKRLTPRTLCPNGYEPAIDPNGVLLHPNLOPKNPSQEPVTL 540
OY 541 DFLDAELENDIKYKIRNKKMIDGSGEKTFTLVKSODERTIDGKNRTYTTPVNGTDYSL 600
Db 541 DFLDAELENDIKYKIRNKKMIDGSGEKTFTLVKSODERTIDGKNRTYTTPVNGTDYSL 600
OY 601 ALVLPYTSFYTIKAKIEETITQARSKKGMKDETLKPNFEESGTYFLAPRYCNDIKI 660
Db 601 ALVLPYTSFYTIKAKIEETITQARSKKGMKDETLKPNFEESGTYFLAPRYCNDIKI 660
OY 661 SDNNTEFLNFEIDRKTPNNPNSCNTDLINRYLLDAGFTNELVQVYWSKQNKIKGVKAR 720
Db 661 SDNNTEFLNFEIDRKTPNNPNSCNTDLINRYLLDAGFTNELVQVYWSKQNKIKGVKAR 720
OY 721 FVYTDGITRVYKKEGEMNENQENPEYEDSFYKRSIDNDNYVTATYFKNKSGGAESEGI 780
Db 721 FVYTDGITRVYKKEGEMNENQENPEYEDSFYKRSIDNDNYVTATYFKNKSGGAESEGI 780
OY 781 MVSAAVEIYIOGKILKRAVVGIKIDVNSWIENTFTKISIRPCAGPVCDCRNSDVMDCV 840
Db 781 MVSAAVEIYIOGKILKRAVVGIKIDVNSWIENTFTKISIRPCAGPVCDCRNSDVMDCV 840
OY 841 LDDGGFLMANHDDYTNOIGRFEGLDPSIMRHLVNI SYAFNKSYDQSVCEPGAAPKQ 900
Db 841 LDDGGFLMANHDDYTNOIGRFEGLDPSIMRHLVNI SYAFNKSYDQSVCEPGAAPKQ 900
OY 901 GAGHRSATVPSIADILHIGWMTAAAMSTLQOFLSLTPRRLLEAVEMEDDDTTASLSQ 960
Db 901 GAGHRSATVPSIADILHIGWMTAAAMSTLQOFLSLTPRRLLEAVEMEDDDTTASLSQ 960
OY 961 SCITTEQYVFFDNDKSFSGVLDGNCNSRI FHEKLMNTLIFIMVESKGTCCDTRLIL 1020
Db 961 SCITTEQYVFFDNDKSFSGVLDGNCNSRI FHEKLMNTLIFIMVESKGTCCDTRLIL 1020
OY 1021 QABQTSDEGDPDCMVKOPRIKRPDVCEDNNALEDYTDGCVS 1063
Db 1021 QABQTSDEGDPDCMVKOPRIKRPDVCEDNNALEDYTDGCVS 1063

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RESULT 5  
AAU01027 standard; Protein: 1091 AA.

AAU01027;

04-JUL-2001 (first entry)

Pig secreted soluble alpha2delta calcium channel subunit #1 protein.

Pig: secreted calcium channel alpha2delta subunit; alpha2delta-2;

alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;

gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;

filter binding assay; wheat germ lectin flashplate assay; porcine.

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XX Sus scrofa.
OS WO200119870-A2.
PN 22-MAR-2001.
PF 18-SEP-2000; 2000WO-EP09137.
PR 16-SEP-1999; 99US-0397550.
PA (WARN ) WARNER LAMBERT CO.
PI Brown JP, Bertelli F;
PI WPI: 2001-235262/24.
DR N-PSDB; AAS01419.
XX
XX Calcium channel alpha2delta subunits, useful in e.g. SPA assays,
XX Flashplate assays, Nickel Flashplate assays, Filter binding assays or
XX Wheat Germ Lectin Flashplate assays -
XX
XX Claim 30; Page 110-113; 160pp; English.
XX
XX The present sequence represents pig secreted calcium channel alpha2delta
XX subunit #1 which is soluble and retains the functional characteristics
XX of the full length or wild type alpha2delta subunit from which it is
XX derived. The invention relates to truncated alpha2delta-2, alpha2delta-3
XX or alpha2delta-4 subunit soluble proteins which retain their affinity for
XX radioactively labelled gabapentin. The alpha2delta subunit is 1 of the
XX components of the heteromultimeric voltage-dependent calcium channel
XX (VDCC) complexes present in neuronal and non-neuronal tissues including
XX heart and skeletal muscle. Numerous soluble forms of the human calcium
XX channel alpha2delta subunits (AAU01014-AAU01024 and AAU01032-AAU01038)
XX and 5 soluble forms of the porcine calcium channel alpha2delta subunits
XX (AAU01027-AAU01031) are described. The secreted soluble alpha2delta
XX subunit may be used in assays e.g. scintillation proximity assay (SPA),
XX flashplate, nickel flashplate, filter binding or wheat germ lectin
XX flashplate assays to detect or measure the binding or interaction of a
XX ligand (e.g. gabapentin, L-Norleucine, L-Allo-isoleucine, L-methionine,
XX L-leucine, L-isoleucine, L-valine, Spermine and/or L-phenylalanine) of
XX a calcium channel alpha2delta subunit.
XX
XX Sequence 1091 AA;
XX
XX Query Match 100.0%; Score 5602; DB 22; Length 1091;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 MAAGCLALTLTLFOSLLIGPSSQEPSPSAVTIKSWDKMOEDLVTLAKTASGYNOIYDI 60
Db 1 MAAGCLALTLTLFOSLLIGPSSQEPSPSAVTIKSWDKMOEDLVTLAKTASGYNOIYDI 60
OY 61 YEKYODLYVEPNNAQVEIARDEIKLSNRKALVRLALEAKVOAHOHREDFASN 120
Db 61 YEKYODLYVEPNNAQVEIARDEIKLSNRKALVRLALEAKVOAHOHREDFASN 120
OY 61 YEKYODLYVEPNNAQVEIARDEIKLSNRKALVRLALEAKVOAHOHREDFASN 120
Db 61 YEKYODLYVEPNNAQVEIARDEIKLSNRKALVRLALEAKVOAHOHREDFASN 120
OY 121 EYVYINAKDDLDPEKNDSEPSQRIKPVFIDANGRGQISYQHAHVHPTDIYEGSTIVL 180
Db 121 EYVYINAKDDLDPEKNDSEPSQRIKPVFIDANGRGQISYQHAHVHPTDIYEGSTIVL 180
OY 121 EYVYINAKDDLDPEKNDSEPSQRIKPVFIDANGRGQISYQHAHVHPTDIYEGSTIVL 180
Db 121 EYVYINAKDDLDPEKNDSEPSQRIKPVFIDANGRGQISYQHAHVHPTDIYEGSTIVL 180
OY 181 NELNMTSALDEVEFKKREDEPSLLMOVFGSATGLARYYPASPMWDNSRTPPKIDLYDVR 240
Db 181 NELNMTSALDEVEFKKREDEPSLLMOVFGSATGLARYYPASPMWDNSRTPPKIDLYDVR 240
OY 241 RPYWIOGAASPKDMLILVDVSGVSGTLTKIRTSVSEMLETLSDDDPVVAVASFNSAOD 300
Db 241 RPYWIOGAASPKDMLILVDVSGVSGTLTKIRTSVSEMLETLSDDDPVVAVASFNSAOD 300
OY 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGTTDYKKGFSFAEQLLNYSRANCKNIIML 360
Db 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGTTDYKKGFSFAEQLLNYSRANCKNIIML 360

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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MAACGLALTLTLFQSLIGPSSOEPPSAVTIKSWDKMOEDLVTLAKTASGVNOLVDI 60
DB 1 MAACGLALTLTLFQSLIGPSSOEPPSAVTIKSWDKMOEDLVTLAKTASGVNOLVDI 60
QY 61 YEKYODLYTEVPNNAROLVEIARDIEKLISNSKALVRLALEAEKVQAHHQREDFASN 120
DB 61 YEKYODLYTEVPNNAROLVEIARDIEKLISNSKALVRLALEAEKVQAHHQREDFASN 120
QY 121 EYVYVYNAKDDLPEKNDSESGSRIKPFVTDANFGROIYQHAHAIIPDIYEGSTIVL 180
DB 121 EYVYVYNAKDDLPEKNDSESGSRIKPFVTDANFGROIYQHAHAIIPDIYEGSTIVL 180
QY 181 NELNMTSALDEVEFKKNEEDPSLLMOVFGSATGLARYPASPVWDSRTPNKIDLYDVR 240
DB 181 NELNMTSALDEVEFKKNEEDPSLLMOVFGSATGLARYPASPVWDSRTPNKIDLYDVR 240
QY 241 RPYWYIOGAASPKMILIVDSSVSGTLTKLIRTSVSEMETLSDDDFVNVASFNSNAD 300
DB 241 RPYWYIOGAASPKMILIVDSSVSGTLTKLIRTSVSEMETLSDDDFVNVASFNSNAD 300
QY 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGITYDKGFSFAFEOQLNYSRANCKIIML 360
DB 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGITYDKGFSFAFEOQLNYSRANCKIIML 360
QY 361 FTGGGERAOEIFAKYNNKKKVVVFVTFVSQAHYDNGPIOMACENKGYEYIPISTGAIR 420
DB 361 FTGGGERAOEIFAKYNNKKKVVVFVTFVSQAHYDNGPIOMACENKGYEYIPISTGAIR 420
QY 421 INTQEVLDVLRPVLADGKAKOVNTNYLDALDELGITGTGTPENTIGNONENTNK 480
DB 421 INTQEVLDVLRPVLADGKAKOVNTNYLDALDELGITGTGTPENTIGNONENTNK 480
QY 481 NOILLEGVNDVSLIEDIKRLPRFTLCPNGYFAIDPNGYVLHPMLQPKNKSQEPVTL 540
DB 481 NOILLEGVNDVSLIEDIKRLPRFTLCPNGYFAIDPNGYVLHPMLQPKNKSQEPVTL 540
QY 541 DFLDALENDIKVEIKNNKIDGSEGEKTRTLVKSODEYIDKGNNTYWTVNGTDSL 600
DB 541 DFLDALENDIKVEIKNNKIDGSEGEKTRTLVKSODEYIDKGNNTYWTVNGTDSL 600
QY 601 ALVLPYSSYYIKAKIETITQARSKKGMKDETLKPDNFESEGTETAPRDYCNLDKI 660
DB 601 ALVLPYSSYYIKAKIETITQARSKKGMKDETLKPDNFESEGTETAPRDYCNLDKI 660
QY 661 SDNNEFLINNEEIDRKTPNPNPSCNTDLINVLDDAGFTNELVONYMSKONIKGVKAR 720
DB 661 SDNNEFLINNEEIDRKTPNPNPSCNTDLINVLDDAGFTNELVONYMSKONIKGVKAR 720
QY 721 FVYTDGGLTRVYPKRAGEWQENPETEYEDSFYKRSIDNDNYVFTAPYFNKSGPGAYESGI 780
DB 721 FVYTDGGLTRVYPKRAGEWQENPETEYEDSFYKRSIDNDNYVFTAPYFNKSGPGAYESGI 780
QY 781 MYSKAVEIITQGLKLPVAVGIIKIDVNSMIENFTKTSIRDPAGPVDCCKRNSDMDCVI 840
DB 781 MYSKAVEIITQGLKLPVAVGIIKIDVNSMIENFTKTSIRDPAGPVDCCKRNSDMDCVI 840
QY 841 LDDGFFLLMANHDYTNIGIRFGEIDPSLMKHLVNIISVAFNKSYSYDQSCCEPAAFKQ 900
DB 841 LDDGFFLLMANHDYTNIGIRFGEIDPSLMKHLVNIISVAFNKSYSYDQSCCEPAAFKQ 900
QY 901 GAGHSASVPSIADILHIGMWATAAAMSIILOFLSLTFEPRLLEVEDEDDDFATASLSKQ 960
DB 901 GAGHSASVPSIADILHIGMWATAAAMSIILOFLSLTFEPRLLEVEDEDDDFATASLSKQ 960
QY 961 SCITQOTQYFEDNDKSSVGLDCGNCRIHVEKLMNTNLIIFIMVESKGTGCPDTRLILI 1020
DB 961 SCITQOTQYFEDNDKSSVGLDCGNCRIHVEKLMNTNLIIFIMVESKGTGCPDTRLILI 1020
QY 1021 QAEQTSDEGPDPCDMVKOPRYRKGPVCFDNNALDEYTDGCGVS 1063
DB 1021 QAEQTSDEGPDPCDMVKOPRYRKGPVCFDNNALDEYTDGCGVS 1063

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DB 1021 QAEQTSDEGPDPCDMVKOPRYRKGPVCFDNNALDEYTDGCGVS 1063
RESULT 4
AAB62255
ID AAB62255 standard; Protein; 1069 AA.
XX
AC AAB62255;
XX
DT 11-JUN-2001 (first entry)
XX
DE Porcine calcium channel subunit alpha2delta-1 deletion mutant.
XX
KW Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;
XX nervous system disorder; pain; epilepsy; anxiety; pig; mutant.
XX
OS Sus scrofa.
XX
PN WO200120336-A2.
XX
PD 22-MAR-2001.
XX
PF 18-SEP-2000; 2000WO-EP09136.
XX
PK 16-SEP-1999; 99US-0397549.
XX
PA (WARNER ) WARNER LAMBERT CO.
XX
PI Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;
XX
WP: 2001-257902/26.
XX
PR Competitive binding assay for screening ligands which bind a cerebral
PT cortical voltage-dependent calcium channel alpha2delta-1 subunit,
PT where the ligands identified are useful for treating disorders of the
PT nervous system, including pain -
XX
PS Claim 8; Page 122-126; 158pp; English.
XX
CC The invention relates to a new method for screening ligands which bind a
CC cerebral cortical voltage-dependent calcium channel alpha2delta subunit,
CC preferably alpha2delta-1 subunit. The method comprises contacting a
CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of
CC interest and a labelled compound which binds the subunit, followed by
CC measuring the level of binding of the labelled compound to alpha2delta-1
CC subunit. The method is useful for screening ligands, preferably
CC biologically active products that modulate a nervous system function,
CC which bind a cerebral cortical voltage-dependent calcium channel
CC alpha2delta-1 subunit. The ligands identified by the method are useful
CC for treating disorders of the nervous system, including pain, epilepsy
CC and anxiety. The present sequence represents a porcine calcium channel
CC subunit alpha2delta-1 deletion mutant.
CC
XX
SQ Sequence 1069 AA.
XX
Query Match 100.0%; Score 5602; DB 22; Length 1069;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAACGLALTLTLFQSLIGPSSOEPPSAVTIKSWDKMOEDLVTLAKTASGVNOLVDI 60
DB 1 MAACGLALTLTLFQSLIGPSSOEPPSAVTIKSWDKMOEDLVTLAKTASGVNOLVDI 60
QY 61 YEKYODLYTEVPNNAROLVEIARDIEKLISNSKALVRLALEAEKVQAHHQREDFASN 120
DB 61 YEKYODLYTEVPNNAROLVEIARDIEKLISNSKALVRLALEAEKVQAHHQREDFASN 120
QY 121 EYVYVYNAKDDLPEKNDSESGSRIKPFVTDANFGROIYQHAHAIIPDIYEGSTIVL 180
DB 121 EYVYVYNAKDDLPEKNDSESGSRIKPFVTDANFGROIYQHAHAIIPDIYEGSTIVL 180
QY 181 NELNMTSALDEVEFKKNEEDPSLLMOVFGSATGLARYPASPVWDSRTPNKIDLYDVR 240
DB 181 NELNMTSALDEVEFKKNEEDPSLLMOVFGSATGLARYPASPVWDSRTPNKIDLYDVR 240

```

CC subunit. The method is useful for screening ligands, preferably  
 CC biologically active products that modulate a nervous system function,  
 CC which bind a cerebral cortical voltage-dependent calcium channel  
 CC alpha2delta-1 subunit. The ligands identified by the method are useful  
 CC for treating disorders of the nervous system, including pain, epilepsy  
 CC and anxiety. The present sequence represents a porcine calcium channel  
 CC subunit alpha2delta-4.

xx Sequence 1063 AA;

Query Match 100.0%; Score 5602; DB 22; Length 1063;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLATLTTLFQSLIGPSSQEPFPAVTIKSWDKMOEDLVTLAKTAGSVNOLVDI 60  
 DB 1 MAAGCLLATLTTLFQSLIGPSSQEPFPAVTIKSWDKMOEDLVTLAKTAGSVNOLVDI 60  
 QY 61 YEKYQDLTYVEPNNAQVLEIAARDIEKLISNSKALVRLALEAEVQAHOHREDFASN 120  
 DB 61 YEKYQDLTYVEPNNAQVLEIAARDIEKLISNSKALVRLALEAEVQAHOHREDFASN 120  
 QY 121 EYVYNAKQDLDEPKNDSEPSORIKPVFTDANFGROI SYOHAHHPIDIEGSTIYL 180  
 DB 121 EYVYNAKQDLDEPKNDSEPSORIKPVFTDANFGROI SYOHAHHPIDIEGSTIYL 180  
 QY 181 NELNMTSALDEVEFKKNEEDPSILMOVFGSATGLARYYPASPVWDSRTPNKIDLYDVR 240  
 DB 181 NELNMTSALDEVEFKKNEEDPSILMOVFGSATGLARYYPASPVWDSRTPNKIDLYDVR 240  
 QY 241 RPYVIGGASPKDMLILVDVSGVSGILTLKITVSSEMETETSDDDFVNVAFSNNAOD 300  
 DB 241 RPYVIGGASPKDMLILVDVSGVSGILTLKITVSSEMETETSDDDFVNVAFSNNAOD 300  
 QY 301 VSCGQHLVQANVNNKVKLADAVNNITAKGTTDYKKGSPAFEOGLNVSRAKCNKTIIM 360  
 DB 301 VSCGQHLVQANVNNKVKLADAVNNITAKGTTDYKKGSPAFEOGLNVSRAKCNKTIIM 360  
 QY 361 FTGGEERRAOEIFAKYNNKDKKVRFTFVSQOHVNDRPIQMACENKGYEETIPSGAIR 420  
 DB 361 FTGGEERRAOEIFAKYNNKDKKVRFTFVSQOHVNDRPIQMACENKGYEETIPSGAIR 420  
 QY 421 INTQETIDVYGRPMVLAGDAKQOVNTNYLDLLEGLVITGTLPPVNTIGQENKNTNLK 480  
 DB 421 INTQETIDVYGRPMVLAGDAKQOVNTNYLDLLEGLVITGTLPPVNTIGQENKNTNLK 480  
 QY 481 NQILIGWGVDSLEDIKRLTPRTLCPPNGYFAIDPNGYVLLHPNLOPNKPSQSEPTVL 540  
 DB 481 NQILIGWGVDSLEDIKRLTPRTLCPPNGYFAIDPNGYVLLHPNLOPNKPSQSEPTVL 540  
 QY 541 DFLDAELNDIKVEIRNMKMDIGESGEKTFRLVKSQDERYIDKGNRTYTWTPVNGTDSL 600  
 DB 541 DFLDAELNDIKVEIRNMKMDIGESGEKTFRLVKSQDERYIDKGNRTYTWTPVNGTDSL 600  
 QY 601 ALVLPYTSFYIRAKIETITQARSKKGAKMDSFTLKPDPNFEESGTYFIFAPROYCNDLKI 660  
 DB 601 ALVLPYTSFYIRAKIETITQARSKKGAKMDSFTLKPDPNFEESGTYFIFAPROYCNDLKI 660  
 QY 661 SDNNTEFLNPNNEFDKTPNPNPCNDLIRVYLLDAGFNLQVONWSQOKNKGKAR 720  
 DB 661 SDNNTEFLNPNNEFDKTPNPNPCNDLIRVYLLDAGFNLQVONWSQOKNKGKAR 720  
 QY 721 FVVYDGGITRYRYPKEAGENQENPEYEDSFYKRSLLDNVYVTFAPYFNKSGPAYBSGT 780  
 DB 721 FVVYDGGITRYRYPKEAGENQENPEYEDSFYKRSLLDNVYVTFAPYFNKSGPAYBSGT 780  
 QY 781 MYSKAVEIYIQGLKLAFAVVGIKIDVNSWLENFTKISIRDPACAPVDCCKRNSVMDCVI 840  
 DB 781 MYSKAVEIYIQGLKLAFAVVGIKIDVNSWLENFTKISIRDPACAPVDCCKRNSVMDCVI 840  
 QY 841 LDDGGLMANHNDYTNQIGRFGEIDPSLMRHLVNISVYAFNKSSTYOSGCEFGAPKQ 900  
 DB 841 LDDGGLMANHNDYTNQIGRFGEIDPSLMRHLVNISVYAFNKSSTYOSGCEFGAPKQ 900

QY 901 GAGHSATVPSIADILATIGMWATAAANSIIQOFLSTLTPRLLFAVEMEDDDFTASISQ 960  
 DB 901 GAGHSATVPSIADILATIGMWATAAANSIIQOFLSTLTPRLLFAVEMEDDDFTASISQ 960  
 QY 961 SCITEQOTQYFFDNDKSKSPSGVLDGNCGRIFRVEKIMNTNLIFFIMESKGTCPDTRILI 1020  
 DB 961 SCITEQOTQYFFDNDKSKSPSGVLDGNCGRIFRVEKIMNTNLIFFIMESKGTCPDTRILI 1020  
 QY 1021 QAEQTSDDPDCDVMYKQPRYRKGPDVCFDNNALBDDYTDCCGSVS 1063  
 DB 1021 QAEQTSDDPDCDVMYKQPRYRKGPDVCFDNNALBDDYTDCCGSVS 1063

RESULT 3  
 AAU01031  
 ID AAU01031 standard; Protein: 1069 AA.

AC AAU01031;

DT 04-JUL-2001 (first entry)

DE Pig secreted soluble alpha2delta calcium channel subunit #5 protein.

KW Pig; secreted calcium channel alpha2delta subunit; alpha2delta-2;  
 KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;  
 KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;  
 KW filter binding assay; wheat germ lectin flashplate assay; porcine.

OS Sus scrofa.

PN WO200119870-A2.

PD 22-MAR-2001.

PF 18-SEP-2000; 2000WO-EP09137.

PR 16-SEP-1999; 99US-0397550.

PA (WARN ) WARNER LAMBERT CO.

PI Brown JP, Bertelli F;

PT WPT; 2001-235262/24.

PT Calcium channel alpha2delta subunits, useful in e.g. SPA assays,  
 PT Flashplate assays, Nickel Flashplate assays, Filter binding assays or  
 PT Wheat germ lectin Flashplate assays -

PS Disclosure: Page 124-127; 160pp; English.

XX The present sequence represents pig secreted calcium channel alpha2delta  
 CC subunit #5 which is soluble and retains the functional characteristics  
 CC of the full length or wild type alpha2delta subunit from which it is  
 CC derived. The invention relates to truncated alpha2delta-2, alpha2delta-3  
 CC or alpha2delta-4 subunit soluble proteins which retain their affinity for  
 CC radioactively labelled gabapentin. The alpha2delta subunit is 1 of the  
 CC components of the heteromultimeric voltage-dependent calcium channel  
 CC (VDCC) complexes present in neuronal and non-neuronal tissues including  
 CC heart and skeletal muscle. Numerous soluble forms of the human calcium  
 CC channel alpha2delta subunits (AAU01014-AAU01024 and AAU01032-AAU01038)  
 CC and 5 soluble forms of the porcine calcium channel alpha2delta subunits  
 CC (AAU01027-AAU01031) are described. The secreted soluble alpha2delta  
 CC subunit may be used in assays e.g. scintillation proximity assay (SPA),  
 CC flashplate, nickel flashplate, filter binding or wheat germ lectin  
 CC flashplate assays to detect or measure the binding or interaction of a  
 CC ligand (e.g. gabapentin, L-Norleucine, L-Allo-Isoleucine, L-methionine,  
 CC L-leucine, L-Isoleucine, L-Valine, Spermine and/or L-Phenylalanine) of  
 CC a calcium channel alpha2delta subunit.

QY Sequence 1069 AA;  
 Query Match 100.0%; Score 5602; DB 22; Length 1069;

D<sub>B</sub> 601 ALVLPYTSFYIIKAKIEETITQARSKGKMKDSETLKPDNFEESGYTFTAPRDYCNLKI 666

secreted soluble recombinant alpha2delta-1 subunit with a ligand of interest and a labelled compound which binds the subunit followed by

CC measuring the level of binding of the labelled compound to  $\alpha$ h2delta-1



100

```
Search completed: February 10, 2003, 14:48:55
Job time : 11.6604 secs
```



```

; SOFTWARE: FastSDQ for Windows Version 4.0
; SED ID NO 5898
; LENGTH: 1349
; TYPE: PRF
; ORGANISM: Staphylococcus aureus
US-09-815-242-5898

```

Query Match	2.8%;	Score 152;	DB 10;	Length 1349;
Best Local Similarity	19.3%;	Pred. No. 0.014;		
Matches 198;	Conservative 124;	Mismatches 337;	Indels 366;	Gaps 48;

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Db      823 LKNEENGEVLQTTKTKDCKOQYQFTGLENGTAKKVEFEETPSCGYFTQVGSQSDIGSINSNST 882
Qy      743 -----NPEYEDSPYKRSLDNNNYEFTAPYENKSGPAGYE-----SGIAMSKEVEITYIQ 791
           : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      883 TGYIKDKNDNTIDSGYKRYFTYINLDYWEPT -NKKNQVDKBEKGISGVTYTLKDE---N 937
Qy      792 GKLLK 796
           : : : :
Db      938 DKVYK 942

```

```

RESULT 15
/ Sequence 13137, Application US/09815242
/ Patent No. US20020061569A1
/ GENERAL INFORMATION:
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Karl L.
/ APPLICANT: Zyskind, Judith W.
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John D.
/ APPLICANT: Carr, Grant J.
/ APPLICANT: Yamamoto, Robert T.
/ APPLICANT: Xu, H. Howard
/ TITLE OF INVENTION: Identification of Essential Genes in
/ TITLE OF INVENTION: Prokaryotes
/ FILE REFERENCE: ELITRA.011A
/ CURRENT APPLICATION NUMBER: US/09/815,242
/ CURRENT FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/151,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ NUMBER OF SEQ ID NOS: 14110
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13137
/ LENGTH: 1349
/ TYPE: prf
/ ORGANISM: Staphylococcus aureus
US-09-815-242-13137

```

Query Match 2.88; Score 152; DB 10; Length 1349;  
Best Local Similarity 19.3%; Pred. No. 0.014;  
Matches 198; Conservative 124; Mismatches 337; Indels 366; Gaps 48;

RESULT 13  
US-09-850-351A-8  
Sequence 8, Application US/09850351A  
Patent No. US20020100080A1  
GENERAL INFORMATION:  
APPLICANT: Feltelson, Jerald S.  
Schnepf, H. Ernest  
Narva, Kenneth E.  
Stockhoff, Brian A.  
Schmeits, James  
Loewer, David  
Dullum, Charles Joseph  
Muller-Cohn, Judy  
Stamp, Lisa  
Morrill, George  
TITLE OF INVENTION: No. US20020100080A1 Pesticidal Toxins and Nucleotide  
Sequences Which Encode These Toxins  
NUMBER OF SEQUENCES: 144  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: US  
ZIP: 32606-6669  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/850,351A  
FILING DATE: 07-MAY-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/073,898  
FILING DATE: 06-MAY-1998  
APPLICATION NUMBER: US 08/960,780  
FILING DATE: 30-OCT-1997  
APPLICATION NUMBER: US 60/029,848  
FILING DATE: 30-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Sanders, Jay M.  
REGISTRATION NUMBER: 39,355  
REFERENCE/DOCKET NUMBER: MA-708CD1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 352-375-8100  
TELEFAX: 352-372-5800  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 790 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: Jay90  
SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-09-850-351A-8  
Query Match 2.98; Score 157.5; DB 10; length 790;  
Best Local Similarity 19.7%; Pred. No. 0.0027;  
Matches 138; Conservative 102; Mismatches 217; Indels 245; Gaps 35;  
QY 231 NKIDLYRRRPWYIGQASPKMDLIVDYSGLTKIRISVSEMLTTSDD-DFV 289  
DB 105 NKLDALINMLKVL-----PKITSMUSDWKKQNYALSLQI--EYLSKQLQEIISDKDI 156  
QY 290 NV-ASFSNMDVVS-----CFQHLVOANVRKKVYLKDA-----VNNIT-----A 327  
DB 157 NVNVLINSLTEITPAORIKYVNEKEFEELTFAETSSKKKKDSSPDIDDELTELTELA 216  
QY 328 KGIDYKKGFSFAEQILN--YVNSRANCKNIMLFTDGEERAQETFAKYNKDKKRVF 385

DB 217 KSVT---KNDVDGFEFEYINTFHDVAVGN-----NLFGRSALKTASBLITKEN-----VKT 264  
QY 386 TFSVGO-HNYDRGPIONMACEKGYVEIPSGARITQOELDYLGPPYLAGDKAKOV 444  
DB 265 GSEVGQVNF---LIVLALOKAKAPLITTCCKLLGLADIDYTSIMNHL-----NKEKE 317  
QY 445 QMTNYYLDALELGLVITGTLTPVFNITGONENKNTNKN-----OIL-----GYMGVDS 493  
DB 318 FRYNI-----LPTLSMTFSNPYAKYKGSDEDAKMIKVEKPGHALIGETS 363  
QY 494 LEDI-----KRLTPR-----TLCPNG-----YYF--AIDPNGVYL 523  
DB 364 NDSITVLKVEEAKLKQNVQVNDKSLSEVIYGDMDKLCPPDQSEQIYTTNNITVPFNEVIT 423  
QY 524 HENLQPKNPKSEPTLTLELDALENDIKVEIRKMKMIDGEGEFTFLYKSODERYTDK 583  
DB 424 KIDFTKKKKKTIRYEVTANFYDSSTG---EIDLNKKV--ESSFAEFTLSANDGQVYVPL 478  
QY 584 GNRITYW-TPVNGTDYSIALVLPYSPFYIKAKIEETITQARSKKGKKMDSFTLKPNE 642  
DB 479 GVISSETFLPINGF-----LQAD--E 498  
QY 643 ESGTIFAPROYCDNKLISDNNTFELNFEIDRKTNNPNSCTDILNR-----VLIDAG 698  
DB 499 NSRLITLCKSYRLRLLA-----TDLNKKETLIVPSC 533  
QY 699 FTNELVN-----YMSKKN-----IKGYKAFVYVDGITYRYREAGEVW 740  
DB 534 FISNIVENGSLIEDNLEPWKANKNAVYDHTGCVNGKALYVHDDGISOF---IGDKL 589  
QY 741 QENPTY-----EDSFYKRSIDNDNVYFTAPYRK----- 770  
DB 590 KPKEEYVLYQTVKGPSPHILKDENTGYIHEDTNNNLEDYQITINKRTTGTDLKGYVIL 649  
QY 771 ---SGPAGESGIVASNAVEIYIOGKLLKPAVVGIKIDVNSW 809  
DB 650 KSONGDEAWGDNFLI---LEISPEKLLSPEL---INTNMW 684  
RESULT 14  
US-09-815-242-5898  
Sequence 5898, Application US/09815242  
Patent No. US20020061569A1  
GENERAL INFORMATION:  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Karl L.  
APPLICANT: Zyskind, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.  
APPLICANT: Yamamoto, Robert T.  
APPLICANT: Xu, H. Howard  
TITLE OF INVENTION: Identification of Essential Genes in  
FILE REFERENCE: ELITRA.011A  
CURRENT APPLICATION NUMBER: US/09/815,242  
CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
NUMBER OF SEQ ID NOS: 14110

QY 200 DPELWQVGSATGLARYYPASPVWNSRTPNKIDLYDVRRP-----WTYOGAA 249  
 DB 252 KPIVAAQ-----RIPSCSR--ETAADGELVYLVDYKREKAGELEFVNGYVHFPA 300  
 QY 250 S-----PMDLILVDYSGSVGLTKLIRTSYSEMLETLSDDDFVNVASFSNAOVSC 303  
 DB 301 PDMLDIPKRIEVLIVDYSVMGVMKQVEMAKTILDLRAEDHPSVIDFQONIR--TW 358  
 QY 304 FOHLVQANRNKVKLDVANNITAKGITUYKKGF---SPAFQILANYNVRANCKNIIL 360  
 DB 359 RNDLFQIQHRLOIARVYERKTOPSGGTINELRALRITLNEANNGLIDRNSVSLIL 418  
 QY 361 FIDG-----GERAEIIFAKYKDKRVVFTFSVGQ--HNYDRGPIOMACENKNG----- 408  
 DB 419 VSDGDPYVGLKSLQKNVKNENIQNISLFSIGMGEDVDYDLKRLSNENHIAQRIYQ 478  
 QY 409 -----YYEET--PSIGAIRIN--TOEYIDLVL-----GRPVYLAG--DKAQ 443  
 DB 479 NODTSOLKAFYQVSTPLRNVOFYPHTSVTDYQNNHNYFGSGSEIVYAGKFDPAK- 537  
 QY 444 VQMTNVLDALELGLVITGTLPEVFNITGONENKTNLKLIGVGVGVDSLEDI---RR 499  
 DB 538 -----LDQIE--SVITA-----TSANTQVLETLAQMDLQDPLSKDH 574  
 QY 500 LTPRETLCPNGYFAIDPNCYVLLHPNLOPKNKSQEPVTLDFLDALENDIKVEIRNKA 559  
 DB 575 ADPDETR-KLMAVLTIN---QLAERSLAP--TAAKRRTIRSILOMSLDHIVTPLSIV 629  
 QY 560 IDGSEKERTLVKSOD 577  
 DB 630 IENAGDERMLADAPPOD 647

RESULT 12  
 US-09-850-351A-6  
 Sequence 6, Application US/09850351A  
 Patent No. US2002010080A1

## GENERAL INFORMATION:

APPLICANT: Feltelson, Jerald S.  
 Schnepf, H. Ernest  
 Narva, Kenneth E.  
 Stockhoff, Brian A.  
 Schmeltz, James  
 Loewer, David  
 Dullum, Charles Joseph  
 Muller-Cohn, Judy  
 Stamp, Lisa

TITLE OF INVENTION: No. US2002010080A1 Pesticidal Toxins and Nucleotide  
 Sequences Which Encode These Toxins

NUMBER OF SEQUENCES: 144

CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanichik, Lloyd & Saliwanichik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: FL

COUNTRY: US

ZIP: 32606-6669

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/850,351A

FILING DATE: 07-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/073,898

FILING DATE: 06-May-1998

APPLICATION NUMBER: US 08/960,780

FILING DATE: 30-Oct-1997

APPLICATION NUMBER: US 60/029,848

FILING DATE: 30-OCT-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sanders, Jay M.  
 REGISTRATION NUMBER: 39,355  
 REFERENCE/DOCKET NUMBER: MA-708CD1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 352-375-8100  
 TELEFAX: 352-372-5800  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 789 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 ORIGINAL SOURCE:  
 INDIVIDUAL ISOLATE: 81F  
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
 US-09-850-351A-6

Query Match 2.9%; Score 157.5; DB 10; Length 789;

Best Local Similarity 20.1%; Pred. No. 0.0026;

Matches 138; Conservative 103; Mismatches 231; Indels 215; Gaps 35;

QY 231 NKIDLYDRRRRWYIQGASPKMDLILVDYSGSVGLTKLIRTSYSEMLETLSDG--DFV 289  
 DB 105 NKIDLYDRRRRWYIQGASPKMDLILVDYSGSVGLTKLIRTSYSEMLETLSDG--DFV 156  
 QY 290 NV-ASFSNAOVDS-----CFQHLVQANRNKVKLDA-----VNNIT-----A 327  
 DB 157 NVNVLINSLTLEITRAYQRIKYNNEKFEITPATETTSKVKKDSRADIIDELFETELA 216  
 QY 328 KGITDYKKGFSAPFQOLN--YNSVRANCKNITLFTDGEERRAOEIFAKYKNDKRVVF 385  
 DB 217 KSVT---KNDVGFEEYLTFFHDVAGN-----NLCRSALKTASLETTKEN---VKT 264  
 QY 386 TFSVQ--HNYDGPPIOMACENKGYEELPSIGAIRINTQOEYLDVGRPVYLAGQAKOV 444  
 DB 265 GSEVGVNYP---LIVLALQAKAPLTLTTCRKLGLADIDYTSIMNEHL---NKEE 317  
 QY 445 QMTNVLDALELGLVITGTLPEVFNITGONENKTNLKN-----QLIL-----GVGVGVDS 493  
 DB 318 FRNTI-----LPTLSNFTSNPNYAKKSGDEDAKMIVEAKPGHALVFEIS 363  
 QY 494 LEDI-----KRLPRF-----TLCPNG-----YF--AIDPNCYVLL 523  
 DB 364 NDSITVLKYEAKLKQNYOVDRDSEVLYIGDMDKLCPDQSEJOIYNNIVFPNREVYT 423  
 QY 524 HPLQPKNKSQEPVTLDFLDALENDIKVEIRNKMIDGSEKERTLVKSODERYIDK 583  
 DB 424 KIDFTKMKTLKREYVTAIFYDSGTG---EIDLKRVV--ESSEAEYRILSANDDGYMPL 478  
 QY 584 GNRFTYV--TPVNG---TYSIALVLPYSPFYIRAKIETITQARSKKGMKDESLKP 638  
 DB 479 GYISEFTLPINFGQADENSRLITLCKSYLRELLATDLSN-----KETRLIAP 530  
 QY 639 -----DNFESGTYFTAPRDYCNLDKISDNNE--PLAFNFPIDRKTPNNSCWTDLIN 691  
 DB 531 PSGFINIVENG-----SIEDNLEPMWANKRNEVYH----- 563  
 QY 692 RVLDAGETVELYQVWYKOKNIKGYKARFVYDGGIT-----RYPK----- 734  
 DB 564 -----TGCVNGTKALVYHDSGISQFIDKLPKREYIYQTVYKX 604  
 QY 735 -----EAG---ENWQENPETYEDSFYKSLNDNVYFAPYFNKSGPAYESGLIN 782  
 DB 605 PSILKQENGTGYIHYEDTNNDYOTITKRFETGDLGVYLLIKSQNGDEAWGDNFI 664  
 QY 783 SKAVEIYQCKLKPAAVVGKIDIVNSM 809  
 DB 665 ---LEISPSKELSPDL---INTNM 884

APPLICATION NUMBER: US 08/960,780  
FILING DATE: 30-OCT-1997  
APPLICATION NUMBER: US 60/029,848  
FILING DATE: 30-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Sanders, Jay M.  
REGISTRATION NUMBER: 39,355  
REFERENCE/DOCKET NUMBER: MA-708CD1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 352-375-8100  
TELEFAX: 352-372-5800  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 790 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: 36a  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-850-351A-4

Query Match 2.9%; Score 160.5; DB 10; Length 790;  
Best Local Similarity 19.7%; Pred. No. 0.0016;

Matches 138; Conservative 103; Mismatches 216; Indels 245; Gaps 35;

231 NKIDYVRRPMTYQGAAPKMDLIVDSGSGVGLTFLKRTSVSEMLTSD-DFV 289  
105 NKLDAMTWLRYL-----PKITSMLSVMKONALSIQT--EYLSKOLGDISKLDIT 156  
290 NV-ASENSAODVS-----CFQHLVQAVYRNNKVKLDA-----VNNIT-----A 327  
157 NVNVLINSLTLEITPAORIKYVNEKFPETSPATETSSKVKCGSPANILDELTELTA 216  
328 KGITDYKGFSPFOLLN--YVSRACNKIMLFTGGERAQEITAKYNNKAYVF 385  
217 KSVT---KNDVGFEEYLFTHDVAVN-----NIFGSAKLTASELTITKEN---VTS 264  
366 TFSVQ--HNDRGPIOMACENKGYVYPIPSIGAIRINTOEYLDVIGRPVLAGDKAQV 444  
265 GSEGVNVNF--LIVTALQAKAFLLTTCRKILGLADIDYTSIMNHL-----NKEKEE 317  
445 QMTNYDALDELGLVITGLTFVNTGNEKNKTNK-----QLTL-----GVMGVDS 493  
318 FRVNI-----LPLSNFSPNPAKVGSGDEDAKMIYEAKPGHALIGFEIS 363  
494 LEDI-----KRLTPRF-----TLCPNG-----YYP--AIDNGVYL 523  
364 NDSITVLKVEAKLKONQVOKDSLEVIYGDMDKLCPCDSEQIYITNNIVFNEYVIT 423  
524 HPNIQPKPKSOEPTVLDLDAELNDIKVEIRNNKIDGESGEKTFRTLVKSODERYIDK 583  
424 KIDFTKKKKTIRYEYTAIFYDSSTG--EIDLNNKV--ESSEAEVYKTLSSANDGVYVPL 478  
584 GNRITYW--TPVNGIDYSLALVPTYSFYIAKIEFTITQARSKKCKMKDSEITLKPNEF 642  
479 GVISEFTLITPFG--L-----LQAD--E 498  
643 ESGYTFIAPRDYCNDKISDNTEFLNFEFIDRKTNNPNSCTDLINR-----VLDAG 698  
499 NSRLITLCKSYRELIA-----TDLSNKETKLIIVPSG 533  
699 FTNELYON-----YNSKON-----IKGVKARFVVTGDTITRVYPRAGEW 740  
534 FTSIVVNGSIEDNLEPMKANNNAVVDHTGVTGKALYVHDKGSIQF--ISDNL 589  
741 QENEFY-----EDSFYKSLDNDNYFTAPYFK-----770  
590 KPKREYVYQTVKGRPSIHLIDETGTYIHEDYNNNNIEDYQTIKKRPTTGTDLKGYLL 649  
771 ---SGPAYESGLVWASKAVETIYQGLKLLKPAVVGIRKIDVNSW 809

DB 650 KSONGDEAMGDNFII---LEISPSKLLSPEL-----INTNNW 684

RESULT 11  
US-09-828-423-3

Sequence 3, Application US/09828423

Patent No. US20020099178A1

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

Guegler, Karl J.

Patterson, Chandra

TITLE OF INVENTION: GROWTH-ASSOCIATED TRYPSIN-TYPE

INHIBITOR HEAVY CHAIN PRECURSOR

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: Word Perfect 6.1/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/828,423

FILING DATE: 05-Apr-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/388,774

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Cerrone, Michael C

REGISTRATION NUMBER: 39,132

REFERENCE/DOCKET NUMBER: PF-0505 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 946 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GENEBANK

CLONE: q133985

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-828-423-3

Query Match 2.9%; Score 160.5; DB 10; Length 946;  
Best Local Similarity 19.8%; Pred. No. 0.0021;  
Matches 134; Conservative 107; Mismatches 248; Indels 169; Gaps 31;

33 IKSMVDMQEDIVTLAKTASGVQVQIDYKQDLYTVPPNNAQOLV-----80  
26 LSEFVD--YEDVEL--APGKFQVLAENRRVORSL--PGSEEMEREDVOTLYSYKV 77  
81 -----IAARDIEKLISNRKALVRLALEAEKVQAHQWRDFAFN-----120  
78 OSTTTRMATFTMQSKVYVANSPOQVNVVFDVQIPKCA-----FISNBSMTYDGTFFNS 131  
121 -----EYVYINAK-----DDIDPEKNDSE--PGSORIKRVFIDANFGRO 158  
132 IREKTVGALVYQARAKGTAGIVSSALDMENFTEVAVLPGAKVQFELHYQEVKMKRL 191  
159 ISYOH-----AAVHIPTDIYEGSTIVLNLNMTSALD-----EYFKRRE-----199  
192 GSEHHIYIQPGRKLKHELVDAVWVIEPQGLRFLHVPDFFEGHFDGVPVITSKQOKAHVSF 251

Db 215 GKGHVSFKSLDQQRSCPTCTDLSLNGDFTTYDVNRESGNAVQVNGVHFEAPDGL 274  
OY 248 AASPDMILVDVSGVSGITLKLRTVSSEMLETLDDEDFVAVASFNADPSCF-OH 306  
Db 275 PVPKNAFVIDISGSMAGKRLQOTKEALLRILEDKKEEDYLNFIIFSG---DVSTWKEH 331  
OY 307 LVQANVKKVLDKAVNNITAKITDYKKGSEFAEQLLNYSR-----ANCNKIML 360  
Db 332 LVQATPENIQEARTFVSMEDKGMTNINDGLGISML--NKAREHRIPEKSTSIIV 388  
OY 361 PTGSG---GERAOEIPAKNK--DKKVRVFTSVGQHNDRDPIQMACEKNYYEIP 414  
Db 389 LTTDGDANVSGSRPEKIOENVRAIIGFEPYLNCFG-NMKNYFLEMLNENGEFARRY 447  
OY 415 SIGAIRINTEYLDVLRPMVLAGDKAKQVMTNLYLDALE-----LGLVITGLP 465  
Db 448 EDSADQLQDGFEEVAVANPL-LNGVEKEYPE--NALIDLQNTYQHFDOSSEIVAGRLV 504  
OY 466 VFNITGONENKTNK-----NQLILGVMDVSLDIEDIKRLTPFTLCPNGYTAIDPN-- 518  
Db 505 DEDM---NSFKADYKGGATNDL---TFTEEVMMKEMEK-----ALQERDYIFG---NYI 550  
OY 519 ---GYLLHPNLQPK---NPKSOEPTLDLDALENDIKVEIRKMKIDGSEGEKTFPT 571  
Db 551 ERLMAYLTITQLEKRNNAHGEKENITARALDSLKYHVTPLTSKVYTKPE----- 603  
OY 572 LVKSODERYI-DKGNRTYTWTPVN-GTDYSLALVLPYSPFYI 612  
Db 604 --DNEDEKATADKPGEDAFKATPVSPAMSYLTSTQPPONPYVV 644

RESULT 9  
US-09-864-761-36461  
; Sequence 36461, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aecmca-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263,6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30

;; PRIOR APPLICATION NUMBER: PCT/US01/00670  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: US 60/234,687  
;; PRIOR FILING DATE: 2000-09-21  
;; PRIOR APPLICATION NUMBER: US 09/608,408  
;; PRIOR FILING DATE: 2000-06-30  
;; PRIOR APPLICATION NUMBER: US 09/774,203  
;; PRIOR FILING DATE: 2001-01-29  
;; NUMBER OF SEQ ID NOS: 49117  
;; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
;; SEQ ID NO 36461  
;; LENGTH: 35  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; OTHER INFORMATION: MAP TO AC008283.2  
;; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.5  
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.67  
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.7  
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.8  
;; OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 1.2  
;; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2  
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3  
;; OTHER INFORMATION: EST\_HUMAN HIT: AM051755.1, EVALU 3.00e-04  
;; OTHER INFORMATION: SWISSPROT HIT: P54290, EVALU 6.00e-15  
US-09-864-761-36461

Query Match 3.3%; Score 182; DB 10; Length 35;  
Best Local Similarity 97.1%; Pred. No. 4.9e-07;  
Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 141 GSORIKPVFIDANFGQISTYQAAVHIPTDIYEG 175  
Db 1 GSORIKPVFIEDANFGQISTYQAAVHIPTDIYEG 35

RESULT 10  
US-09-850-351A-4  
; Sequence 4, Application US/09850351A  
; Patent No. US20020100080A1  
; GENERAL INFORMATION:  
; APPLICANT: Feltelson, Jerald S.  
; APPLICANT: Schnepf, H. Ernest  
; APPLICANT: Narva, Kenneth E.  
; APPLICANT: Stockhoff, Brian A.  
; APPLICANT: Schmeltz, James  
; APPLICANT: Loewer, David  
; APPLICANT: Dullum, Charles Joseph  
; APPLICANT: Muller-Cohn, Judy  
; APPLICANT: Stamp, Lisa  
; TITLE OF INVENTION: No. US20020100080A1 Pesticidal Toxins and Nucleotide  
; Sequences Which Encode These Toxins  
; NUMBER OF SEQUENCES: 144  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: US  
; ZIP: 32606-6669  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/850,351A  
; FILING DATE: 07-May-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 09/073,898  
; FILING DATE: 06-MAY-1998



RESULT 5  
US-09-864-761-44281  
Sequence 44281, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: Aecm1ca-X-1  
CURRENT FILING DATE: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR FILING DATE: 2000-02-04  
PRIOR FILING DATE: US 60/180,312  
PRIOR FILING DATE: 2000-05-26  
PRIOR FILING DATE: US 60/207,456  
PRIOR FILING DATE: 2000-08-03  
PRIOR FILING DATE: US 09/632,366  
PRIOR FILING DATE: 2000-10-04  
PRIOR FILING DATE: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR FILING DATE: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR FILING DATE: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR FILING DATE: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR FILING DATE: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR FILING DATE: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR FILING DATE: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR FILING DATE: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR FILING DATE: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR FILING DATE: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR FILING DATE: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR FILING DATE: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR FILING DATE: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR FILING DATE: US 09/774,203  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 44281  
LENGTH: 51  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC006145.2  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1  
OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 0.86  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.91  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.93  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.81  
OTHER INFORMATION: SWISSPROT HIT: P54289, EVALUATE 4.00e-25  
OTHER INFORMATION: EST\_HUMAN HIT: H86016.1, EVALUATE 1.00e-02  
US-09-864-761-44281  
Query Match 5.0%; Score 272; DB 10; Length 51;  
Best Local Similarity 100.0%; Pred. No. 3.1e-13;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 859 IGRFGEIDPSLMRLVNIISYAFNKSVDYOSVCEPAGAPKOGAGHSAYV 909  
DB 1 IGRFGEIDPSLMRLVNIISYAFNKSVDYOSVCEPAGAPKOGAGHSAYV 51  
RESULT 6  
US-09-864-761-38267  
Sequence 38267, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO  
FILE REFERENCE: Aecm1ca-X-1  
CURRENT FILING DATE: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR FILING DATE: 2000-02-04  
PRIOR FILING DATE: US 60/180,312  
PRIOR FILING DATE: 2000-05-26  
PRIOR FILING DATE: US 60/207,456  
PRIOR FILING DATE: 2000-08-03  
PRIOR FILING DATE: US 09/632,366  
PRIOR FILING DATE: 2000-10-04  
PRIOR FILING DATE: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR FILING DATE: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR FILING DATE: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR FILING DATE: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR FILING DATE: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR FILING DATE: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR FILING DATE: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR FILING DATE: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR FILING DATE: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR FILING DATE: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR FILING DATE: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR FILING DATE: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR FILING DATE: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR FILING DATE: US 09/774,203  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 38267  
LENGTH: 53  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC008283.3  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.86  
OTHER INFORMATION: EST\_HUMAN HIT: AL134437.1, EVALUATE 3.00e-24  
OTHER INFORMATION: SWISSPROT HIT: P54289, EVALUATE 4.00e-25  
US-09-864-761-38267  
Query Match 5.0%; Score 272; DB 10; Length 53;  
Best Local Similarity 100.0%; Pred. No. 3.3e-13;  
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 918 HGLDPRKAL-----SAKKWIMTELIVLVEF-----NCSWMSHSDMTAKAKOIKOTLE 967  
 QY 961 SCITEQYQFFDNDKSFSGVLDCGNCRIEHEKIMNTNLIPIVIESKQTCDDT 1016  
 Db 968 PCDETPAFVSERTIKETTGINCEDCSKSFVIOQLPSSMLFVAVDS--SCLCES 1021

## RESULT 3

US-09-875-423-2  
 ; Sequence 2, Application US/09875423  
 ; Patent No. US20020081657A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Curtis, Roy A.J.  
 ; TITLE OF INVENTION: 21784, A NOVEL HUMAN CALCIUM CHANNEL  
 ; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF  
 ; FILE REFERENCE: 10448-059001  
 ; CURRENT APPLICATION NUMBER: US/09/875,423  
 ; CURRENT FILING DATE: 2001-06-05  
 ; PRIOR APPLICATION NUMBER: US 60/209,257  
 ; PRIOR FILING DATE: 2000-06-05  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; TYPE: PRF  
 ; LENGTH: 1091  
 ; ORGANISM: Homo sapiens  
 ; US-09-875-423-2

Query Match 20.4%; Score 1111; DB 10; Length 1091;  
 Best Local Similarity 28.7%; Pred. No. 3e-71;

Matches 308; Conservative 224; Mismatches 417; Indels 124; Gaps 38;

QY 3 AGCLALILTLFOSLIGBSSOEPPSAVTIKSVWDMQEDLVTLAKTASGVNQLVDIYE 62  
 Db 14 ASALLAAL-LYALGDVYRSEQIPLSV-VLMAAFGEGETKSTAYKSSQLQKKYK 71  
 QY 63 KYODLYTEPNNAQOLVEIARDIEKLNSKSLVRLALEKQVQAHOHREDFASNEV 122  
 Db 72 EYKXVAIEHIDGIDLVLKKLAKNMEHFKKSEAVRRLVEAEHKLHEPDADL--QY 128  
 QY 123 VYTNK--DDIDPEKNDSEPSQRIKPFVIDDANGROISYOHAAVHIPTDIYEGSTVL 180  
 Db 129 EYFNVLINERDKDGNFELKEFT--LAPNDHFNMLPVNLSLSQVQPTMMYKKDPAIV 186  
 QY 181 NEMNTSALDIEVFKKREDEPSILMOVGSGATGLARYYPASPVWDSNTPNKIDLYVVR 240  
 Db 187 NGYVSESLNKVFYDNEFDPSLIMQYFGSAKGEFFROYPGIKWEPDE--NGVIAFCRN 243  
 QY 241 RPWYIOGAASFMDLILVDVSGVSGTLKLTISVSEMLETSLDDDFVNVASNSNAOD 300  
 Db 244 RKWTIOATSPKDVYLLVDVSGSKGLRLITAKOTVSSILDTLDDDFNTIAYNEELHY 303  
 QY 301 VS-CFO-HLVQANRANKVLDAAVNNITAKGITDYKKGSFAFQOLNINYSRAN--CNK 356  
 Db 304 VEPCLNGTLVQADRTNNEHREHDKLFAKIGMDIALNAFNLSDENHTGGGSCSQ 363  
 QY 357 IIMFTDGGERRAEITAKYV-KKKYRVETFSVGOHNYDRGPLOMACENKGYEIPS 415  
 Db 364 AIMLTGADVDTYDTITAKITMPPRKVIFLYLIGREAPADNLKMAACANKGFFTOIST 423  
 QY 416 IGAIIRINTOEYLDVGRPNVLADGKAKOVOMTNYLDAL-----ELG--LVITGL 464  
 Db 424 LADVOENMEYLVLSRPVY--DQEHVYVTEAYIDSTLRQAKLITDDGPPVLMNTVAM 481  
 QY 465 PVFNITQONENKTYLAKQULILGVGVDSVLEDKRLTPRETLCPNGYFAIDPNGVYLH 524  
 Db 482 PVFS---KONETRSKG-ILGVGVGVDPVKEELKITPKYKLGHYAFAITNGVYLH 536  
 QY 525 PNLQ---PKPKPSQEP--VTLDFLDAELNDIYEIRNKKIDGESGKTRPTLVKSODER 579  
 Db 537 PELRLIYEEOKKKRKKRPYSSVDLSEVEMEDRDV-LNNAMVNRKTGK--FSMEVK---K 589

QY 580 YIDKGNRT-----YTWTPVNGTOYSLAVLP-YSFYITAK--IEETIQASKSKGM 630  
 Db 590 TYDKKRVLYMTNDYIYDIDKGTPELSGVALSRGKXFFFGNVTIERGL----- 639  
 QY 631 KDSEITLKDNEEESGYFIAPRDYCN-DLKISDNTTEFLNMFNEIPRKFPNNPCNTDL 689  
 Db 640 -----HDLHPDVSILADEMSYCNLDLHREHRLSLLEAKIYKKEP-LLOCKREL 690  
 QY 690 INRVLLDAGFTNELVQNTWS-----KOKNIKYKARPVYTDGRTYRP----- 733  
 Db 691 IOEVLFDA-VVSAPLEAVWTSLALNKSSENSDKGEVAFIAGRTLSRLNLFVGAEOQLNQ 749  
 QY 734 --KEAGENMOENPETEESFYKRSIDN--DNVYTAAYFNKSGGALESGLMVAEYI 789  
 Db 750 DELKAGDENLEFNADHPLMTYRRAEQIPGSFYISIP--STGVNKSNNVYASTSIOL 807  
 QY 790 IQGILKPAVVGIRIDVNSWIENTFTKTSIRPCAGPYCDKRNSDVMDVYILDGCGFLM 849  
 Db 808 DERKSPVVAAGIQMKLEFFQKFWTASRQCSLIDGCSISCDDETYNCLYLDNNGFTLV 867  
 QY 850 ANHDYTMQIGRFGELDPSLMRLVNI SYAFKSTDYOSVCEPGAAPKGA-GRSAY 908  
 Db 868 S--EDYT-QTDPFGELEGAVNNKLTMGSEFKRTITLYDOAMCRANKESSDCAHGLIDPY 924  
 QY 909 VPSIADILHIGMATTAAMSIIQOFLSTLTPRLLAEVEMEDDFTASLSK-----QSCI 963  
 Db 925 -----NAFLSAKVMIMTELIVLVEF-----NCSWMSHSDMTAKAKOIKOTLEPCD 970  
 QY 964 TEQYQYFFDNDKSFSGVLDCGNCRIEHEKIMNTNLIPIVIESKQTCDDT 1016  
 Db 971 TEYAFVSERTIKETTGINCEDCSKSFVIOQLPSSMLFVAVVDS--SCLCES 1021

## RESULT 4

US-10-005-168-2  
 ; Sequence 2, Application US/10005168  
 ; Patent No. US20020133840A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brennan, Thomas J.  
 ; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING DISRUPTIONS  
 ; FILE REFERENCE: R-10  
 ; CURRENT APPLICATION NUMBER: US/10/005,168  
 ; CURRENT FILING DATE: 2001-12-04  
 ; PRIOR APPLICATION NUMBER: US 60/299,668  
 ; PRIOR FILING DATE: 2001-06-19  
 ; PRIOR APPLICATION NUMBER: US 60/282,685  
 ; PRIOR FILING DATE: 2001-04-09  
 ; PRIOR APPLICATION NUMBER: US 60/254,802  
 ; PRIOR FILING DATE: 2000-12-11  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; TYPE: PRF  
 ; LENGTH: 223  
 ; ORGANISM: Mus musculus  
 ; US-10-005-168-2

Query Match 6.8%; Score 369.5; DB 12; Length 223;  
 Best Local Similarity 40.9%; Pred. No. 2.9e-19;

Matches 65; Conservative 34; Mismatches 59; Indels 1; Gaps 1;

QY 878 SYVAFNKSYDYOSVCEPGAAPKGAHRSAYVPSIADILHIGMATTAAMSIILOOFLSL 937  
 Db 2 SFYTRKESYDYQAAACAPQPPGNLGAAPRVFVPTIADPLNTLMAWLSAAMSILFOOLLGL 61  
 QY 938 TTPRLLEAVEMEDDFTLSKQSCITEQYQYFFDNDKSFSGVLDCGNCRIEHEKIM 997  
 Db 62 IYHSWFOADPAEAEG-SPEYTRSSCYMKQYQYFSGVNASVALIDCGNCRIEHEKIM 120  
 QY 998 NTNLIPIVIESKQTCDDTIRLLIOAEDTSIDGPPCDWYK 1036  
 Db 121 NTNLIPIVIESKQTCDDTIRLLIOAEDTSIDGPPCDWYK 159



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Db 241 RPYIGGASPKMLLIVDSSVSGLTLLKLTSTSEMLFTLSDDETFNVAASFNSNAD 300
Qy 301 VSCFQHLVQANVRNKKVYLKDAVNNITAKGITYDKGFSAPBQLLNVNVRANCKNTIML 360
Db 301 VSCFQHLVQANVRNKKVYLKDAVNNITAKGITYDKGFSAPBQLLNVNVRANCKNTIML 360
Qy 361 FTGGERBOEITAKXNKKKRVVFVFSYGOHNYDGRPIOMWACENKGYIEIPSGAIR 420
Db 361 FTGGERBOEITAKXNKKKRVVFVFSYGOHNYDGRPIOMWACENKGYIEIPSGAIR 420
Qy 421 INTQEXYLDVLRPMVLADGRKAKOVMTNYYLDALDELGLYTGTLTPFNITGONENKTNLK 480
Db 421 INTQEXYLDVLRPMVLADGRKAKOVMTNYYLDALDELGLYTGTLTPFNITGONENKTNLK 480
Qy 481 NOILICVMGVDSLEDIKLTLPRTLCPNGYFPAIDPNGYVLLHPNLQPKNKSGEPVTL 540
Db 481 NOILICVMGVDSLEDIKLTLPRTLCPNGYFPAIDPNGYVLLHPNLQPKNKSGEPVTL 540
Qy 541 DFLDAELNDIWEITRNKMIIDEGSEKERTLVKSODEXYIDKGRNTYTWTYNGTIDSL 600
Db 541 DFLDAELNDIWEITRNKMIIDEGSEKERTLVKSODEXYIDKGRNTYTWTYNGTIDSL 600
Qy 601 ALVLPYSEYITKAKIETITQARSKKGMKDETLKPNFEESGYTFIAPRDYCNDLKI 660
Db 601 ALVLPYSEYITKAKIETITQARSKKGMKDETLKPNFEESGYTFIAPRDYCNDLKI 660
Qy 661 SNNNPFLLNPFEDIRKTPNPNPSCNTDLINRVLLDAGFTNELVONVMSKORNIKGVAR 720
Db 661 SNNNPFLLNPFEDIRKTPNPNPSCNTDLINRVLLDAGFTNELVONVMSKORNIKGVAR 720
Qy 721 FVYTDGIRTRYPKRAGEWMOENPETIEDSEFKRSIDNNONYTAPYFKSPGAYESGI 780
Db 721 FVYTDGIRTRYPKRAGEWMOENPETIEDSEFKRSIDNNONYTAPYFKSPGAYESGI 780
Qy 781 MYSKAVEIYIOGKLLKPAVVGIRKIDVNSWIEFTKTSIRDPAGVCCCKRSDVMDCVI 840
Db 781 MYSKAVEIYIOGKLLKPAVVGIRKIDVNSWIEFTKTSIRDPAGVCCCKRSDVMDCVI 840
Qy 841 LDDGGELMANHDYTNQGRFGEIDPSLMHLVNIISVYAFNKSYDYQSCPCGAAPKO 900
Db 841 LDDGGELMANHDYTNQGRFGEIDPSLMHLVNIISVYAFNKSYDYQSCPCGAAPKO 900
Qy 901 GAGHSAAVPSIADILHIGMWATAAMSTLOOFLSTLTFPRLEAVEMEDDFTASLSKO 960
Db 901 GAGHSAAVPSIADILHIGMWATAAMSTLOOFLSTLTFPRLEAVEMEDDFTASLSKO 960
Qy 961 SCITEQTOYFEFNDKSKFSGLVDCGNCRIPEVEKLMNTLFIIVESKGTCPDTRLII 1020
Db 961 SCITEQTOYFEFNDKSKFSGLVDCGNCRIPEVEKLMNTLFIIVESKGTCPDTRLII 1020
Qy 1021 QAEQTSIDGPPCDMYK 1036
Db 1021 QAEQTSIDGPPCDMYK 1036

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# RESULT 2

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US-09-875-423-5
; Sequence 5, Application US/09875423
; Patent No. US20020081657A1
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Rory A.J.
; TITLE OF INVENTION: FAMILY MEMBER AND USER THEREOF
; FILE REFERENCE: 10448-059001
; CURRENT APPLICATION NUMBER: US/09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,257
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1091

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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-875-423-5
Query Match 20.4%; Score 1112; DB 10; Length 1091;
Best Local Similarity 28.9%; Pred. No. 2,56-71;
Matches 311; Conservative 224; Mismatches 411; Indels 130; Gaps 39;
Qy 3 AGCLIALTLTFLFOSLLIPSSQEPFPAVITKSWDMQOEVLVLTATASGVNLVDYIE 62
Db 14 ASALLA-TALLYAALGDVVRSEQDPLSV-VKMAASAFGKIKIAKYSQSLQKKK 71
Qy 63 KYODLTYEPNNAQOLVEIARIDIEKLLSNSKALVRLALEAEKVOAHOHREDPASNEV 122
Db 72 EYKQVAAIEEIDGLQYVKKLAKIMEEMPHKSEAVRRLVEAEBAHLKHEFDAL--QY 128
Qy 123 VYVNAK--DIDLPEKNDSEPSQRIKPFIDANFGROIQOAAVAIIPDIYEGSTIVL 180
Db 129 EFNNAVLINEKDKGNFLELKEFT--LAPNDHFNMLPVNISLSDYQVPTMYNKKDPAIV 186
Qy 181 NELNMTSALDEVFKKNREDEPSILMOVFSATGLARYPASPWYDNRTPNKTIDLYDVR 240
Db 187 NGVYWSLSLNVFVQDNFDRDPSLIWQYFGSAKGFQYPGIKWEPDE--NGYIAFDGRN 243
Qy 241 RPYIIGGASPKMLLIVDSSVSGLTLLKLTSTSEMLFTLSDDETFNVAASFNSNAD 300
Db 244 RKWYIOAATSPKDVYLLVDVSGSMKGLRLTAKQTVSSILDTLGDGDDFFNITYNELHY 303
Qy 301 VS-CEO-HLVQANVRNKKVYLKDAVNNITAKGITYDKGFSAPBQLLNVNVRAN--CNK 356
Db 304 VEPCLNGTLVQADRTNKEHEFHLDKLEAKIGIMDALNEAFNISLDFNHTGSGISCSQ 363
Qy 357 IIMFTDGEERAOEIPAKYN-KDKRVVFEVFSYGOHNYDGRPIOMWACENKGYIEIP 415
Db 364 AIMLITGAVDTYPTIFAKYVWPKRVIRIFTYILIGREAAADNLKMAACANKGFQIOIS 423
Qy 416 IGARINTQEXYLDVLRPMVLADGRKAKOVMTNYYLD-----ALEGLYI--TGT 464
Db 424 LADQEVNMEYLVLSRPKVI--DOEHVYVTEAVYIDSTLPQAKLADDOGLVIMTTVAM 481
Qy 465 PVFNITGONENKTKMLKQOLIGVWGVDVSLDIKRLPRTLCPNGYFPAIDPNGYVLLH 524
Db 482 PVFS-----KQNETSKG-TLGGVGTDPYKELKLTIPKRLIGHGAFTYNGYLTH 536
Qy 525 PNIQP---KNKRSQEP--VTLDPLDAELNDIWEITRNKMIIDEGSEKERTLVKSODER 579
Db 537 PELRPLVEEGKRRKRPYSSVDSLSEVEMEDRDY-LNMAVNNKTKG--FSMEVK-----K 589
Qy 580 YIDGNT-----YTWTPVNGDYSIALVLP--YSEYITKAK--IEETITQARSKGKM 630
Db 590 TVDKGRVLYWNTDYTYTDIKTPFSLGVALSRGHCKYFFRGVWTTIEGL----- 639
Qy 631 KDSFTLKPDPNFEESGYTFIAPRDYCN-DLKISDNNTEFLNPFEDIRKTPNPNPSCNTDL 689
Db 640 -----HDLHPDVSADLDEWSTCNTDLHPERHHSQLEAIVLYLKGRP-LLOQDEL 690
Qy 690 INRVLLDAGFTNELVONVMS-----KQNIKGVKARFVYTDGIRTRYV----- 733
Db 691 IOEVLFDA-VVSAPIEAYWISLANKSENSDKGEVAFLCTRGISRLINLFVABQLTNO 749
Qy 734 --KAGENMOENPETYDSTYKRSLDN--DNYFTAPY---FNKSGPGAYESGIVAKRA 785
Db 750 DFLKAGDENIFNADHPPLMYRRAAEIOASFYISIPFSGTVNKS-----NVYASFS 803
Qy 786 VEIYIOGKLLKPAVVGIRKIDVNSWIEFTKTSIRDPAGVCCCKRNSDVMOCVILLDDG 845
Db 804 IQLDKKSYVAVAVGIOKMLEFFQKRFWTASQKASLDGKSCISCDDETVNCTYLLDNG 863
Qy 846 FLMANHDYTNQGRFGEIDPSLMHLVNIISVYAFNKSYDYQSCPCGAAPKQAGAR 905
Db 864 FILVVS--EDYT-OTGDFGEVGAVMNKLITGMSFRLITLYDQAMCR--ANKESDSA 917
Qy 906 SAYVPSIADILHIGMWATAAMSTLOOFLSTLTFPRLEAVEMEDDFTASLSK-----Q 960

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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2003, 14:22:34 ; Search time 7.66041 Seconds

(without alignments)  
2998.192 Million cell updates/sec

Title: US-10-090-827-7

Perfect score: 5446

Sequence: 1 MAAGCLLALTLTLFQSLILG.....RLLIQAEQTSDEGPDPCDMVK 1036

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 129505 seqs, 22169297 residues

Total number of hits satisfying chosen parameters: 129505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

1: PublishedApplications\_AA.\*  
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3: /cgn2\_6/ptodata/2/pubpaa/PCOT\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5380	98.8	1091	10	US-09-875-423-4
2	1112	20.4	1091	10	US-09-875-423-5
3	1111	20.4	1091	10	US-09-875-423-5
4	369.5	6.8	223	12	US-10-005-168-2
5	272	5.0	51	10	US-09-864-761-38267
6	272	5.0	51	10	US-09-864-761-38267
7	190	3.5	35	10	US-09-864-761-38267
8	185	3.4	885	10	US-09-828-423-5
9	182	3.3	35	10	US-09-864-761-38267
10	160.5	2.9	790	10	US-09-828-423-4
11	160.5	2.9	946	10	US-09-828-423-3
12	157.5	2.9	789	10	US-09-850-351A-6
13	157.5	2.9	790	10	US-09-850-351A-8
14	152	2.8	1349	10	US-09-815-242-5898
15	152	2.8	1349	10	US-09-815-242-5898
16	146.5	2.7	1781	9	US-09-995-749A-2
17	140	2.6	3169	9	US-10-114-170-257
18	133.5	2.5	764	9	US-10-105-695-4
19	133.5	2.5	764	9	US-10-105-694-4

20	133.5	2.5	764	10	US-09-747-521-4	Sequence 4, Appl1
21	133.5	2.5	764	12	US-10-106-014-4	Sequence 4, Appl1
22	131.5	2.4	2125	10	US-09-919-172-29	Sequence 29, Appl1
23	130.5	2.4	1323	10	US-09-801-368-34	Sequence 34, Appl1
24	130	2.4	3712	9	US-10-108-605-103	Sequence 103, Appl1
25	127.5	2.3	956	9	US-10-121-032-63	Sequence 63, Appl1
26	126	2.3	876	10	US-09-815-242-12623	Sequence 12623, A
27	124	2.3	2285	10	US-09-932-183A-2	Sequence 2, Appl1
28	118.5	2.2	1183	9	US-09-870-759-45	Sequence 45, Appl1
29	118	2.2	1050	9	US-10-050-183-9	Sequence 9, Appl1
30	118	2.2	5795	10	US-09-815-242-12610	Sequence 12610, A
31	117	2.1	3594	9	US-10-150-821-4	Sequence 4, Appl1
32	117	2.1	3594	10	US-09-911-842-4	Sequence 4, Appl1
33	116	2.1	911	10	US-09-828-423-4	Sequence 4, Appl1
34	114	2.1	549	10	US-09-712-363-190	Sequence 190, Appl1
35	114	2.1	698	9	US-09-801-220-4	Sequence 4, Appl1
36	113.5	2.1	1430	10	US-09-740-274-6	Sequence 6, Appl1
37	113.5	2.1	3571	9	US-10-150-821-2	Sequence 2, Appl1
38	113.5	2.1	3571	10	US-09-911-842-2	Sequence 2, Appl1
39	113	2.1	1066	9	US-09-423-126-3	Sequence 3, Appl1
40	113	2.1	1066	10	US-09-280-197-5	Sequence 5, Appl1
41	112	2.1	2835	10	US-09-885-535-4	Sequence 10, Appl1
42	111.5	2.0	836	9	US-09-858-525A-10	Sequence 2, Appl1
43	111.5	2.0	871	9	US-09-858-525A-2	Sequence 32, Appl1
44	111.5	2.0	871	10	US-09-850-351A-32	Sequence 29, Appl1
45	111	2.0	811	9	US-10-011-588-29	

## ALIGNMENTS

### RESULT 1

US-09-875-423-4  
; Sequence 4, Application US/09875423  
; Patient No. US20020081657A1  
; GENERAL INFORMATION:  
; APPLICANT: Curtiss, Rory A.J.  
; TITLE OF INVENTION: 21784, A NOVEL HUMAN CALCIUM CHANNEL  
; FILE OF INVENTION: FAMILY MEMBER AND USRS THEROF  
; FILE REFERENCE: 10448-059001  
; CURRENT APPLICATION NUMBER: US/09/875,423  
; CURRENT FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US 60/209,257  
; PRIOR FILING DATE: 2000-06-05  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 1091  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-875-423-4

Query Match	98.8%	Score 5380	DB 10	Length 1091
Best Local Similarity	98.7%	Pred. No. 0		
Matches 1023	Conservative	6	Mismatches	7
			Indels	0
			Gaps	0
QY	1	MAAGCLLALTLTLFQSLILGSSOPPPSAVIRKQVWKMOMEDVTLAKTASGVQIYDI	60	
DB	1	MAAGCLLALTLTLFQSLILGSSOPPPSAVIRKQVWKMOMEDVTLAKTASGVQIYDI	60	
QY	61	YKRYODLVYEPNNARQVEIARDIEKLSNRSAFYALAEAKVOAHQWREDFASN	120	
DB	61	YKRYODLVYEPNNARQVEIARDIEKLSNRSAFYALAEAKVOAHQWREDFASN	120	
QY	121	EVVYNNAKDDLPKRNDSFGSQRIRKPFIDANGROISYQHAHVHPTIYEGSTVL	180	
DB	121	EVVYNNAKDDLPKRNDSFGSQRIRKPFIDANGROISYQHAHVHPTIYEGSTVL	180	
QY	181	NEIWNMTSALDEVFKKRNREDFSLIMQVGSAGLRRYPASPVWNSRTPKIDYDVR	240	
DB	181	NEIWNMTSALDEVFKKRNREDFSLIMQVGSAGLRRYPASPVWNSRTPKIDYDVR	240	
QY	241	RPWYIOGAASPRDMLIVDVSGSVGLTLKIRTSVSEMLETLSDDFEVNVAFSNSAOD	300	

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Db 211 LF-----GRMSVVGITNAHL-LLELAPQAHAI-VKRYVAQSEPMDLT-VQ 254
Qy 481 NQILIGVMGVDSLEDIRKAPRFTLCPNGYFAIDPNGYVLLHNPQKPKSQE----- 536
Db 255 NQALIEVVLGDLMTDOERV-----LLNLVLDQLLPQOHVIGQVQIYDDPASQTNLL 309
Qy 537 ----PYTDLFDELENDIKVEIRKMKMDGSEKTE--FRLLVKSQDERITDKGRITYTW 590
Db 310 SUPPLPTIO-VQTOYQSTPDVQVQESILTLAKYRQTOIAEKLKMGDQGAATMLQTA 368
Qy 591 TPVNGTDSLALVLPYSEFYIKAKIEFTITQARSKGKMDSELTLP 638
Db 369 TLOMGDKNGATITQTN---TRLOSGEDLSGDKRKTRMWSKTTLP 413

RESULT 15
140884
cytotoxin L - Clostridium sordeilli
C.Species: Clostridium sordeilli
C.Date: 16-Aug-1996 #sequence revision 16-Aug-1996 #text change 15-Oct-1999
C.Accession: 140884
R.Green, G.A.; Schue, V.; Montell, H.
Gene 161, 57-61, 1995
A.Title: Cloning and characterization of the cytotoxin L-encoding gene of Clostridium sc
A.Reference number: 140884; MUID:95369733; PMID:7642137
A.Accession: 140884
A.Status: preliminary; translated from GB/EMBL/DBU
A.Molecule type: DNA
A.Residues: 1-2364 <RES>
A.Cross-references: EMBL:X82638; NID:g1000694; PID:CAAS7959.1; PID:g1000695
C.Superfamily: cpl repeat homology
C.Keywords: cytotoxin

Query Match 2.9%; Score 160.5; DB 2; Length 2364;
Best Local Similarity 18.0%; Pred. No. 0.64;
Matches 219; Conservative 142; Mismatches 346; Indels 513; Gaps 58;

Qy 6 LALALLFLFOSLLIGPSOEPSPASVITKSWDKMOEDLVTLAKTASGVNOLVD----- 59
Db 1066 IMAVMTLTAATAIV-----TSALGASGFSIL--LVPLAGISAGIPSLVNNELLQ 1114
Qy 60 ----IYKYODLYVEPNNAKOLV-----EIAARDIEKLNSRKALVRLAE 105
Db 1115 DKATVVIDPFKHTSLAETEGATLLDDKIIMPQDVLVSEID--FNNSITLGCETMRA 1172
Qy 106 KYQAAHQRRED---FASNEVVY-----YNA---KDDLDPEK----- 135
Db 1173 EGGSGHTLDDIDHFSSPSITRYRKPMLSTYDVNLKKEKIDFSKDLAVLNAAPRVRGY 1232
Qy 136 -----NDSEPGSQRIKP-----VFIDANFGR-QISYQAAVHIPTD 171
Db 1233 EMGWTPGRFSLDNDGTCKLIDRIHDEGQFYWRPAFIADALITKLKRPREDYTVRIMLD 1292
Qy 172 IYEGSTIVLNLMTSALDEVFKKREDPRLMVGESATGLAAYPASPWVNSKTPN 231
Db 1293 GNTRFPIV-----PVITTEQIRKN-----LSYSFYS--GGSYSLSPYNNM----- 1333
Qy 233 KIDLVDVRRRPVYIGGAASPKDMLLVDSGSVSGTLKLRISVPMLETLSDDDFVNV 291
Db 1334 -IDLNLVENDTW-----VIDVNVKNITTESDEIQGELIENI----- 1371
Qy 292 ASFNSNADVSCFOHLVOANVRNKKVLKDAVNNITAK--GITDYKKGSPAFBOLLNVN 348
Db 1372 -----LSKRLINIEDNKII--LNNHTINFGDINESNRFTISLFTLEDIN 1413
Qy 349 -----VSRA-----NCKIIMLFTD-----GGEERQELIFA-----KYN- 377
Db 1414 IITIEDLVSKSKILLSGCKMLIENSSDIQOKIDHIGFNGEHOXYIPYSYIDMETKYNG 1473
Qy 378 ---KDKKRVVETFSVGOHNDYDGPQIOMMACENKGYEYIPISGAIRINTQEVLVIGRPM 434
Db 1474 FIDYSKKKGLFTAEFSNSIIFN--IYMPDSNNLFTYSSKDLKDIRIINK-----GDVK 1525

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Qy 435 VLADGKAKQ-----VQWTVNYDLALELGLVITGTLPVENITGQENKTNL 479
Db 1526 LLICNVFKDKDMKYSLSFTIEDTNTIKINGVYLD-----NGVAQILKFMNNAKALMT 1578
Qy 480 KNOILIGVMGVDSLEDIRKAPRFTLCPNGYFAIDPNGYVLLHNPQKPKSQEPT 539
Db 1579 SNSIMNLESTINIK-----NIFYNNLDPNLEFLDTNF----- 1611
Qy 540 LDFLDAELENDIKVEIRKMKMDGSEKTEPTLVKSODERYIDKGNRTYTPWNGTDS 599
Db 1612 -----IISGSNSIGQFE-LICQDKN----- 1631
Qy 600 LALVLPYSEFYIAKIEFTITQARSKGKMDSETLKPNFEESGYTAPRQYNDIK 659
Db 1632 ---IQP---YFINFKIKET-----SYTLVGNRON---LIVEPSYHLD-- 1666
Qy 660 ISDNTEFEILNFE---FIDR---KTPNNSCNTDLIN-----RVLLDAGE 699
Db 1667 -SGNISSTVINEFSOKLYLIDRYVKNVYIAPNLYTDEINITPYKPNYICPEVIILDANT 1725
Qy 700 TNE-----LVQNYW-----SKQKINIGVAKRPVVDGITRVYPREAGE 738
Db 1726 INEKINNINDLSIRYWDNDGSDLLILIANSEEDNOPVAKIRY-----NFKSDTAA 1778
Qy 739 ---NMQENPE-----TYEDSFYKR---SLDNDNYVTAPYFNKSGPGA 775
Db 1779 DKLSFNFSKQDVSVSKIISTFSLAAYSDGFYEFGLVSLDND-----YFINSFGN 1831
Qy 776 YESGIMSKAVEYIIOCKL--LKP---AVVGT-KIDVNSMINETKTSIRDCAQVCD 828
Db 1832 MVSGL-----IYINDSLYFKRPPKNNLITGFTTIDGNKYFPDPKSG---AASI- 1877
Qy 829 CKRNSDVMDCVILDDGGFLMANHDDYTN---QIG-----RPF---GEIDPSLMR 872
Db 1878 -----GEIITDGDYFNKOGILQYVINTSDGLAFAPAGLIDENLGS 1921
Qy 873 HLNYI-----SVYAFNKSVDYOSVCEPGAAPKQAGHRSAYVDSIADLIHGMWATA 924
Db 1922 ESYVFIKLNIDGKIYFEDNY-----RAA 1946
Qy 925 AAMSILQGFLLSTFFPRLLEAVEMEDDFTASLSKSCITEOTOFPPDNDKSFSGVLOC 984
Db 1947 VEMKLLD-----DETYFNPKTGEALKGLHOI 1973
Qy 985 GNCSTRIFHEKLMNTNLFIT 1004
Db 1974 GDNKYYFDDNGIMQTFIT 1993

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Search completed: February 10, 2003, 14:21:53  
 Job time : 27.7185 secs

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 A:Residues: 1-889 <NA>  
 A:Cross-references: DDBJ:D89287  
 A:Experimental source: Liver  
 A:Accession: PC4486  
 A:Molecule type: protein  
 A:Residues: 34-53;449-475;509-526 <NA>  
 C:Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3 were  
 that the complexes play important role for pancreatic cancer.  
 C:Superfamily: inter-alpha-trypsin inhibitor complex component II  
 F:236-239,664-865/Distulfide bonds: #status predicted

Query Match 3.0%; Score 166; DB 2; Length 889;  
 Best Local Similarity 23.2%; Pred. No. 0.064;  
 Matches 66; Conservative 57; Mismatches 111; Indels 51; Gaps 11;

QY 202 SLIMOVGATGLARYPPSPWVNSRT--PNKID-----LYVRRR-PWYTOGA-- 248  
 Db 211 SLITKFSFGKGVSRFP--IDQOSCEPTCSLLNGDFTIVYVNRSPGVVAVNG 267  
 QY 249 -----ASPKDMLIVDGSVSGLTILRTSVSEMLTISDDDFVNVASFNS 296  
 Db 268 YEVHFAFGGLPVPRKNIVVIDISGSMAGRIQOTRVALLKIDMKDDYINFLFET 327  
 QY 297 NADVSCFOHLVQANVRNKKVLDVANNITAKGITDYKGFSPAEQLLN---YVNSRA 352  
 Db 328 GV--TTWKDSLVOATPANLEARTFVRSISDQGMTNINDGLIGIMLTDAREQHTVPER 385  
 QY 353 NCKKIIMLFIDG---GEERAOEIFPKYNNKDKVVRFTSVG-QHNYDGPIDMACENK 407  
 Db 386 STSIIIML-TDGNANTGESPEKIQENVRKALEGRFPLNGLGNNLNPLETMALENH 444  
 QY 408 GYYEIPISGAIRINTOEYLDVGRPMVLADGAKOVONTNYLD 452  
 Db 445 GVARRIYEDSDANLQLOGFEYEVANPL-----TNVEVE 478

## RESULT 13

F64688  
 protease (EC 3.4.-.-) - Helicobacter pylori (strain 26695)  
 C:Species: Helicobacter pylori  
 C:Date: 09-Aug-1997 #sequence\_revision 15-Aug-1997 #text\_change 29-Sep-1999  
 C:Accession: F64688  
 R:Tombl, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, J.; Loftus, B.; Richardson, D.; Dodson, R.; Khakh, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Matthey, L.; Nature 388, 539-547, 1997  
 A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.  
 A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.  
 A:Reference number: A64520; MUID:97394467; PMID:9252185  
 A:Accession: F64688  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-459 <TOM>  
 A:Cross-references: GB:AE000636; GB:AE000511; NID:g2314517; PIDN:AA08394.1; PID:g231452  
 C:Genetics:  
 A:Start codon: GTG  
 C:Superfamily: carboxyl-terminal processing proteinase  
 C:Keywords: hydrolase

Query Match 3.0%; Score 165; DB 2; Length 459;  
 Best Local Similarity 22.2%; Pred. No. 0.026;  
 Matches 138; Conservative 69; Mismatches 198; Indels 216; Gaps 30;

QY 6 LALATLTLFOSLLIGSSQEPFSAVTIKSWDKMOEDLVTLAKTASGV-----NOLV 58  
 Db 3 LLMTRRLKGLAVSLAGGEVKEKKVPKVEDQOELA--AKRYEASRSNVAS 60  
 QY 59 DIYEKYDYLYTEPNNAKRLVEIARDIEKLISRSKALVRLALEAKYQAOAHOMREDA 118  
 Db 61 EIKKVVYDKRIS-----ELMTAKISGLSLND-----AHS----- 91  
 QY 119 SNEVYVYNAKDLDPEKNSEPSQRIKPVFIDANFGQISYOHAAVHIPTDIYEGSTI 178

Db 92 ----AYLN-----EKKFKE-----FOAQTEGEGGIGITVGRDGLT 125  
 QY 179 VLNELMTLSAL-----DEVFKKREEDPSLTMQVFSASGLARYYPASWVNSRPN 231  
 Db 126 VIAPLEGTPAKAGVSKSDNLIKINNE--STLSMSIDDAINLMGRKRTD----- 173  
 QY 233 KIDLVDVRRRPYIIOGAAPKDM--LIVDVSQSVSGLTILRTSVSEMLTISDDDFV 289  
 Db 174 -IQLIVKRN-----EPKPIVENIIRDI-----IKLPSYVKKIKET--PLIVY 214  
 QY 290 NVASFNNAQDVSCFOHLVQANVRNKKVLDVANNITAKGITDYKGFSPAEF----- 341  
 Db 215 RVSGFDKAVTK--SVLEG--KANPKAKGIVLDLRGN--PGGLNOAVGINSIFKEGYLS 270  
 QY 342 -----EOLLNVSRAN-----CKIIMLTDSGEERAOEIFPKYNNKDKVVRFTSVG 390  
 Db 271 QKGRKKEENLEY--KANGRAPYTNLPLAVLVNGSASASIVAGALQDHRAYI---IG 324  
 QY 391 QHNYDRCPIDMACENKGYEYIISGAIIRINTOEYLDVGRPMVLADGAKOVONTNYV 450  
 Db 325 EKTFFKGSVQMLLPVKNK-----EAKITTAITYLPSGR-----TIQAGIT 366  
 QY 451 IDALEGLVITGTLPEVNTIQONENKTNLKNOLLIGVGVDSLEDIKRLTPRETLCPNG 510  
 Db 367 PDI-----VIYGEKVP-----ENENKFSLEK-----ADLKH----- 392  
 QY 511 YFALDIPNGYVLLH-----PNIQPRKPSOEPVILDFDALENDIVKINNKIDG-- 563  
 Db 393 -----HLEQELKTIKIDTPNSKE-----ADKKKDEEKEIYPMIINDIQ 433  
 QY 564 -----SGEKTEITLVKSDER 579  
 Db 434 LKTAIDSLKTSIVDEKMDK 454

## RESULT 14

S76691  
 hypothetical protein - Synechocystis sp. (strain PCC 6803)  
 C:Species: Synechocystis sp.  
 A:Variety: PCC 6803  
 C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 08-Oct-1999  
 C:Accession: S76691  
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O. K.; Okumura, S.; Shimizu, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas  
 DNA Res. 3, 109-116, 1996  
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys  
 S:Reference number: S74322; MUID:97061201; PMID:8905231  
 A:Accession: S76691  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-420 <KAN>  
 A:Cross-references: EMBL:D64004; GB:AB001339; NID:g1001701; PIDN:BA10635.1; PID:d101  
 A>Note: The nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 2.9%; Score 160.5; DB 2; Length 420;  
 Best Local Similarity 21.1%; Pred. No. 0.042;  
 Matches 86; Conservative 86; Mismatches 181; Indels 55; Gaps 16;

QY 251 PKDMLILVDGSVSGLTILRTSVSEMLTISDDDFVNVASFNSNAQDVSCFOHLVQA 310  
 Db 41 PLNLCLVLDHSGSDGQPLETVKSAALGLIDRLIEDRLSYIARDHRAKIV-----IENQ 95  
 QY 311 NVNRNKKVLDVANNITAKGITDYKGFSPAEQLNVVNSAKNKKIIMLTDSGEERAQ 370  
 Db 96 QVRNCAALAKAIERLKAAGGTAIDGKLGLOEAKGKEDVVS--HIFLLTDSENRGD 152  
 QY 371 E-----IFAKYNNKDKVVRFTSVGQHNDRGPIDMACENKNG--YYEITPISGAIRINTO 424  
 Db 153 NDRCLAKLTGVSADYKLTLYHTLGFQGH-WNOVLEAIAASAGSISYIENPS-EALHFRQ 210  
 QY 425 EYLDVLRPMVLADGAKOVONTNYLDALBELG---LVITGTLPEVNTIQONENKTNLK 480

Matches 194; Conservative 153; Mismatches 334; Indels 351; Gaps 53;

QY 24 QEPFSAVITKSVNDKQEDL-VTLAKTAGVNOQVLD-----IYKYQDIYTVEPNNA 75  
 Db 133 EQOIKKARTSKG-ADLTKEIDGTTIANTSDISIKGIDRMTKGTAVVSDYQIFLITGVN 191  
 QY 76 RQVLEIARDIEKLNSRSLV-----RLAEAEVQAAHOMREDFASNEVYYNA 127  
 Db 192 N-----LQDINSMLTKRVALSKILSTVYDKITTAVSNNINNAHDESPFALQI--YAV 243  
 QY 128 KDDLDEKND-----SEPGSQRKPVFD-----DA-----NFGD-OISYQH--A 164  
 Db 244 QEDLVFLENNISAKKNNKSGDLSSEITVYKDSIKLQDALERINLQGITLDYHFG 303  
 QY 165 AVIIPDIDYEGSTTVLNEIWNMTSALDEVEFKNR--EEDPSLLQV--FGSATGLARYPA 220  
 Db 304 AANVDNNIEMEDVNGMANGKGM-----FERNNAIEINSIVEPLSRKNSGSTADYDA 356  
 QY 221 --SPWYDNGSRTPY-----KIDLYVRRRPMTYQGA 248  
 Db 357 IOVDGVDNNNDIKSVIAEKQOLKGNLNLAEINSAVEEYKTVLDFYDLIKR-----GT 411  
 QY 249 ASPKD--MLILVDS--GSVSGL-----TLKLIPTSVSEMLTSLD-----DD 287  
 Db 412 AKVSDYNAIGLVTEEDNTDNNELLKNDITLKNLQDNINSIISKLNINAGDTDPD 471  
 QY 288 FVNVASFNSADVSCF-----OHLVQANVR--NKKVLDAVNNITAK----- 328  
 Db 472 YNML--MISSVTDNLSIFIDIDIKTAQANGSDLNKGIQDSVNNSLRLSAMDRIAGSA 530  
 QY 329 GIDYK-----KGFSAFEGDLNMYNSRANCNKLIMFTGGEGERQEIFAKNR----- 378  
 Db 531 ALDDYVNLLEIGVTSNLTFFVNNQVKGSKCTIDELKTIVSD--ALKLIDSVKNNGDA 588  
 QY 379 --DKKRV--FTSVGQHNDRGPQIWMACENKGY--YEIPSG--ALRIN----- 422  
 Db 589 YDDYKIKIGVIAKIEEYTYNG-----YFKGNYFTLEELKAGINIAVVRSTENIKNG 643  
 QY 423 -----QOELDVLRPMVLAKGAKOV-----QWNTNYL 451  
 Db 644 VGSVEDFTAGYGVTEENIKYINIKVILRGDAPSAISNITTEVNEIQLSKRMSSQGV 703  
 QY 452 ---DALELGLVITGLPVENITGN-----ENKTKLNQOLLIGVGVDSLEDIR 499  
 Db 704 TAEDEVKSLQSLT-----VTEENISYIMDRVYKNTYYSKELLLEAEVAILKEEYIER 755  
 QY 500 LIPREFTLCNGYYPAI-----DPNGYVLLHPNLOPKNPKSOEPTVLDLDALEND 550  
 Db 756 INLGQATVADYEYIKVTVSYNITSINDY-----KSGNLTRELQAKI--D 802  
 QY 551 IYVE-----IRKKHIDSESEKTFR-----TLVKSQDERYIDCKNRYTWTVPNGT 596  
 Db 803 VVEIQTOSAAHTDVAIGRVNIGEANISDFEFGITVVSFNFOYVDHLKDKKQYTTIDAI 862  
 QY 597 DVSLLALVLPYTFYFIKAKIEETITQARSKGKMKDSEFLKDNFEESGYTPIARDON 656  
 Db 863 KAAYVYFGVGYIY-----EIN-----KGTATL-----DIYN 890  
 QY 657 DKLISDNTEPLINFEIDRTKTPNNPSCNTDLINRVLDACTNELVQYNTWSKOKNIG 716  
 Db 891 SLGITGVTEENTITYINLNIKESSEYFNAS--DIQTKV-----NALLSVGYEIEIKNG 940  
 QY 717 VKAREVYVDDGITTRYVPRKAGENMOENPEYTSFYSKSLDNQVVFAPYFNKSGCPAY 776  
 Db 941 EKVTVDYISLGIYV-----TKENILFINIYIYKE--COY 972  
 QY 777 ESGINWAKAVEI-----YIQ--GKILPVAVGIKIDVNSMINETFTSIRDCACAPV 826  
 Db 973 FLUTSLKSSVEVLEEKYEAYVATISGK--AVVG-----DYTKVGKIKDYTEENI 1018  
 QY 827 CCKCRNSDVMD 838  
 Db 1019 AVININLIDLCNG 1030

RESULT 11  
 D64998  
 hypothetical protein b2270 - Escherichia coli (strain K-12)  
 C:Species: Escherichia coli  
 C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002  
 C:Accession: D64998  
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;  
 A:Rose, D.J.; Mau, B.; Shao, Y.  
 Science 277, 1453-1462, 1997  
 A:Title: The complete genome sequence of Escherichia coli K-12.  
 A:Reference number: A64720; MUID:97426617; PMID:9278503  
 A:Accession: D64998  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-575 <BLAT>  
 A:Cross-references: GB:AE000317; GB:U00096; NID:g1788605; PIDN:AAC75330.1; PID:g17886  
 A:Experimental source: strain K-12, substrain M61655

Query Match 3.1%; Score 168.5; DB 2; Length 575;  
 Best Local Similarity 21.6%; Pred. No. 0.023;  
 Matches 111; Conservative 94; Mismatches 205; Indels 105; Gaps 24;

QY 71 EPNNAQVLEIARDIEKLNSRSLVRLAEKYQAAHOMREDFASNEVYYNAKD 130  
 Db 22 OPENKESQOQPSPTTEQOVLAAQQAIRK--EADQSA--AKALAQEYQYQSDKA 75  
 QY 131 LDPEKND-----SEPGSQRKPVITDANGROISTYQAA--VHIFPDI 172  
 Db 76 LQRIQEPAPRAAKAKATHIANPGRYQOF--DDNPVQYVQNPPLATFSLDVTGS 132  
 QY 173 YEGSTIVNE-----LNMTSALDEVEFKNRREDPSLMOVGSATGLARY 218  
 Db 133 YANVRRELNGQLLPDPDAVRYEELVNFPSDMDI--KDSQIPASKPIPRAMRELA-- 187  
 QY 219 PASPVNDSRTPKPKIDLYVRRRPMTYQGAASPKDMLILVDVSGS--VSGTLKIRTSVS 277  
 Db 188 PA-PW-MEQRILKVDILAKRKEELPAS--NLVFLIDTSGSMISDRPLIQSLK 241  
 QY 278 EMLETLSDDDPVNVAFSNSADVSCFOHLVQANVRKKVLDKAVNNITAKGJTDYKGF 337  
 Db 242 LLVELREODNIAIYTAGDSRIA-----LPSIGSKAEINAIYDLDDEGSTNGAGL 296  
 QY 338 SPAREQLLNIVNSBRANCKITMLFTDG-----GEERAQEIFAYNKDKKVRVFTSVGQ 391  
 Db 297 ELAVQQAIRK-GFIRGGINR--TLATDGFVNGIDDPKISVMYKQRESGVTLSTPVCN 354  
 QY 392 HNYDRGPLOMACENKGYEYIETPSIGAIRINTQETLYDLVGRPMYL--AGDKAKOVQ-- 445  
 Db 355 SNYDEAMVVRADVNGVSYIDTLS---EAKQVLNSEMROMLITVAKDVKKAIEFPNA 410  
 QY 446 WTNVYLLALELGLVITGLPVENITGNENKTNLKNOLLIGVGVQ--VSLEDI--KRLT 501  
 Db 411 WATPEY--RQIGYE-----KRLRVEHENNDVNDAGDIGAGKHIT 447  
 QY 502 PFTFLCPNGYYFAIDPNGYVLLHPNLOPKNPKSQE 536  
 Db 448 LLFELTLNGQASIDKLRYA--PDNKLAKSKTKE 480

RESULT 12  
 JC5576  
 Inter-alpha-trypsin inhibitor heavy chain 3 - golden hamster  
 C:Species: Mesocricetus auratus (golden hamster)  
 C:Date: 23-Sep-1997 #sequence\_revision 23-Sep-1997 #text\_change 17-Mar-1999  
 C:Accession: JC5576; PC4486  
 R:Nakatan, I.; Suzuki, Y.; Yamamoto, T.; Sinohara, H.  
 J. Biochem. 122, 71-82, 1997  
 A:Title: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precurs  
 sin inhibitor heavy chain family.  
 A:Reference number: JC5574; MUID:97420688; PMID:9276673  
 A:Accession: JC5576

R:Bourguignon, J.; Diarra-Mehrpour, M.; Thiberville, L.; Bost, F.; Seebouee, R.; Martin, Eur. J. Biochem. 212, 771-776, 1993  
 A:Title: Human pre-alpha-1-trypsin inhibitor-precursor heavy chain cDNA and deduced amino  
 A:Reference number: S30350; MUID:93215656; PMID:7681778  
 A:Accession: S30350  
 A:Molecule type: mRNA  
 A:Residues: 1-885 <BOU1>  
 A:Cross-references: EMBL:X67055; NID:9288562  
 R:Bourguignon, J.  
 Submitted to the EMBL Data Library, June 1992  
 A:Reference number: S34123  
 A:Accession: S34123  
 A:Molecule type: mRNA  
 A:Residues: 1-310, 'K', 312-343, 'R', 345-885 <BOU2>  
 A:Cross-references: EMBL:X67055; NID:9288562; PIDN:CAA47439.1; PID:9288563  
 R:Diarra-Mehrpour, M.; Bourguignon, J.; Seebouee, R.; Mattei, M.G.; Passage, E.; Salier, Eur. J. Biochem. 179, 147-154, 1989  
 A:Title: Human plasma inter-alpha-trypsin inhibitor is encoded by four genes on three ch  
 A:Reference number: S02141; MUID:89137072; PMID:2465147  
 A:Accession: S02141  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 341-356, 'G', 358-845, 'H', 847-885 <DIA1>  
 A:Cross-references: EMBL:X14690; NID:935464; PIDN:CAA32821.1; PID:935465  
 R:Englund, J.; Thøgersen, I.B.; Pizzo, S.V.; Salvesen, G.  
 J. Biol. Chem. 264, 15975-15981, 1989  
 A:Title: Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-a  
 A:Reference number: A92736; MUID:89380192; PMID:2476436  
 A:Accession: D34245  
 A:Molecule type: protein  
 A:Residues: 30-48 <ENG1>  
 R:Englund, J.; Salvesen, G.; Hefta, S.A.; Thøgersen, I.B.; Rutherford, S.; Pizzo, S.V.  
 J. Biol. Chem. 266, 747-751, 1991  
 A:Title: Chondroitin 4-sulfate covalently cross-links the chains of the human blood pro  
 A:Reference number: A39079; MUID:91093267; PMID:1898736  
 A:Accession: A39079  
 A:Molecule type: protein  
 A:Residues: 631-647 <ENG2>  
 R:Diarra-Mehrpour, M.; Bourguignon, J.; Sarafan, N.; Bost, F.; Seebouee, R.; Muschio-Bon  
 Biochim. Biophys. Acta 1219, 551-554, 1994  
 A:Title: Random orientation of the inter-alpha-trypsin inhibitor heavy chain H1 and H3 g  
 A:Reference number: S50132; MUID:95002176; PMID:7522574  
 A:Accession: S50132  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-27 <DIA2>  
 R:Wisniewski, H.G.; Burgess, W.H.; Oppenheim, J.D.; Vilcek, J.  
 Biochemistry 33, 7423-7429, 1994  
 A:Title: TSG-6, an arthritis-associated hyaluronan binding protein, forms a stable comp  
 A:Reference number: A53642; MUID:94271799; PMID:7516184  
 A:Accession: B53642  
 A:Molecule type: protein  
 A:Residues: 30-34, 'X', <WIS>  
 R:Jessen, T.E.; Paarray, K.L.; Ploug, M.  
 FEBS Lett. 230, 195-200, 1988  
 A:Title: Carbohydrate as covalent crosslink in human inter-alpha-trypsin inhibitor: a no  
 A:Reference number: S02431; MUID:88167187; PMID:2450785  
 A:Accession: A59167  
 A:Molecule type: protein  
 A:Residues: 30-32, 'GEKQAVPT' <JES>  
 C:Comment: As pre-alpha-inhibitor, this protein is covalently cross-linked by chondroitin  
 C:Genetics:  
 A:Gene: GDB:ITIH3  
 A:Cross-references: GDB:120109; OMIM:146650  
 A:Map position: 3p13-3p12  
 C:Superfamily: Inter-alpha-trypsin inhibitor complex component II  
 C:Keywords: chondroitin sulfate proteoglycan; glycoprotein; heterodimer; proteinase inh  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-29/Domain: propeptide #status predicted <PRO>  
 F:30-647/Product: inter-alpha-trypsin inhibitor heavy chain 3 #status experimental <MAT>  
 F:648-885/Domain: carboxyl-terminal propeptide #status predicted <CTP>  
 F:87,576/Binding site: carboxylate (Asn) (covalent) #status predicted

F:647/Modified site: chondroitin sulfate ester carboxyl end (Asp) (in mature form) #s  
 Query Match 3.5%; Score 188; DB 2; Length 885;  
 Best local similarity 21.5%; Pred. No. 0.003;  
 Matches 138; Conservative 112; Mismatches 243; Indels 150; Gaps 36;  
 QY 45 VTLAKTAGSVNOLVDIERKODLYVEPNNAQLVEIARDIEKLISNRKALVALAE 104  
 DB 77 VELPKTAFTINFTLT-----DGVTY-PGNVKE-KEVAKQYERKAVSOGKTGL----- 123  
 QY 105 EKYQAHHQMRDE-----ASNEVYYNAKDDDPENKDSFGQRKIPFTIDANGR 157  
 DB 124 --VKASGRKLEKFWYSVNAAGSKVTELTVEELLRHKRYEMLYKQP-----K 172  
 QY 158 QISYQAAAHIFPTDIYEGSTIYLNEIMNTSALDEVEFKKREEDPSLLMQVFSA-----T 212  
 DB 173 QL-VKHFEEIV--DIFEPGI-----SMD-----AASRTYNDLGSALTKFS 214  
 QY 213 GLARYYPASPMWNSRT-PNKID-----LYVRRRP-----WTI-----OG- 247  
 DB 215 GKKGHSFKPSLDQKSCPTCTDLSLNGDFTTYDVNRESPGNVQIVNGEVHFPAPGGL 274  
 QY 248 AASPKMILLVDYSGVSGTLTKLRTSVSEMLETLSDDFVNVASFNSMODVSCF-QH 306  
 DB 275 PVPKNAVAVFVLDISGMAARKLEQTEALRLTEMQEEDYLNFLFSG--DVSTWKEH 331  
 QY 307 LVQANRNKKVLDVANNITAKITDYKKGFSAEQLNLYNVS-----ANCKIIML 360  
 DB 332 LVQATPENLQEAKEPTFKSMDKGMNINDLRLGISML--NKANEHRIPRSTSIYM 388  
 QY 361 FPDG---GEBAQETFAKYNK--DKRVVPTFSVQOHNYDRGPIQMACENKGYEIP 414  
 DB 389 LIDGDANVESPREKIQEENVNNAIGKPELYMIGFG--NNLANNFLNNALNENHGFARRIY 447  
 QY 415 SIGAIRINQEYLDVGRMVLASGKAKOVNTYIALD-----LGLVTGLP 465  
 DB 448 EDSADLQLOGFEEVAVNP-LTGVMETPE--NALIDLTQNTYQHFIDGSEIVAGRLV 504  
 QY 466 VFNITGONENKNTLK-----NOLLIGVMGVDSLEDIKRLPRFTLCPNGYFAIDPN-- 518  
 DB 505 DEEM--NSFKADYKKGATNDL--TFEEVDMMEMEK-----ALQENDYIFG--NYI 550  
 QY 519 ----GYLLHPNLQPK--NPKSQEPVYLDPLDAELNDIKVEIRNKMTDGSGETRT 571  
 DB 551 ERLMAYLTTEOLEKRNKHAHEKENTARALDSLKYFHTVPLTSMVYTKPE----- 603  
 QY 572 LVKSODERTI-DKGNRTYTPVN-CTDYSLLVLPYTSFYFI 612  
 DB 604 --DNEDERAIADKPGDAEATPVSPAMSTYLTSTOPQNPYTV 644  
 RESULT 10  
 D97033  
 uncharacterized protein, probably surface-located [imported] - Clostridium acetobutyli  
 C:Species: Clostridium acetobutylicum  
 C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001  
 R:Collings, D. 197033  
 C:Accession: D97033  
 J. Bacteriol. 183, 4823-4838, 2001  
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium  
 A:Reference number: A96900; MUID:21359325; PMID:21359325  
 A:Accession: D97033  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1819 <KUP>  
 A:Cross-references: GB:AE001437; PIDN:AAK79055.1; PID:915023996; GSPDB:GN00168  
 A:Experimental source: Clostridium acetobutylicum ATCC824  
 C:Genetics:  
 A:Gene: CAC1081  
 Query Match 3.1%; Score 170.5; DB 2; Length 1819;  
 Best local similarity 18.8%; Pred. No. 0.11;

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Db 333 LVQATPANKLEAKTEFVNKNIDHOSMTNINDLKGIEML--NKAREDTVPERSITIM 389
QY 361 FIDG-----GERRAOEFAKYNK--DKKRVVFTFVSQOHYDGPDIOMMACEKGYVEIP 414
Db 390 LIDGANTGSRPEKIOENVRNAIGKFPPLYNUGFC--NMLNPFLETLLENHGLARRIY 448
QY 415 SIGAIRINTOEYLDVIGRPMVLADGKAKOVMTNYLDALGLVITGTLPEVNTIGONE 474
Db 449 ESDGANLQIQGFEEVAVNPL-----TNVEVEPEANA-----ILLDLTRNSY 489
QY 475 NKTNLKNLILGVWGVDSLEDIKRLTPRTLCPNGYTAIDPNGVLLHPMLQKRNPKS 534
Db 490 PHFYDSEIYVAGRLVDRMMDN-----FKADVKGHALN-----DLTF 527
QY 535 QEPVTLDPDLAELENDIKVEIRNMIDGSEGEK--TFRTLVKSODERYIDKGNRTYTWP 592
Db 528 TEEDVMEEDDAIK-----EGYTFPGDIYERLMAVILITBOLLERKNAKDERENIT- 579
QY 593 VNGTDSLAL--LVLPYTFYIKAKIETITTOARSKKMKDSE-----LKPDNFEESG 645
Db 580 AEALDLSLKYHFVPLTSMVTPPEEDNEQTSIADNAGEAFAETTTMSFLTTOOSSQSP 639
QY 646 YTFIARDCNDLKISDNTTEFLNNEFIDKTRPNNSCNDLIRVILLDAGFTNELYO 705
Db 640 YYYV-----DGPHEFTIQ-----PKNDSTICFNIDKPGTYLRLIQ 676
QY 706 NYMSKONIKYKARFVVDIGITRYVPKPEAGENMOENPEYEDSKRSLDNDNYVFTA 765
Db 677 D-----PVT--GIT--VTGQLIGD-----KKS--NASRTRGK 702
QY 766 PYNKSQPGAYESGIMWKAVEIYIOGKLKIPAVVIGIKIDVNSWITNFKTSTRDCAP 825
Db 703 TYFGKLGITNAMMDPVEVEVTEKIIIG-----TGAEISTESWIDTIVTQ-----TGL 750
QY 826 VCCCKRSDVMDCVIILDDG--GFLLMAN-----HDDYTNOIGRFGEDPSLMRLVN 876
Db 751 SVTINRKKANV--VSGDGISEVILHQQWKKHPRHODELG-----FYVDSHRMSAQTH 803
QY 877 ISVAFNKSXYQSV--CEPGAAP 898
Db 804 GLIGOFFQPPDFKVFGRPCSDP 826

RESULT 8
C86880
hypothetical protein yycC [imported] - Lactococcus lactis subsp. lactis (strain 111403)
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C:Accession: C86880
R:Bolotin, A.; Wincker, P.; Manger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s.s.
A:Reference number: AB6625; M01D:2135186; PMID:11337471
A:Accession: C86880
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1450 (S10)
A:Cross-references: GB:AE005176; PID:g12725093; PIDN:AA06141.1; GSPDB:GN00146
A:Experimental source: strain 111403
C:Genetics:
A:Gene: yycC

Query Match 3.5%; Score 190.5; DB 2; Length 1450;
Best Local Similarity 19.4%; Pred. No. 0.0046;
Matches 203; Conservative 148; Mismatches 359; Indels 339; Gaps 51;

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QY 128 KDDLDPEKNDSEPGSQRKIP---VFIDANRGROISYOHAVH----- 167
Db 181 EEVLNNESSQEEYLSQKKDSQALFAFVPSNNGIASRNDLAQVNTSPEYRDETGISP 240
QY 168 ----IPDIYGGSTIVNELMWTSALEDEVEKKNEDDEPSLIQVFGSATGLARYPASW 223
Db 241 NWSWIP-----GNTVYVHQQMSNF-----SSQMGVNSWN--GEATNLENSIYAG 287
QY 224 VDN-----SRPNKIDLY--DYRRRPWYIOGAASPKDMLIIVDVGSGVSLTLK 270
Db 268 VNNPVPALRKRYAKETETPGILDYVLNNGN--VQNPVKFVDVLVIDSGSMQAKET 344
QY 271 LIRTSVSEMLETISDD---DEVNV--ASFNSMAOVSCFOHLVOANYRNKVLKD-----A 321
Db 345 AVRGQVDSFLESTIQNTAVADYVNVGIVGSSPGVYVVGASGIVTVPL--DKVSSESHVS 402
QY 322 VNNITA---KGIIDYKKKFSFAFQGLNLYNVRANKCKIIMFLFDGGEERAOEFAKYNK 378
Db 403 INQALAPQFSQGTQQLRKGTEML--EODSSDNOKMMLMTDQ---VPTFSYVNS 455
QY 379 DKVR--VFTFVSQOHYNDRG---PIQ---WMAECNKGYEYI-----PSGAIRINTOE 425
Db 426 YLDVLGRPMVLADG-----KAKQVQMTNYLDALGLVITGTLPEVNTIGONE 474
QY 426 YLDVLGRPMVLADG-----KAKQVQMTNYLDALGLVITGTLPEVNTIGONE 474
Db 516 ISEIHTLGIQNGDSYLSQEBKSRSLIAFTGLQYQANSAN-----DITVLYK 565
QY 475 NKTN-----LKNOLLGVWGVDSLEDIK----- 498
Db 566 NQANVLSRFNTITGLDPLDGAQFEYKDKFEITSYGEDSIDNLPKTKNEKGLISN 625
QY 499 -----RLTPRFLCPNGYFPAIDPBGVYLLHPNLQPKPKSQ----- 535
Db 626 LNIGKNOEVOIHQYRLMTEDDEFTKNWYQM--NGETTLAPN--GSPMDKAVFQVPSA 681
QY 536 --EPVTLFLDALENDIKVEIRNMIDG-----SGEFTRLVKSODERYIDKGNRTY 588
Db 682 KSSGINTLEKQWMLANSRNIPEVVELLIGRSQAQISSDMTIVLKEDE----- 731
QY 589 TWTTPVNGTDSLALVLPYVS-----FYIRAKI-----BETITQARSKKG 629
Db 732 -WR-----SOLENDPKYSILGEEFYIENDEYLNSEIYDWTITIGDKTTIANIEFR 783
QY 630 MKDSETLKPDNFEESGYTFIARDCYN--DLKISDNTTEFL-----LNFNE--FIDRKT 679
Db 784 LQILKTSNHDNPEPLSEVEFVLKNSGEEIDKAVTNEKEGELLFDKRLVNGEYQJHEIKS 843
QY 680 PMN-----PSCNTD-----LINRVLLDAGFTNEL--YQYMSKOKNI 714
Db 844 PCHSLEGPWKIKTERENGOPILIKVGEQIALDEHYNKKPMISLNTINDINVEEF---RNS 899
QY 715 KGVKARFVYT---DGITRVYPKEA--GENMOENP-----EYEDSFPYK 753
Db 900 VTIKRAVDSEKLDGAVNVLNQLIESVDDELQQLKPLEITNNLLPGLALADESPSPNY 959
QY 754 RSLDNDNYVFTA-----PYNKSQPGAYESGIMWKA--EIIYQGLL 795
Db 960 R--DDEVHFRVYKFNGLSIVAIISGEDIPIFLDENESG--KNGLVNEBENDLHLTLIFY 1015
QY 796 KPAVYGIKIDVNSWIENTFKTSTRDCAG 824
Db 1016 NQAVPPLQLEVDKIDDDP-----SPLAG 1039

RESULT 9
S30350
inter-alpha-trypsin inhibitor heavy chain 3 precursor - human
N:Alternate names: HC3; inter-alpha-trypsin inhibitor chain H3; pre-alpha-inhibitor h
C:Species: Homo sapiens (man)
C:Date: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change 04-Feb-2000
C:Accession: S30350; S34123; S02141; D34245; A39079; S50133; B53642; A59167

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submitted to the EMBL Data Library, June 1995  
 A:Reference number: Z19019  
 A:Accession: T18770  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1148 <W12>  
 A:Cross-references: EMBL:Z49907; PIDN:CAA90091.1; GSPDB:GN00020; CESP:T24FL.6  
 A:Experimental source: clone B0491  
 R:Chnl, C.  
 submitted to the EMBL Data Library, June 1995  
 A:Reference number: Z20004  
 A:Accession: T25249  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1148 <W12>  
 A:Cross-references: EMBL:Z49912; PIDN:CAA90141.1; GSPDB:GN00020; CESP:T24FL.6  
 A:Experimental source: clone T24FL  
 C:Genetics:  
 A:Gene: CESP:T24FL.6  
 A:Map position: 2  
 A:Insertions: 91/2; 131/3; 170/3; 283/1; 322/2; 410/3; 487/1; 563/1; 602/3; 654/3; 683/3; 7

Query Match 10.5%; Score 571; DB 2; Length 1148;  
 Best Local Similarity 21.6%; Pred. No. 3.9e-26;  
 Matches 243; Conservative 212; Mismatches 417; Indels 254; Gaps 45;

QY 37 VDKMQLDYLTA-----KTASGVNQLVDYERKODLYVEPNNAKQLEIARDI 86  
 DB 99 VDTIEEPASIAOFSANILRDFETQSRSFLVCEFEKLDKSKEDAEKLRVATEHL 158  
 QY 87 EKLNSKALVRLALEAEVQAHOHREDFASNEVYVYNAKDDLPKNDSEPSOR-- 144  
 DB 159 DRLVTNVDLKLKLAASAESAFAV-----DEYDQAVAPQAKRRE 201  
 QY 145 --IKPVEIDANRGOISYOH--AAVHPTDIEGSTLYLNLMTSA--LDEVEKKR 197  
 DB 202 AYKKNMESDMHFVSNM-VEHNSKSGIHITVESYQCDPRMRPFMDTGKHEKTSMDK 260  
 QY 198 EEPDSLMQVFSATGLARYTPASPVNDSPNPKITLDYVRRRPYIGGAAPKMDLIL 257  
 DB 261 EKAPENGHQYIGTYSGLTRMYPRRHW-KVEPFTITLIDPDRRPFVNAESVPCDIFVL 319  
 QY 258 VDSGVSGLTTLKLRISVSEMLEFTLSDDFVAVAFSNAOD-VSCFQH-LVQANVRK 315  
 DB 320 LDVSGSVKPTMLIKITMYTILSTSPNDYFEGVYFNHNEPILISCANRTMPATTSK 379  
 QY 316 KVLKDAVNNITAKGIDYKGSFAFEOL--LNVNVS-----RANCKNIMFTDGE 367  
 DB 380 KVFEEELGLEEKDQAHFATPLKFLSLDVLKGNLDSNOSLFADYRSCHKLITFTDGVDE 439  
 QY 368 RAOEIT---FAKNKDKKRVFTFSVQJHNYDRPI-QMMACENKGYEIPISGAIRIN 422  
 DB 440 WPHQILDEEFQRTNSE-LRIRFGFSMG-YGTSILLPQOYMAKSHSGSEISIDMVKPO 497  
 QY 423 TOEYLDVLRPMVLADGDKAK-----QYOWTNVYDALDELGLVITGTLPVNNITQGNAN 475  
 DB 498 SRIOVNLQ---VRDEELKGTNAEKREPSWOLIMETGCTGPVYLSLPIL-----TSE 549  
 QY 476 KTNLKNQILIGVGVDSLEDIKRLTPRTLCPNGYFAIDPNGYVLLPNLO-PKNPK- 533  
 DB 550 ORIMROKLAGVAIDISIKFTKHLR-TSSROMYGYIVDNNGMILYHPQOIKTEVH 607  
 QY 534 -----SOEPV-----TIDFDLDELNDIKVEI 555  
 DB 608 CVRRSACYDAQVQKAGSGLRVHVGFSDEYRRLVGLIDSIPITLMDYLEDGSTAIRDL 667  
 QY 556 RNMKIDGSEGEKFTFLVYSODERTYDKNRTYTWTPVNGTDYSIALV-LPTYSFYIK 613  
 DB 668 RR-----RTTTCYEEPAIKDSKSKYHSHIDSFPFLVYNNIQLKTVYDD 715  
 QY 614 ARIETITQ-----ASKKGGKMDSETLKPDNFEESGYTFIAPDYC--NDLKISDN 663  
 DB 716 SVQELGLTGNKLVTFEPPYRSDYCCWKLDEYLAHDFRV--WSDISEKEICADDDRLR 773

QY 664 NTEELLNFEFLDRKUPNPNSCNTDLINRVLLDAGFTNELVQNMYSKOKNIGKAVRPV 723  
 DB 774 FTKGLGSLQSPKSDIEHTTC-----LDAQPENASVPHVNS-----FVH 815  
 QY 724 TDGQITRVYPKBAENWQENPETYEDSFYKSLDNDVYFAPYPNKSGPAGESIGIMVS 783  
 DB 816 TSKLTLAFYPTCSHDMKAVNKKFDEI--KTLDNNDVY-----QFSMR-----SSLLIT 864  
 QY 784 KAVEIYIGKLLKPAVVGKIDVN--SKIEFTYTSIRDPACGPFVCCCKRNSD-----V 835  
 DB 865 KTIADYDNRL--AVVGQMKENEPDQYFDNFT-----RONPDMKIDRK 906  
 QY 836 MDCVILDDGFLIMNHDDYTNOGRFGEIDPSTLMRHLVNSYAFNKSVDYOSVCP-P 894  
 DB 907 QECSTIIRNGHYIASAHRAHKLKF--DPQLFESLVKYNLSTMSWTEVSECKAK 962  
 QY 895 GAAPKQAGHRSAYVPSIADILHIGMATAA--AWSIIQOFLSLTFPRLLEAVEMEDDD 952  
 DB 963 RVAP-----WSSAARGSSILRYFTVSI-----FKIAKTS 992  
 QY 953 FTASLSKOSCIETQYTFENDSKSFSGVLDGNC-SHIFHEKLMNTLIFIVESKGT 1011  
 DB 993 FWRNLLESALLVDAPSPMTGNTCTFOKIKPFCRFMFFHYRMTLNTTK-QLDITGMS 1051  
 QY 1012 C-----PCDTRLILQAEQTSDDPP-----CDMV 1035  
 DB 1052 CSRYAKLVYPPHTTILSIADACSQYRPRKLFSESPKLEKCDVY 1097

RESULT 7  
 S54355  
 Inter-alpha-trypsin inhibitor heavy chain 3 precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 04-Feb-2000  
 R:Chan, P.; Ristler, J.L.; Raguenez, G.; Saller, J.P.  
 Biochem. J. 306, 505-512, 1995  
 A>Title: The three heavy-chain precursors for the inter-alpha-inhibitor family in mou  
 A:Reference number: S54353; MUID:95194326; PMID:7554067  
 A:Accession: S54355  
 A>Status: preliminary; nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-886 <CHA>  
 A:Cross-references: EMBL:X70393; NID:9695635; PIDN:CA449843.1; PID:9695636  
 C:Superfamily: Inter-alpha-trypsin inhibitor complex component II

Query Match 3.6%; Score 196.5; DB 2; Length 886;  
 Best Local Similarity 20.5%; Pred. No. 0.00092;  
 Matches 189; Conservative 142; Mismatches 349; Indels 243; Gaps 46;

QY 45 VTIARTAGVNOVDYERKODLYVEPNNAKQLEIARIEKLLNSRSALVRLALEA 104  
 DB 78 VELRPTATITFTLTI-----DGVTY-PGNVKE-KEVAQOYEAASOGKTAGI----- 124  
 QY 105 EKVQAAMQWREDF-----ASNEVYVYNAKDDLPKNDSEPSORIKPFVIDANFGR 157  
 DB 125 --VNASGRKLEKFTVSVNVAAGSVTFELTYEELKKNKGYEYKLVQP-----K 173  
 QY 158 QISYQHAHVIPTDIYEGSTIVLNLMTWSALDVEFKKRNREDEPSLIMQVFGSA-----T 212  
 DB 174 QL-VRH--FELDAHIFEPQI-----SMID-----AASFTINDLGLSMTKFS 215  
 QY 213 GLARYTPASPVNDSPNPKID-----LVDVRRP-----WYI-----QG- 247  
 DB 216 GKRGHVSFKPSLDQRCPTCTDLSLNGDFTIYDVARESPGNVAVNGVFFHFAPAGL 275  
 QY 248 AASPMDLILVDVSGVSGTLKLRISVSEMLETTSDDFVAVAFSNAODVSCFO-H 306  
 DB 276 FVPEKNITVIVDVSGSGRKRIQOTREALKIIDVAKEDYILNFIEST--DYTIMKH 332  
 QY 307 LVQANVRKVKLVKAVNNTAKGTTDYKGFSAFEOLLVYNVSRAN-----CNKIML 360



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Db      72  EYKDAVIEIDLOLVKYLAKIMEMPHKSSAVRLEAAEALMLKEFPADL---OY 128
      123  VYTNAR--DDLDPEKNDSEPGSQRKIPVTDANEGROIISYOHAAVHPITDIYEGSTIYL 180
      129  EYFNANVLINERDKGNFLEIGKEFI--LAPNDHFNLPVNTSLSDVQVPTNNYNNDPAIV 186
      181  NELNMVSAIDEPYKRRREDPSILMVGSSATGLARYTASWVDNSRTPNKIDLYDVR 240
      187  NGYVWSESINKYFVNDPDDPSILMVGSSATGLARYTASWVDNSRTPNKIDLYDVR 243
      241  RPYVIGASPKDMLLVVSGSVSGTLTKLRTSYSEMLETLLSDDDFVNASPSMNAQ 300
      244  RKMYIOATSPKDVVILVYVSGSMKRLITAKQVYSLTLDLGDDEFNITTYNEELHY 303
      301  VS-CFO-HLVQANVRNKVYLKAVNNITAKGITDYKKGFSFAFEDLLNYNSRAN--CNK 356
      304  VERCLNGTLVQADRNRKEHFREHLDFAKGIGMLDIALNEAFNLLSDPHNGQGSICSG 363
      357  IIMLFIDGGEERAOEIFAYYN-KDKKVRVFTSVGOHNDROPVOMACENKGYTEPDS 415
      364  AMLITLDGAVDYDTLEAFYNNPDRKVRITFTYLGREAFADNLKMMACANNGFEQIIST 423
      416  IGAIRINTOEYLDVLCRPVWLAGDKAKOYQVNTNYLD-----ALEGLVI--TGTL 464
      424  LADVOENWMEYLVLSRPVY--DOEHVYVTEATYIDSTLPQAKLADDOGLVMTYAM 481
      465  PVFNITGONENKTNLKNQILIGVGVDSLEDIKRLTPRTLCPNGYFAIDPNGYVLH 524
      482  PVFS-----KONETRSKG-ILGCVGTDPVKEELKTIPTKLGINGYAFALITNGYILTH 536
      525  PNLQF---KNKSOEP--VTLDFDLAELNDIKVELRNKIMIDEGSEKTEFLVYSQDER 579
      537  PELRLPYEGEKKRRKRVSSVDSLEWEDRDV--LRNMAVRKTKG--FSMEVK---K 589
      580  YIDKGNRT-----YTFPVGNGTDYSIALVLPY--YSFYIKAK--LEETITQARSKGKM 630
      590  YVDKGRVLYMNDYYTIDIKGTPSLGVALSRGHGKYFRGNVITIEBL----- 639
      631  KQSEITLKPNEFSGYTFLAPDYCN-DLKISDNTTEFLNFNEFIDRKTTPNNSCNTDL 689
      640  -----HDLRHPVSLADEWSYCNNTDLRPHRHISOLEAIKYLKKEP--LQCDKEL 690
      690  IIRVLDAFTNELYONVMS-----KONIKGVKARPVNTGCGITRYV----- 733
      691  IOEVLFDA-VVSAPLEATWTSIALKSENSDKGEVAFELGTGTSRLINLVEGABQLNQ 749
      734  --KEAGENMOENPEYEDSFYKRSIDN--DNYVFTAPY---FNKSGPQAYESGIWVSKA 785
      750  DFLKAGDKENINADHFLPMYRRAAQLAGSFYISIPSTGIVNKS-----NVYTAISTS 803
      786  VEITYOGKLLKPAVVGIKIDVNSWIENTFTKTSIRDPGAPVCDCKRNSDVMDCVILDDG 845
      804  IOLLEBKSPVVAAGVIOKMLEFFQKFEWTASRQASLDGKCSICDDDETVCYLLDNG 863
      846  FLLMANHDYTNQIOREFGEIDPSLRHLVNTSVYAFKSYTOSVCEGAPKRGACAGR 905
      864  FLVVS--EDYT-QTGDPEVEGAVYNNKLLTGSKFRKTLTDYQAMCR--ANKESSOSA 917
      906  SAYVPSIADILHIGWATTAAMSIIQOFLSLTFPRLLEAVEMEDDFTASLSK-----Q 960
      918  HGLIDPYKAFL-----SAKAKIMTELVLFLVEF-----NLCSMWMSDMTAKAKOKILE 967
      961  SCITETOTQFFPNDKSKSVGLDGCNCSRIHFVERKMLNTLFIIVESKGTGCPDCT 1016
      968  PDTEYPAVVSERTIKETGTINACEDCSKSFVIOQIPSSNLFMVVVD--SCLCES 1021

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RESULT 5  
 S44617  
 C50C3.11 protein - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 30-Jun-2001

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C:Accession: S44617
R:Ravello, A.D.
submitted to the EMBL Data Library, May 1993
A:Description: Sequence of the C. elegans cosmid C50C3.
A:Reference number: S44627
A:Accession: S44617
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-734 <FAV>
A:Cross-references: EMBL:L14433; NID:g289649; PID:g289650
C:Genetics:
A:Insertions: 24/2; 87/3; 175/1; 259/1; 290/3; 346/3; 460/3; 538/3

Query Match          11.2%; Score 611; DB 2; Length 734;
Best local similarity 26.5%; Pred. No. 7.5e-29;
Matches 179; Conservative 127; Mismatches 261; Indels 108; Gaps 19;

      47  LAKTASGVNOLVDIYEKQDITYEPNNARQVLTAARDIEKLISNSKAL--VRLALEA 104
      36  MKETFSKISHETIKQNEKLVEEQDFPRAELKSKHRIEDYLKVSOPAYKAKISLEA 95
      105  EKVQAHQWRDFAFASNEVYVYNAKDDLDPEK--NDSEPGSQRKP-----VFIDANF-G 156
      96  RSVRNDSTVNDPQSKSPFRMSAKOGNDCTTYSNHLGKRLKYNKTSFNLTQANFYT 155
      157  ROISYOHAAVHPIDYEGSTIVLNELNMTSALDEVEKKNREEDPSILMVGSSATGLAR 216
      156  LPTSSVSAAVHIPPLVDNRNEDLRLKIDW--SDIDAVYRTNREETKDLAFOLFCSEAGYMR 214
      217  YYPASPWV--DMSRTPNKIDLYDVRRRPRYTOGAASPRDMLLVDSVSGSLTKLIRTS 275
      215  YYPASWFMWQ--DEHIDLPDCRNTETVINSATNSVNLIMLDMSSMGLGOREYVAKOT 272
      276  VSEMLETSDDDFVNVAFSNSNA---QDVSCFQHLVQANVRNKVYLKAVNNITAKGTD 332
      273  TEALITELTSHNDYINIMTFKSKNTFLDGCNCTNLLDQATPRNKKALKRKMDTYOSBKA 332
      333  YKKGFSFAFEDLLVYN-----VSRANCKIIMLFIDGGEERAOEIFAKYKDKKRVYTF 387
      333  YEKALPLAFSVLLDINNCGDNNRGACENVIMLTDDAPNAYKKIFPMYNAKDKVRVTF 392
      388  SVGQHNDRGRLOMACEKNGKYEIEISIGAIRINTOEYL-----DVIGRWVLAGDKAKQ 443
      393  LVGDAIDENVEKEMACNNRGYVAVNMAVDVDEKIHYYIRMSRVVGRHYKESGOLS-- 450
      444  VQVNTNYLDALDELQ--VITGLPVPNITGONENKTN----- 478
      451  -WMTGVYHERLYLDRPELFAFPVPTITNOSFVNMKMASRKRIRLOKSEARSKEFTVTYST 509
      479  --LKNQILIGVGVDSLEDIKRLTPRTLCPNGYFAIDPNGYVLHLPNIQPRNP----- 532
      510  PVIYNETFMGVAANVILPEVAQKSHPANIGSKSYFPMIDONGVMTHPQLRIPDPTTX 569
      533  KSGEPVTLDFD-----AELENDIKYEIRNKMIDGE 563
      570  HKQVNNMDLLELEVQONQVNRSSQKSAVSDLVCEGANYARCEVDLRLKRAVRKMIIDCD 629
      564  SGEKTFFLVYSQDERY---IDK---GNRTYTTVPNGTDYSIALVLPYYSYTIKAKI 616
      630  NSD-----VQGLDVILATLDELDRVYPTQMTYTAECINHANFVLGLAVAKGDDRYVYKK- 682
      617  EETITQARSKKGMK 631
      683  -----QRKYDFGRVYK 692

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RESULT 6  
 T18770  
 probable calcium channel protein - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 29-Oct-1999  
 C:Accession: T18770; T25249  
 R:Stulston, J.

Db 1020 MQAEQTSIDGPDPCDMVK 1036

## RESULT 3

CHRA2

calcium channel protein alpha-2 chain precursor - rabbit  
N:Alternate names: dihydropyridine-binding protein, 140K  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 22-Jun-1999

C:Accession: S10579; A39518; A33409

R:Ellis, S.B.; Williams, M.E.; Ways, N.R.; Brenner, R.; Sharp, A.H.; Leung, A.T.; Campbell, A.T.;

Science 241, 1661-1664, 1988

A:Title: Sequence and expression of mRNAs encoding the alpha(1) and alpha(2) subunits of

A:Reference number: S10579; M01D:88336904; PMID:2458626

A:Accession: S10579

A:Molecule type: mRNA

A:Residues: 1-1106 &lt;EUC&gt;

A:Cross-references: EMBL:M21948; NID:g164762; PIDN:AAA81562.1; PID:g164763

A:Note: 57-Asn, 106-Lys, and deletion of 620-Ser were also found

R:Day, S.D.; Sharp, A.H.; Kahl, S.D.; Vedvick, T.S.; Harpold, M.M.; Campbell, K.P.

J. Biol. Chem. 266, 3287-3293, 1991

A:Title: Structural characterization of the dihydropyridine-sensitive calcium channel al

A:Reference number: A39518; M01D:91131638; PMID:1847144

A:Accession: A39518

A:Molecule type: protein

A:Residues: 961-973 &lt;JAY&gt;

A:Note: this sequence represents the amino end of a glycosylated peptide that appears at

e at the amino end and identical molecular weights (17K) following deglycosylation

R:Hamilton, S.L.; Hawkes, M.J.; Brush, K.; Cook, R.

Biochemistry 28, 7820-7828, 1989

A:Title: Subunit composition of the purified dihydropyridine binding protein from skelet

A:Reference number: A33409; M01D:90122765; PMID:2558713

A:Accession: A33409

A:Status: preliminary

A:Molecule type: protein

A:Residues: 27-44, 'S', '46-47' &lt;HAM&gt;

C:Superfamily: calcium channel alpha-2 chain

C:Keywords: calcium; disulfide bond; glycoprotein; ion channel; membrane protein; phosph

F:1-26/Domain: signal sequence #status predicted &lt;SIG&gt;

F:27-1106/Product: calcium channel alpha-2 chain #status predicted &lt;MNT&gt;

F:94,138,186,326,350,470,477,606,615,678,697,784,827,891,898,988,1001,1081/Binding site:

Query Match

Best Local Similarity 96.5%; Score 5253.5; DB 1; Length 1106;

Matches 1009; Conservative 11; Mismatches 9; Indels 29; Gaps 4;

QY 1 MAAGCLATLTLTFFOS--LIGPSSEPPPSAVTITKSWDKMEDLVTLAKTASGVNOLY 58  
 DB 1 MAAGCLATLTLTMOALILIGPSSEPPPSAVTITKSWDKMEDLVTLAKTASGVNOLY 60  
 QY 59 DIYEKQDLYTVEPNNAKQLEIAARDIEKILSNRSKALVRLALEAKYQAOAHQWREDA 118  
 DB 61 DIYEKQDLYTVEPNNAKQLEIAARDIEKILSNRSKALVRLALEAKYQAOAHQWREDA 120  
 QY 119 SNEVYVYNAKDDLDPEKNSEPPSQRIKPYFIDANFGRQISTQOAAVHPIPDYGCSTI 178  
 DB 121 SNEVYVYNAKDDLDPEKNSEPPSQRIKPYFIDANFGRQISTQOAAVHPIPDYGCSTI 180  
 QY 179 VLENLMTSLADEVFKKRNREDEPSLLMOYVGSATGLARYYPASPWNDSRTPKIDLYGY 238  
 DB 181 VLENLMTSLADYFKNKRNREDEPSLLMOYVGSATGLARYYPASPWNDSRTPKIDLYGY 240  
 QY 239 RRRPWTYOGAASPDKMLILVYGSVSGTLKILRTSVSEMLETLLSDDDFVNVAASFNNA 298  
 DB 241 RRRPWTYOGAASPDKMLILVYGSVSGTLKILRTSVSEMLETLLSDDDFVNVAASFNNA 300  
 QY 299 QDVSCQHLVQAVNRKKVYLKADVANNITAKGIDYKKGSPFAEQLLNINVASANCNKII 358  
 DB 301 QDVSCQHLVQAVNRKKVYLKADVANNITAKGIDYKKGSPFAEQLLNINVASANCNKII 360  
 QY 359 MLFTDGEERAQELFAKYNNDKVRVETFSVGOHNDRGIOMACENKGYEIPISICA 418  
 DB 361 MLFTDGEERAQELFAKYNNDKVRVETFSVGOHNDRGIOMACENKGYEIPISICA 420

QY 419 IRIINTEYLDVLRPMVLADGKAKOVMTNVYLDALDELGITVTGTLPEVNTIGONENKTN 478  
 DB 421 IRIINTEYLDVLRPMVLADGKAKOVMTNVYLDALDELGITVTGTLPEVNTIGOFENKTN 480  
 QY 479 LKNQILGVGVSVLEIDIKRLTPRFTLCPNGVPAIDPNGVILLHPMLQPK----- 530  
 DB 481 LKNQILGVGVSVLEIDIKRLTPRFTLCPNGVPAIDPNGVILLHPMLQPKIGVIGPT 540  
 QY 531 -----NPKSEPVTLDFDAELENDIKVEIRKMKIDGSEGETFTFTVKSQDER 579  
 DB 541 INLRKRPVQVQKSEPVTLDFDAELENDIKVEIRKMKIDGSEGETFTFTVKSQDER 600  
 QY 580 YIDKGNRTYTPVNGTGY-SLALVPIYSFYIAKLEETITQARSKKGMKSEITPK 638  
 DB 601 YIDKGNRTYTPVNGTGY-SLALVPIYSFYIAKLEETITQARSKKGMKSEITPK 653  
 QY 639 DNFEESGYTFLAPRDYCDNLIKISDNTEFLNFNEFIDRKTPNPNPSCMTDLINRYLDAG 698  
 DB 654 DNFEESGYTFLAPRDYCDNLIKISDNTEFLNFNEFIDRKTPNPNPSCMTDLINRYLDAG 713  
 QY 699 FPNELVQVWWSKQKNIKVKAFVYTTDGTIRVYRKKEGEMWQENPEFYEDSFYKRSIDN 758  
 DB 714 FPNELVQVWWSKQKNIKVKAFVYTTDGTIRVYRKKEGEMWQENPEFYEDSFYKRSIDN 773  
 QY 759 DNVYFTAPYFNKSGGAVESGIMVSKAVEIYIOGKILPVAVGIKIDVNSWIENTFTSI 818  
 DB 774 DNVYFTAPYFNKSGGAVESGIMVSKAVEIYIOGKILPVAVGIKIDVNSWIENTFTSI 833  
 QY 819 RPPCAGPVDCCKRNSDVMDCVILDDGFLMANHDDYTNQIGRFGETIDPSLMRLVNI 878  
 DB 834 RPPCAGPVDCCKRNSDVMDCVILDDGFLMANHDDYTNQIGRFGETIDPSLMRLVNI 893  
 QY 879 VYAFNKSYDYGSCERGAAPKOGAGRSAYPSTADIIHGMWATAAWSLLOQFLSLT 938  
 DB 894 VYAFNKSYDYGSCERGAAPKOGAGRSAYPSTADIIHGMWATAAWSLLOQFLSLT 953  
 QY 939 FPRLLAEVEMEDDPTASISKOSCTEOTOFYFENDSKSFGSVLDDCGNCSIFVHEKLMN 998  
 DB 954 FPRLLAEVEMEDDPTASISKOSCTEOTOFYFENDSKSFGSVLDDCGNCSIFVHEKLMN 1013  
 QY 999 TMLIFIVWSKGTCCDTRLILQAEQTSIDGPDPCDMVK 1036  
 DB 1014 TMLIFIVWSKGTCCDTRLILQAEQTSIDGPDPCDMVK 1051

## RESULT 4

T30256

calcium channel alpha-2-delta-C chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 20-Jun-2000

C:Accession: T30256

R:Klugbauer, N.; Iachova, L.; Marais, E.; Hobom, M.; Hofmann, F.

J. Neurosci. 19, 648-691, 1999

A:Title: Molecular diversity of the calcium channel alpha2delta subunit.

A:Reference number: Z20794

A:Accession: T30256

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1091 &lt;KUD&gt;

A:Cross-references: EMBL:AJ010949; PIDN:CAA09423.1

A:Experimental source: brain

C:Superfamily: calcium channel alpha-2 chain

Query Match

Best Local Similarity 20.4%; Score 1112; DB 2; Length 1091;

Matches 311; Conservative 224; Mismatches 411; Indels 130; Gaps 39;

QY 3 AGCLATLTLTFFOSLIGPSSEPPPSAVTITKSWDKMEDLVTLAKTASGVNOLVLDIYE 62  
 DB 14 ASALLA-TALLYALAGDVVRSEQIPLSV-VKMAASAGGEIKSIKAKYSSQLQKKYK 71  
 QY 63 KYQDLYTVEPNNAKQLEIAARDIEKILSNRSKALVRLALEAKYQAOAHQWREDA 122

```

|||||
Db 301 VSCFHLVQANRNKRVLDVANNITAKGTTDKKGFSEFQOLLNYSRANCKNTIML 360
QY 361 FTGGEERAOEIFAKYNNKKVAVTFEVSQGHNDYRGPLOMMACENKGYEIEPSGAIR 420
Db 361 FTGGEERAOEIFAKYNNKKVAVTFEVSQGHNDYRGPLOMMACENKGYEIEPSGAIR 420
QY 421 INTQYELVLDVGRPMVLADGKAKOVONTNVLDALELGLVITGTLPPVNTIGONENKTNL 480
Db 421 INTQYELVLDVGRPMVLADGKAKOVONTNVLDALELGLVITGTLPPVNTIGONENKTNL 480
QY 481 NQILIGVGVDSLEDIKRLTPRTLCPPNGYGFADIPNGYVLLHPLOPKNKSOEPTVL 540
Db 481 NQILIGVGVDSLEDIKRLTPRTLCPPNGYGFADIPNGYVLLHPLOPKNKSOEPTVL 540
QY 541 DFLDALENDIKVEIRNNKIDGESSEKTRTLVKSODEYIKNKNTYTWTPVNGDYSL 600
Db 541 DFLDALENDIKVEIRNNKIDGESSEKTRTLVKSODEYIKNKNTYTWTPVNGDYSL 600
QY 601 ALVLPYSEFYIYAKIEETITQARSKKGMKODETLKPDNFEESGYTFIAPRDYCNLDKI 660
Db 601 ALVLPYSEFYIYAKIEETITQARSKKGMKODETLKPDNFEESGYTFIAPRDYCNLDKI 660
QY 661 SDNTEFLNENEFIDRKTPNNPSCNTDLINRYLDAGFTNELVONYSKONIKGVKAR 720
Db 661 SDNTEFLNENEFIDRKTPNNPSCNTDLINRYLDAGFTNELVONYSKONIKGVKAR 720
QY 721 FVVTDSGITRVYKPEAGENMOENPEYEDSFYKRSIDNINNYFTAPYFNKSGGAYESGI 780
Db 721 FVVTDSGITRVYKPEAGENMOENPEYEDSFYKRSIDNINNYFTAPYFNKSGGAYESGI 780
QY 781 MYSKAVEITYIOGKLLKPAVYVGIKIDVNSWIENTKTSINDPCAGPYCCKRNSDVMDCVI 840
Db 781 MYSKAVEITYIOGKLLKPAVYVGIKIDVNSWIENTKTSINDPCAGPYCCKRNSDVMDCVI 840
QY 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRLVNI SYAFNKSVDYQVCEPGAAPK 900
Db 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRLVNI SYAFNKSVDYQVCEPGAAPK 900
QY 901 GAGHRSAVYPSIADILHIGMATTAAMSILQOFLSLTFPRLLLEAVEMDDDTASTLSK 960
Db 901 GAGHRSAVYPSIADILHIGMATTAAMSILQOFLSLTFPRLLLEAVEMDDDTASTLSK 960
QY 961 SCITEOTQYFFDNDKSFSGVLDGNCSTRIFHEKLMNTNLIFIMESKGTCCDTRLI 1020
Db 961 SCITEOTQYFFDNDKSFSGVLDGNCSTRIFHEKLMNTNLIFIMESKGTCCDTRLI 1020
QY 1021 QAEOTSDGPPDCMVK 1036
Db 1021 QAEOTSDGPPDCMVK 1036

```

## RESULT 2

A44147

calcium channel protein alpha-2 chain precursor - rat

N/Alternate names: dihydropyridine-sensitive L-type

N/Contains: calcium channel alpha-2 chain

C/Species: Rattus norvegicus (Norway rat)

C/Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 20-Aug-1999

C/Accession: A44147

R:Klm, H.L.; Lee, P.; King, R.G.; Chin, H.

Proc. Natl. Acad. Sci. U.S.A. 89, 3251-3255, 1992

A/Title: Rat brain expresses an alternatively spliced form of the dihydropyridine-sensit

A/Reference number: A44147; MUID:92228762; PMID:1314383

A/Accession: A44147

A/Status: Preliminary

A/Molecule type: mRNA

A/Residues: 1-1091 &lt;KIM&gt;

C/Cross-references: GB:M86621; NID:9203954; PIDN:AAA41088.1; PID:9203955

C/Superfamily: calcium channel alpha-2 chain

C/Keywords: calcium; glycoprotein; ion channel; transmembrane protein

Query Match 96.7%; Score 5268; DB 2; Length 1091;

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Best Local Similarity 96.2%; Pred. No. 4,6e-309;
Matches 998; Conservative 23; Mismatches 14; Indels 2; Gaps 2;
QY 1 MAAGLLALTTLTFOSSILGSSOEPFSAVITKSWDKMEDIVTAKASGNOLVDI 60
Db 1 MAAGLLALTTLTFOSSILGSSOEPFSAVITKSWDKMEDIVTAKASGNOLVDI 60
QY 61 YEKYODLVTEBPNNARQVLEIARDIEKLSNRKALVRLALEAKYQAAHOMREDEASN 120
Db 61 YEKYODLVTEBPNNARQVLEIARDIEKLSNRKALVRLALEAKYQAAHOMREDEASN 120
QY 121 EYVYNNADDDLPKNDSEPSQRIKPYFIDANFGROIISQHAHVHPDIDYEGSTIVL 180
Db 121 EYVYNNADDDLPKNDSEPSQRIKPYFIDANFGROIISQHAHVHPDIDYEGSTIVL 180
QY 181 NELNMTSALDEYFKNNRDEPTLLMQYF-AADRILARYIPASPWDNSRTPKIDLYVRR 240
Db 181 NELNMTSALDEYFKNNRDEPTLLMQYF-AADRILARYIPASPWDNSRTPKIDLYVRR 240
QY 241 RPWYIOGAASPKDMLIVDVSQVSGTLTKLIRTSVSEMETLSDDDFVNVASFNSAOD 300
Db 241 RPWYIOGAASPKDMLIVDVSQVSGTLTKLIRTSVSEMETLSDDDFVNVASFNSAOD 300
QY 301 VSCFHLVQANRNKRVLDVANNITAKGTTDKKGFSEFQOLLNYSRANCKNTIML 360
Db 301 VSCFHLVQANRNKRVLDVANNITAKGTTDKKGFSEFQOLLNYSRANCKNTIML 360
QY 361 FTGGEERAOEIFAKYNNKKVAVTFEVSQGHNDYRGPLOMMACENKGYEIEPSGAIR 420
Db 361 FTGGEERAOEIFAKYNNKKVAVTFEVSQGHNDYRGPLOMMACENKGYEIEPSGAIR 420
QY 421 INTQYELVLDVGRPMVLADGKAKOVONTNVLDALELGLVITGTLPPVNTIGONENKTNL 480
Db 421 INTQYELVLDVGRPMVLADGKAKOVONTNVLDALELGLVITGTLPPVNTIGONENKTNL 480
QY 481 NQILIGVGVDSLEDIKRLTPRTLCPPNGYGFADIPNGYVLLHPLOPKNKSOEPTVL 540
Db 481 NQILIGVGVDSLEDIKRLTPRTLCPPNGYGFADIPNGYVLLHPLOPKNKSOEPTVL 540
QY 541 DFLDALENDIKVEIRNNKIDGESSEKTRTLVKSODEYIKNKNTYTWTPVNGDYSL 600
Db 541 DFLDALENDIKVEIRNNKIDGESSEKTRTLVKSODEYIKNKNTYTWTPVNGDYSL 600
QY 601 ALVLPYSEFYIYAKIEETITQARSKKGMKODETLKPDNFEESGYTFIAPRDYCNLDKI 660
Db 601 ALVLPYSEFYIYAKIEETITQARSKKGMKODETLKPDNFEESGYTFIAPRDYCNLDKI 660
QY 661 SDNTEFLNENEFIDRKTPNNPSCNTDLINRYLDAGFTNELVONYSKONIKGVKAR 720
Db 661 SDNTEFLNENEFIDRKTPNNPSCNTDLINRYLDAGFTNELVONYSKONIKGVKAR 720
QY 721 FVVTDSGITRVYKPEAGENMOENPEYEDSFYKRSIDNINNYFTAPYFNKSGGAYESGI 780
Db 721 FVVTDSGITRVYKPEAGENMOENPEYEDSFYKRSIDNINNYFTAPYFNKSGGAYESGI 780
QY 781 MYSKAVEITYIOGKLLKPAVYVGIKIDVNSWIENTKTSINDPCAGPYCCKRNSDVMDCVI 840
Db 781 MYSKAVEITYIOGKLLKPAVYVGIKIDVNSWIENTKTSINDPCAGPYCCKRNSDVMDCVI 840
QY 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRLVNI SYAFNKSVDYQVCEPGAAPK 900
Db 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRLVNI SYAFNKSVDYQVCEPGAAPK 900
QY 901 GAGHRSAVYPSIADILHIGMATTAAMSILQOFLSLTFPRLLLEAVEMDDDTASTLSK 960
Db 901 GAGHRSAVYPSIADILHIGMATTAAMSILQOFLSLTFPRLLLEAVEMDDDTASTLSK 960
QY 961 SCITEOTQYFFDNDKSFSGVLDGNCSTRIFHEKLMNTNLIFIMESKGTCCDTRLI 1020
Db 961 SCITEOTQYFFDNDKSFSGVLDGNCSTRIFHEKLMNTNLIFIMESKGTCCDTRLI 1020
QY 1021 QAEOTSDGPPDCMVK 1036
Db 1021 QAEOTSDGPPDCMVK 1036

```

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 10, 2003, 14:13:54 ; Search time 19.7185 Seconds

(without alignments)  
5050.861 Million cell updates/sec

Title: US-10-090-827-7

Perfect score: 5446

Sequence: 1 MAAGCLLALTLTFLFSLIG.....RLLIQAETSDGPDPCDMWK 1036

Scoring table: BL0SUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5360	98.8	1091	2 JH0565	calcium channel al
2	5268	96.7	1091	2 A44147	calcium channel pr
3	5253.5	96.5	1106	1 CHRAA2	calcium channel al
4	1112	20.4	1091	2 T30256	calcium channel al
5	611	11.2	734	2 S44617	C50C3.11 protein
6	571	10.5	1148	2 T18770	probable calcium c
7	196.5	3.6	886	2 S54355	inter-alpha-trypsi
8	190.5	3.5	1450	2 C86880	hypothetical prote
9	188	3.5	885	2 S30350	inter-alpha-trypsi
10	170.5	3.1	1819	2 D97033	uncharacterized pr
11	168.5	3.1	575	2 D64998	hypothetical prote
12	166	3.0	889	2 UC5576	inter-alpha-trypsi
13	165	3.0	459	2 F64688	protease (EC 3.4
14	160.5	2.9	420	2 S76691	hypothetical prote
15	160.5	2.9	2364	2 T40884	cytotoxin L - Clo
16	159	2.9	932	2 JC5953	inter-alpha-inh1b1
17	158.5	2.9	918	2 E90542	lipoprotein (impor
18	153.5	2.9	946	1 T1H02	inter-alpha-trypsi
19	155	2.8	1315	2 T28679	fibronogen-binding
20	155	2.8	1984	2 A44396	P-type cation tran
21	154	2.8	1426	2 D96930	methyl-accepting c
22	153.5	2.8	946	2 A99580	hypothetical prote
23	153	2.8	5005	2 JC5575	inter-alpha-trypsi
24	152.5	2.8	5005	2 F82884	hypothetical prote
25	152	2.8	1516	2 E71619	membrane associate
26	150.5	2.7	680	2 A97331	methyl-accepting c
27	149.5	2.7	921	2 JC4625	inter-alpha-trypsi
28	149.5	2.7	926	2 D86897	hypothetical prote

30	149.5	2.7	3216	2 C90538	hypothetical prote
31	148.5	2.7	1285	2 B72420	hypothetical prote
32	148	2.7	2706	2 T28155	variant-specific s
33	147.5	2.7	689	2 F84811	probable retroelem
34	147.5	2.7	1237	2 AC1583	interalpha protein
35	147	2.7	1087	1 S41797	cellulose 1,4-beta
36	146.5	2.7	676	2 T47637	hypothetical prote
37	146	2.7	1027	2 B90527	atp-binding prote
38	145	2.7	1385	2 D89824	hypothetical prote
39	145	2.7	1599	2 S22737	glucosyltransferas
40	145	2.7	1864	2 T18485	hypothetical prote
41	145	2.7	2401	2 T28676	thioxy protein -
42	144.5	2.7	929	2 I51027	type XII collagen
43	144	2.6	930	2 JX0368	inter-alpha-trypsi
44	144	2.6	1091	2 S33850	fibronectin-binding
45	143.5	2.6	1243	2 S60138	sex factor aggrega

## ALIGNMENTS

## RESULT 1

JH0565  
Calcium channel alpha-2b chain precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 20-Aug-1999  
C:Accession: JH0565

R.Williams, M.E., Feldman, D.H., McCue, A.F., Brenner, R., Velicelebi, G., Ellis, S.B.  
Neuron 8, 71-84, 1992

A>Title: Structure and functional expression of alpha1, alpha2, and beta subunits of  
A:Reference number: JH0564; PMID:92110010; PMID:1309651

A:Accession: JH0565  
A:Molecule type: mRNA

A:Residues: 1-1091 <WIL>  
A:Cross-references: GB:M6559; NID:q179761; PIDN:AAA51903.1; PID:q179762

A:Experimental source: basal ganglia  
A:Note: Several conflicts are found between Genbank submission, authors' translation

C:Comment: This protein is a subunit of the voltage dependent calcium channel.  
C:Superfamily: calcium channel alpha-2 chain

C:Keywords: glycoprotein; phosphoprotein  
F.1-24/Domain: signal sequence #status predicted <SIG>

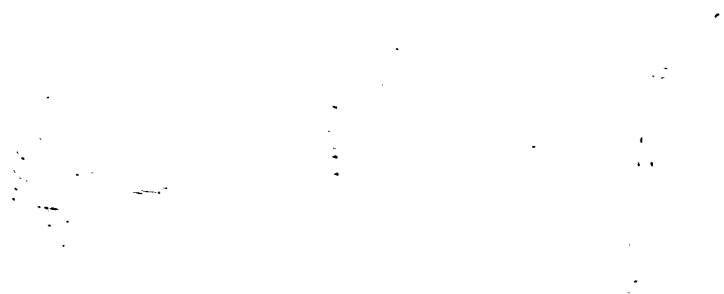
F.25-1067/Product: calcium channel alpha-2b chain #status predicted <CAL>  
F.32,268,326,539,635,1087/Binding site: phosphate (Thr) (covalent) (by protein kinase

F.91,142,250,625,817/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #  
F.92,136,184,324,348,468,475,585,594,663,682,769,812,876,883,973,986/Binding site: ca

F.501/Binding site: phosphate (Thr) (covalent) #status predicted  
F.833/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status pre

Query Match 98.8%; Score 5380; DB 2; Length 1091;  
Best Local Similarity 98.7%; Pred. No. 8.3e-316;  
Matches 1023; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY	1	MAAGCLLALTLTFLFSLIGSSQPPPSATYIKSWYKMDLVTLAKTASGVQVLDI 60	
DB	1	MAAGCLLALTLTFLFSLIGSSQPPPSATYIKSWYKMDLVTLAKTASGVQVLDI 60	
QY	61	YKKYODLTVEPNNAKRLVEIAARDIEKILSRSAVLRLLEAKVOAAHQWREDFASN 120	
DB	61	YKKYODLTVEPNNAKRLVEIAARDIEKILSRSAVLRLLEAKVOAAHQWREDFASN 120	
QY	121	EVVYNNAKDDLDPEKNDESPGSQRIKPVFIDANGFROIYSOHAHVIPTDIYEGSTIVL 180	
DB	121	EVVYNNAKDDLDPEKNDESPGSQRIKPVFIDANGFROIYSOHAHVIPTDIYEGSTIVL 180	
QY	181	NELNMTSALDEYFKKRNREDESSLIMQVGSATGLARYYPASPVWDSNTPKIDLYDVR 240	
DB	181	NELNMTSALDEYFKKRNREDESSLIMQVGSATGLARYYPASPVWDSNTPKIDLYDVR 240	
QY	241	RMWYTGAAAPKMDLILVDGSGVSGTLKILRTSVSMLETLDDDPVNVNASFNSNAD 300	
DB	241	RMWYTGAAAPKMDLILVDGSGVSGTLKILRTSVSMLETLDDDPVNVNASFNSNAD 300	
QY	301	VSCFQHLVQAVNRRKKVLDAVNNITAKGITDYKKGSFAFEQLLNVNFRANCKIIML 360	



US-08-435-675B-5  
 : Sequence 5, Application US/08435675B  
 : Patent No. 5710250  
 :  
 : GENERAL INFORMATION:  
 : APPLICANT: Ellis, Steven Bradley  
 : APPLICANT: Williams, Mark E.  
 : APPLICANT: Harpold, Michael Miller  
 : APPLICANT: Schwartz, Arnold  
 : APPLICANT: Brenner, Robert  
 : TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS  
 : NUMBER OF SEQUENCES: 6  
 :  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Brown, Martin, Haller & McClain  
 : STREET: 1660 Union Street  
 : CITY: San Diego  
 : STATE: CA  
 : COUNTRY: USA  
 : ZIP: 92101-2926  
 :  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Diskette  
 : COMPUTER: IBM Compatible  
 : OPERATING SYSTEM: DOS  
 : SOFTWARE: FASTSEQ Version 1.5  
 :  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/435,675B  
 : FILING DATE: 05-MAY-1995  
 : CLASSIFICATION: 435  
 :  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 08/314,083  
 : FILING DATE: 28-SEP-1994  
 : APPLICATION NUMBER: US 07/914,231  
 : FILING DATE: 13-JUL-1992  
 : APPLICATION NUMBER: US 07/603,751  
 : FILING DATE: 08-NOV-1990  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Seidman, Stephanie L.  
 : REGISTRATION NUMBER: 33,779  
 : REFERENCE/DOCKET NUMBER: 6362-53193  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 619-238-0999  
 : TELEFAX: 619-238-0062  
 :  
 : INFORMATION FOR SEQ ID NO: 5:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 1106 amino acids  
 : TYPE: amino acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: protein  
 : FRAGMENT TYPE: internal  
 : US-08-435-675B-5

Query Match 96.6%; Score 5410.5; DB 1; Length 1106;  
 Best local similarity 95.5%; Pred. No. 0;  
 Matches 1036; Conservative 10; Mismatches 10; Indels 29; Gaps 4;

QY 1 MAAGCLLALTTLEFGS--LLIGPSSQEPFSPAVTIKSWDKMQEDLVTLAATASGVNOLV 58  
 DB 1 MAAGRLAMWTLTLMQAMLLILIGPSSSEFPSPAVTIKSWDKMQEDLVTLAATASGVNOLV 60  
 QY 59 DIYEKYGDLTYEPNNAQOLVEIARQLEKLLSNRSKALVRLALEAEVQAHHQREFEA 118  
 DB 61 DIYEKYGDLTYEPNNAQOLVEIARQLEKLLSNRSKALVRLALEAEVQAHHQREDEFA 120  
 QY 119 SNEVYVYNAKDDLDPEKNDSEPGSORIKPFVIDANFGROI SYOHAHVITPDIYEGSTI 178  
 DB 121 SNEVYVYNAKDDLDPEKNDSEPGSORIKPFVIDANFRÖVSYOHAHVITPDIYEGSTI 180  
 QY 179 VLNELNMTSALDEVFKKRNREDPSLLMQVFGSATGLARYTPASPWNDSRTPNKIDLYDV 238  
 DB 181 VLNELNMTSALDEVFKKRNREDPSLLMQVFGSATGLARYTPASPWNDSRTPNKIDLYDV 240  
 QY 239 RRRPWYIOGAASPKDMLILVDVSGSVGLTLKLTIVSEMIETLSDDDFVNVA SFNSNA 298

DB 241 RRRPWYIOGAASPKDMLILVDVSGSVGLTLKLTIVSEMIETLSDDDFVNVA SFNSNA 300  
 QY 299 QDVSCFOHLVQAVNRKKVYKADAVNNITAKGITDYKKGSPFAFEOILLNNTVNSANCKIT 358  
 DB 301 QDVSCFOHLVQAVNRKKVYKADAVNNITAKGITDYKKGSPFAFEOILLNNTVNSANCKIT 360  
 QY 359 MLPTDGGEEBAOELFAKYNKDKVRYFTSVGQHNDRGPIQMACENKGYEYFISGA 418  
 DB 361 MLPTDGGEEBAOELFAKYNKDKVRYFTSVGQHNDRGPIQMACENKGYEYFISGA 420  
 QY 419 IRIINTOEYLDVIGRPVYIADGKAKQVQWNTVYLDALGLVITGTLPVENITGQNEKTN 478  
 DB 421 IRIINTOEYLDVIGRPVYIADGKAKQVQWNTVYLDALGLVITGTLPVENITGQNEKTN 480  
 QY 479 LKNQOLLIGVGVDSIEDIKRLTPRETLCPNGYFAIDPBGVYLLHPNLPQK----- 530  
 DB 481 LKNQOLLIGVGVDSIEDIKRLTPRETLCPNGYFAIDPBGVYLLHPNLPQKIGVIGPT 540  
 QY 531 -----NPKSQEPVTLDFLDAELENDIKVEIRNKKIDEGSEKTFRTLYKSQDR 579  
 DB 541 INLRKRRPNQNRKSGQEPVTLDFLDAELENDIKVEIRNKKIDEGSEKTFRTLYKSQDR 600  
 QY 580 YIDKGNFTYTWTPVNGTDY-SLALVLPYSFYIAKIEETITQANSKKKKMSSETLKP 638  
 DB 601 YIDKGNFTYTWTPVNGTDYSLALVLPYSFYIAKIEETITQARY-----SETLKP 653  
 QY 639 DNEESGYTFIAPRDYCNQDKISDNTEFLNNEEDIRKTPNNSCNTDLINRYLIDG 698  
 DB 654 DNEESGYTFIAPRDYCNQDKISDNTEFLNNEEDIRKTPNNSCNTDLINRYLIDG 713  
 QY 699 FTNELVQNYWSKONIKGVAKRFVTDGCTIRYVPRKAGENMOENBETEDSEYKKSILN 758  
 DB 714 FTNELVQNYWSKONIKGVAKRFVTDGCTIRYVPRKAGENMOENBETEDSEYKKSILN 773  
 QY 759 DNYVFTAPYFNKSGPGAYESGIWKAVEIYIOGKLLKPAVVICIKIDVNSMIENFTKTSI 818  
 DB 774 DNYVFTAPYFNKSGPGAYESGIWKAVEIYIOGKLLKPAVVICIKIDVNSMIENFTKTSI 833  
 QY 819 RDPGAGVPCCKRNSDVMDCVIIDGGFLLMANHDDYTNOIGRFGEIDPSLMRHLVNTS 878  
 DB 834 RDPGAGVPCCKRNSDVMDCVIIDGGFLLMANHDDYTNOIGRFGEIDPSLMRHLVNTS 893  
 QY 879 VYAFNKSVDYQVCEPQAPKQAGHRSAYVPSIADILHIGWATAAAMSTIQQFLSLT 938  
 DB 894 VYAFNKSVDYQVCEPQAPKQAGHRSAYVPSIADILHIGWATAAAMSTIQQFLSLT 953  
 QY 939 FPRLLAEVEMEDDFTASLSKQSCITEQTYFFDNDNSKSFSGVLDGNCSTRIFHYEKLNN 998  
 DB 954 FPRLLAEVEMEDDFTASLSKQSCITEQTYFFDNDNSKSFSGVLDGNCSTRIFHYEKLNN 1013  
 QY 999 TNLIFIVESKGTCPCTRLILIAEQTSDGPDGCDMWKQPRYKRGDPVCFDNNALLETYD 1058  
 DB 1014 TNLIFIVESKGTCPCTRLILIAEQTSDGPDGCDMWKQPRYKRGDPVCFDNNALLETYD 1073  
 QY 1059 CGGVS 1063  
 DB 1074 CGGVS 1078

Search completed: February 10, 2003, 14:23:17  
 Job time : 16.7901 secs

## RESULT 14

US-08-223-305C-55

; Sequence 55. Application US/08223305C

; Patent No. 5851824

; GENERAL INFORMATION:

; APPLICANT: Harpold, Michael

; APPLICANT: Ellis, Steven

; APPLICANT: Williams, Mark

; APPLICANT: Feldman, Daniel

; APPLICANT: McCue, Ann

; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

; NUMBER OF SEQUENCES: 57

; CORRESPONDENCE ADDRESS: 57

; ADDRESSER: Brown, Martin, Haller &amp; McClain

; STREET: 1660 Union Street

; CITY: San Diego

; STATE: California

; COUNTRY: USA

; ZIP: 92101-2926

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/223,305C

; FILING DATE: April 4, 1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/868,354

; FILING DATE: April 10, 1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/745,206

; FILING DATE: 15-AUG-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/620,250

; FILING DATE: 30-NOV-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/482,384

; FILING DATE: 20-FEB-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/603,751

; FILING DATE: 04-APR-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US89/01408

; FILING DATE: 04-APR-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/176,899

; FILING DATE: 04-APR-1988

; ATTORNEY/AGENT INFORMATION:

; NAME: Seidman, Stephanie L.

; REGISTRATION NUMBER: 33,779

; REFERENCE/DOCKET NUMBER: 52516 (P519739)

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619)238-0999

; TELEFAX: (619)238-0062

; INFORMATION FOR SEQ ID NO: 55:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1079 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FRAGMENT TYPE: internal

; US-08-223-305C-55

Query Match 97.0%; Score 5436; DB 2; Length 1079;

Best Local Similarity 97.5%; Pred. No. 0;

Matches 1036; Conservative 6; Mismatches 9; Indels 12; Gaps 2;

QY 1 MAAGCLALTLTLFQSLILIGPSSEPPSAVTIKSWVDKQEDLVTLAKTASGVNLVDI 60

Db 1 MAAGCLALTLTLFQSLILIGPSSEPPSAVTIKSWVDKQEDLVTLAKTASGVNLVDI 60

QY 61 YKKYODLTVPEPNNAKQVETIARADIEKILSNRSKATVRLAEAKVQAQAHQMEDFASN 120

Db 61 YKKYODLTVPEPNNAKQVETIARADIEKILSNRSKATVRLAEAKVQAQAHQMEDFASN 120

QY 121 EYVYVNAKDDLPKNDSPGSRQIKPVFIDDANFGROIYQHAHVHPTDIYEGSTIVL 180

Db 121 EYVYVNAKDDLPKNDSPGSRQIKPVFIDDANFGROIYQHAHVHPTDIYEGSTIVL 180

QY 181 NELNMTSALDEVEFKKREDDPSLIMOVGSATGLARVYPAAPWVNSRTPKIDLYDR 240

Db 181 NELNMTSALDEVEFKKREDDPSLIMOVGSATGLARVYPAAPWVNSRTPKIDLYDR 240

QY 241 RPYVYOGAASPKDMLLVDSVSGSLTLKRLTSVSEMLFETLSDDDPVNVAASFNSNAD 300

Db 241 RPYVYOGAASPKDMLLVDSVSGSLTLKRLTSVSEMLFETLSDDDPVNVAASFNSNAD 300

QY 301 VSCFOHLVQANVRNKKVYLKDAVNNITAKGIDYKKGFSAFEOQLNIVNSRANCKIIML 360

Db 301 VSCFOHLVQANVRNKKVYLKDAVNNITAKGIDYKKGFSAFEOQLNIVNSRANCKIIML 360

QY 361 FTDDGGERAOEIEFAYNKKDKYRVFTSVGQHNDRGPIONMACENKGYEIPISGAIR 420

Db 361 FTDDGGERAOEIEFAYNKKDKYRVFTSVGQHNDRGPIONMACENKGYEIPISGAIR 420

QY 421 INTOEYLDVIGRPVYLAGDKAKOVQWTVNYLDALGLVITGTLPLVFNITGONENKTIK 480

Db 421 INTOEYLDVIGRPVYLAGDKAKOVQWTVNYLDALGLVITGTLPLVFNITGONENKTIK 480

QY 481 NOLILGKMGVDSLEEDIKRLTRFTLCRPGYFAIDPNKYVYLHNNIDPKNKSEPTL 540

Db 481 NOLILGKMGVDSLEEDIKRLTRFTLCRPGYFAIDPNKYVYLHNNIDPKNKSEPTL 540

QY 541 DFLDAELNDIKVEIRNKMIDSESGEKTFTLYKSODERYIDKGRRTYTWTPVNGTDSL 600

Db 541 DFLDAELNDIKVEIRNKMIDSESGEKTFTLYKSODERYIDKGRRTYTWTPVNGTDSL 600

QY 536 DFLDAELNDIKVEIRNKMIDSESGEKTFTLYKSODERYIDKGRRTYTWTPVNGTDSL 595

Db 536 DFLDAELNDIKVEIRNKMIDSESGEKTFTLYKSODERYIDKGRRTYTWTPVNGTDSL 595

QY 601 ALVLPYTSFYIYKAKIEETITQARSKKKMKSEITLKPNEESGYTFLAPDYCNLDKI 660

Db 601 ALVLPYTSFYIYKAKIEETITQARSKKKMKSEITLKPNEESGYTFLAPDYCNLDKI 660

QY 596 ALVLPYTSFYIYKAKIEETITQARSKKKMKSEITLKPNEESGYTFLAPDYCNLDKI 648

Db 596 ALVLPYTSFYIYKAKIEETITQARSKKKMKSEITLKPNEESGYTFLAPDYCNLDKI 648

QY 661 SDNTEFLNENFIDRKTNNPNSCNTDLINRYLDAGFTNELVQVNSKONINGVAR 720

Db 661 SDNTEFLNENFIDRKTNNPNSCNTDLINRYLDAGFTNELVQVNSKONINGVAR 720

QY 649 SDNTEFLNENFIDRKTNNPNSCNTDLINRYLDAGFTNELVQVNSKONINGVAR 708

Db 649 SDNTEFLNENFIDRKTNNPNSCNTDLINRYLDAGFTNELVQVNSKONINGVAR 708

QY 721 FVYTDGIGTRVYKKEAGENMOENPETEYDSFYKRSIDNDNYVFTAPYFKSGPAYESGI 780

Db 721 FVYTDGIGTRVYKKEAGENMOENPETEYDSFYKRSIDNDNYVFTAPYFKSGPAYESGI 780

QY 709 FVYTDGIGTRVYKKEAGENMOENPETEYDSFYKRSIDNDNYVFTAPYFKSGPAYESGI 768

Db 709 FVYTDGIGTRVYKKEAGENMOENPETEYDSFYKRSIDNDNYVFTAPYFKSGPAYESGI 768

60

120

120

180

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300

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420

480

540

600

595

660

648

720

708

780

768

840

828

900

888

948

960

1020

1008

1063

1051

1008

1063

1051

1008

1063

RESULT 13  
US-08-455-543A-55  
Sequence 55, Application US/08455543A  
Patent No. 5792846  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: Pasteo Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,543A  
FILING DATE: May 31, 1995  
APPLICATION NUMBER: 08/223,305  
FILING DATE: April 4, 1994  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-52517  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1079 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-455-543A-55

Query Match 97.0%; Score 5436; DB 1; Length 1079;  
Best Local Similarity 97.5%; Pred. No. 0;  
Matches 1036; Conservative 6; Mismatches 9; Indels 12; Gaps 2;

QY 1 MAAGCLLTLTLFOSLLIGPSSOEPPSAVTKSGWDMKQEDVTLAKTASGVNQLVDI 60  
DB 1 MAAGCLLTLTLFOSLLIGPSSOEPPSAVTKSGWDMKQEDVTLAKTASGVNQLVDI 60  
QY 61 YEKYODLYVEEPNNARQLEIAARDIEKLSRSKALVRLALEAKVOAAHQRDEFSN 120  
DB 61 YEKYODLYVEEPNNARQLEIAARDIEKLSRSKALVRLALEAKVOAAHQRDEFSN 120  
QY 121 EYVYINAKDDLDPEKNDSEPSQRIKPVFIDANFGROIYQHAHVIPTDIYEGSTIVL 180  
DB 121 EYVYINAKDDLDPEKNDSEPSQRIKPVFIDANFGROIYQHAHVIPTDIYEGSTIVL 180  
QY 181 NELNMTSALDEVEFKKREDEPSLMQVGSATGLARYYPASPWDNSRTPKIDLYVRR 240  
DB 181 NELNMTSALDEVEFKKREDEPSLMQVGSATGLARYYPASPWDNSRTPKIDLYVRR 240  
QY 241 RPYITOGAASPDKMLILDVSGSVGLTLKLRISVSEMLTSLDDPFVNVASFNSNAD 300  
DB 241 RPYITOGAASPDKMLILDVSGSVGLTLKLRISVSEMLTSLDDPFVNVASFNSNAD 300  
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGSFAEQLLNTVSRANCKTIML 360  
DB 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGSFAEQLLNTVSRANCKTIML 360  
QY 361 FTDGGEERAQELFAKYNKDKVRFVTFSGOHNDROGQIOMACENKGYEIEPSIGAIR 420  
DB 361 FTDGGEERAQELFAKYNKDKVRFVTFSGOHNDROGQIOMACENKGYEIEPSIGAIR 420  
QY 421 INFOEYLDVIGRPVYLAGDKAKOVWNTVYLDALDELGLVITGTLVPVNTIGONENKTNLK 480  
DB 421 INFOEYLDVIGRPVYLAGDKAKOVWNTVYLDALDELGLVITGTLVPVNTIGONENKTNLK 480  
QY 481 NOLLIGVGVVSLIEDIKRLPRTLCNGYFPAIDNGVYLLHPNLOPKNPKSOEPTVL 540  
DB 481 NOLLIGVGVVSLIEDIKRLPRTLCNGYFPAIDNGVYLLHPNLOPKNPKSOEPTVL 540  
QY 541 DFLDAELENDIKVELRNKMGIDEGSEKTFRTLVKSODERYIDKGNRTYMPVNGTYSL 600  
DB 541 DFLDAELENDIKVELRNKMGIDEGSEKTFRTLVKSODERYIDKGNRTYMPVNGTYSL 600  
QY 596 ALVLPYTSFYIYKAKLEETITQARY-----SETLKPNDFEESGYFIAPRDYCNLKI 648  
DB 596 ALVLPYTSFYIYKAKLEETITQARY-----SETLKPNDFEESGYFIAPRDYCNLKI 648  
QY 661 SDNNTTEFLNNEFIIDRTKTPNNPSCNDLIRVYLDAGFTNELVQNTWSKQKNIKGYKAR 720  
DB 661 SDNNTTEFLNNEFIIDRTKTPNNPSCNDLIRVYLDAGFTNELVQNTWSKQKNIKGYKAR 720  
QY 721 FVVTIDGITTIRVYPRKEAGENQENPEYEDSFYKSLDNDVYVFTAPYFNKSGQAYESGI 780  
DB 721 FVVTIDGITTIRVYPRKEAGENQENPEYEDSFYKSLDNDVYVFTAPYFNKSGQAYESGI 780  
QY 781 MYSKAVELYIQQKLLKAAVYGIKIDVNSWLENFTKTSIRDPGAGVCDCKRNSDNDVCYI 840  
DB 781 MYSKAVELYIQQKLLKAAVYGIKIDVNSWLENFTKTSIRDPGAGVCDCKRNSDNDVCYI 840  
QY 841 LDDGGLFLMANHDDYTQIGRFGEIDPSLMRHLVNTSVYAFNKSVDYOSVCEPAGAPRO 888  
DB 841 LDDGGLFLMANHDDYTQIGRFGEIDPSLMRHLVNTSVYAFNKSVDYOSVCEPAGAPRO 888  
QY 901 GAGHRSAVYPSIADILHIGMATAAWSIIQOELSLTSPRRLLEAVEMEDDDTATSLSKQ 960  
DB 901 GAGHRSAVYPSIADILHIGMATAAWSIIQOELSLTSPRRLLEAVEMEDDDTATSLSKQ 960  
QY 949 SCITEQTYOFFDNDKSFSESVLDCGNCSTRIFHEKELMTNLLPIVNESKGTGCDTRLILI 1008  
DB 949 SCITEQTYOFFDNDKSFSESVLDCGNCSTRIFHEKELMTNLLPIVNESKGTGCDTRLILI 1008  
QY 1021 QAEQTSQDPDCDMVKOPRYRKGPVOCFDMNALEDYTDGCGVS 1063  
DB 1021 QAEQTSQDPDCDMVKOPRYRKGPVOCFDMNALEDYTDGCGVS 1063



Sequence 53, Application US/08223305C  
Patent No. 5851824  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
ZIP: 92101-2926  
COUNTRY: USA  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/223,305C  
FILING DATE: April 4, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
TELECOMMUNICATION INFORMATION:  
REFERENCE/DOCKET NUMBER: 52516 (P519739)  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1103 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-223-305C-53

Query Match 97.4%; Score 5456; DB 2; Length 1103;  
Best Local Similarity 96.2%; Pred. No. 0;  
Matches 1041; Conservative 6; Mismatches 9; Indels 26; Gaps 2;

QY 1 MAAGCIIATLTITFOSILIGSSQEPFPPSAVITIKSWVDKMOEDLVYLTATASGVNOVDVI 60  
DB 1 MAAGCIIATLTITFOSILIGSSQEPFPPSAVITIKSWVDKMOEDLVYLTATASGVNOVDVI 60

QY 61 YKYQDLYTVERNNAROLVEIAPADIEKLNSRKALVRLALEAKVOAHQWREDFASN 120  
DB 61 YKYQDLYTVERNNAROLVEIAPADIEKLNSRKALVRLALEAKVOAHQWREDFASN 120  
QY 121 EYVYNNAKDLDPEKNDSPGSRIRKPFIDANGRISVQHAHVHPTIYEGSTVYL 180  
DB 121 EYVYNNAKDLDPEKNDSPGSRIRKPFIDANGRISVQHAHVHPTIYEGSTVYL 180  
QY 181 NELNMTSALDEVFKKRNREDPISLWQVFSATGLARYPASPMWNSRTPKIDLYDVR 240  
DB 181 NELNMTSALDEVFKKRNREDPISLWQVFSATGLARYPASPMWNSRTPKIDLYDVR 240  
QY 241 RFWYIQAASPRDMLILDVSGSVGLTKLRISVSKMLETLSDDPVNVAFSNSNAD 300  
DB 241 RFWYIQAASPRDMLILDVSGSVGLTKLRISVSKMLETLSDDPVNVAFSNSNAD 300  
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAGITDYKGFSAFEOILNTVSRANCKIIML 360  
DB 301 VSCFQHLVQANVRNKKVLDKAVNNITAGITDYKGFSAFEOILNTVSRANCKIIML 360  
QY 361 FTDGEERAQELIFARYNDRKRVFTFSVQHNDRGIOMWAGENKGYEIPISGAIR 420  
DB 361 FTDGEERAQELIFARYNDRKRVFTFSVQHNDRGIOMWAGENKGYEIPISGAIR 420  
QY 421 INTQETLDVGLRPVYLAQDKAKOVQWTVYLDALBLGIVTGTLPVNIQONENKTNLK 480  
DB 421 INTQETLDVGLRPVYLAQDKAKOVQWTVYLDALBLGIVTGTLPVNIQONENKTNLK 480  
QY 481 NOLIIQVGVQVDSLEDIKRLPRFTLCNGYFFALDPGVYLLHPNLOPK----- 530  
DB 481 NOLIIQVGVQVDSLEDIKRLPRFTLCNGYFFALDPGVYLLHPNLOPKIGIPIIN 540  
QY 531 -----NPKSDEPVTLDFLDELLENDIKVEIKRNKIDESGKERTLVKSODERYI 581  
DB 531 LKRRPNIONPKSDEPVTLDFLDELLENDIKVEIKRNKIDESGKERTLVKSODERYI 600  
QY 582 DKGNRTYTWTPNGNDYSIALVPTYSFYIKAKIEETITQARSKKGMKSEFLKDPNF 641  
DB 582 DKGNRTYTWTPNGNDYSIALVPTYSFYIKAKIEETITQARSKKGMKSEFLKDPNF 653  
QY 642 EESGYTFIAPRDYCNLDKISDNTEFLNFEFIDRKTPNPNPCNTDLINRYLDAGFTN 701  
DB 642 EESGYTFIAPRDYCNLDKISDNTEFLNFEFIDRKTPNPNPCNTDLINRYLDAGFTN 713  
QY 702 ELVQYVWSKQKNIKGVKARFVYTDGIRVYPKEAGENWQENPETYEDSFYKSLDNDY 761  
DB 702 ELVQYVWSKQKNIKGVKARFVYTDGIRVYPKEAGENWQENPETYEDSFYKSLDNDY 773  
QY 762 VFTAPYFNKSGGAYESGIMVSKAVEIYIOGKLKPAVVGIRKIDVNSVTEMTSTIRDP 821  
DB 762 VFTAPYFNKSGGAYESGIMVSKAVEIYIOGKLKPAVVGIRKIDVNSVTEMTSTIRDP 833  
QY 822 CAGPYCDCKRNSDVADCVILDDGFLMANHDDYTNOIGRFGFEDISLMLHVNISVYA 881  
DB 822 CAGPYCDCKRNSDVADCVILDDGFLMANHDDYTNOIGRFGFEDISLMLHVNISVYA 893  
QY 882 FNSKSYDYSVCEPGAAPKQAGHRSAYVPSIADILIHGMWATAAAMSTILOQFLSLTFPR 941  
DB 882 FNSKSYDYSVCEPGAAPKQAGHRSAYVPSIADILIHGMWATAAAMSTILOQFLSLTFPR 953  
QY 942 LLEAVEMEDDDFTASLQSCCTTETOTYFFPNDKSFSGVLDCCNCSIRFVEXLMTNTL 1001  
DB 942 LLEAVEMEDDDFTASLQSCCTTETOTYFFPNDKSFSGVLDCCNCSIRFVEXLMTNTL 1013  
QY 1002 IFIVESKGTCCDTRLLIOAEQTSDDGPPCDVMYKQPRYRKGPVCEFNALLETYDCGG 1061  
DB 1002 IFIVESKGTCCDTRLLIOAEQTSDDGPPCDVMYKQPRYRKGPVCEFNALLETYDCGG 1073  
QY 1062 VS 1063  
DB 1062 VS 1075

APPLICANT: Williams, Mark  
 APPLICANT: Feldman, Daniel  
 APPLICANT: McCue, Ann  
 APPLICANT: Brenner, Robert  
 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
 TITLE OF INVENTION: METHODS  
 NUMBER OF SEQUENCES: 57  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Brown, Martin, Haller & McClain  
 STREET: 1660 Union Street  
 City: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92101-2926  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/455,543A  
 FILING DATE: May 31, 1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/223,305  
 FILING DATE: April 4, 1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/868,354  
 FILING DATE: April 10, 1992  
 PRIOR APPLICATION DATA:  
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 FILING DATE: 30-NOV-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/482,384  
 FILING DATE: 20-FEB-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/603,751  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/US89/01408  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/176,899  
 FILING DATE: 04-APR-1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie L.  
 REGISTRATION NUMBER: 33,779  
 REFERENCE/DOCKET NUMBER: 6362-52517  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619)238-0999  
 TELEFAX: (619)238-0062  
 INFORMATION FOR SEQ ID NO: 53:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1103 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-455-543A-53

Query Match 97.4%; Score 5456; DB 1; Length 1103;  
 Best Local Similarity 96.2%; Pred. No. 0;  
 Matches 1041; Conservative 6; Mismatches 9; Indels 26; Gaps 2;

QY 1 MAAGCLATLTFQSLILGFSQSEFPBSAVTIKSWDKMQEDLYTLAKTASGVQQLVDI 60  
 DB 1 MAAGCLATLTLFQSLILGFSQSEFPBSAVTIKSWDKMQEDLYTLAKTASGVQQLVDI 60  
 QY 61 YEKYODLYVEPNNAQLVEIARDIEKLLSNRSKALVRLAEKVQAHHQWREDFASN 120  
 DB 61 YEKYODLYVEPNNAQLVEIARDIEKLLSNRSKALVRLAEKVQAHHQWREDFASN 120

DB 61 YEKYODLYVEPNNAQLVEIARDIEKLLSNRSKALVRLAEKVQAHHQWREDFASN 120  
 QY 121 EYVYVNAKDLDPEKNDSPGSRIRKPYIDDANGROIISQHAVALPTDIYEGSTIVL 180  
 DB 121 EYVYVNAKDLDPEKNDSPGSRIRKPYIDDANGROIISQHAVALPTDIYEGSTIVL 180  
 QY 181 NELNNTSALDEVEFKKREEDPSLIMQVGSATGLARYYPAPMWNSPTPKIDLYDVR 240  
 DB 181 NELNNTSALDEVEFKKREEDPSLIMQVGSATGLARYYPAPMWNSPTPKIDLYDVR 240  
 QY 241 RPYWIOGAASPKDMLILVDVSGSVGLTKLRISVSEMLFTLSDDDFVNVAFSNSNAD 300  
 DB 241 RPYWIOGAASPKDMLILVDVSGSVGLTKLRISVSEMLFTLSDDDFVNVAFSNSNAD 300  
 QY 301 VSCFOHLYOANRNKKVLDKDAVNNITAGTIDYKKGSEFARBDLLNTVSAKCKIIML 360  
 DB 301 VSCFOHLYOANRNKKVLDKDAVNNITAGTIDYKKGSEFARBDLLNTVSAKCKIIML 360  
 QY 361 FTDGGEERAOEIFAKYNNKDKVRVFTFSVGOHNDYRGPQIMACENKGYEIPISGAIR 420  
 DB 361 FTDGGEERAOEIFAKYNNKDKVRVFTFSVGOHNDYRGPQIMACENKGYEIPISGAIR 420  
 QY 421 INTQETLDVILGRPVYLADGKAKOVQWTVNYLDALDELGLVITGTLPVENITGONENKTNLK 480  
 DB 421 INTQETLDVILGRPVYLADGKAKOVQWTVNYLDALDELGLVITGTLPVENITGONENKTNLK 480  
 QY 481 NOLILGVMGVDVSLIEDIRLTPRFTLCNGYFATDPGCVLLPNQOPK 530  
 DB 481 NOLILGVMGVDVSLIEDIRLTPRFTLCNGYFATDPGCVLLPNQOPK 530  
 QY 531 -----NPKSOEPTVTLDFLDALENDIKVEIIRKMKIDSESEKFTRLVKSQDERYI 581  
 DB 531 -----NPKSOEPTVTLDFLDALENDIKVEIIRKMKIDSESEKFTRLVKSQDERYI 581  
 QY 581 LKRRPNQNPSPQEPVTLDFLDALENDIKVEIIRKMKIDSESEKFTRLVKSQDERYI 600  
 DB 581 LKRRPNQNPSPQEPVTLDFLDALENDIKVEIIRKMKIDSESEKFTRLVKSQDERYI 600  
 QY 601 DKGNTTYTWTPVNGTDYSALVLPYTSFYIKAKIETTTQARSKKGMKDSFLKPDNF 641  
 DB 601 DKGNTTYTWTPVNGTDYSALVLPYTSFYIKAKIETTTQARSKKGMKDSFLKPDNF 641  
 QY 641 EESGYTFIAPRDYCNLDKISDNNTFELNFEFIDRKPNNPSCNTDILNVLLDAGFTN 701  
 DB 641 EESGYTFIAPRDYCNLDKISDNNTFELNFEFIDRKPNNPSCNTDILNVLLDAGFTN 701  
 QY 701 ELVQNTWSKQKNIKGVKARFVYTDGKITRVYPKEAGENWQENPETYEDSFYKSLDNDY 761  
 DB 701 ELVQNTWSKQKNIKGVKARFVYTDGKITRVYPKEAGENWQENPETYEDSFYKSLDNDY 761  
 QY 761 VFTAPYENKSGRGAEESGIMSKAVEIYIOGKLLKPAVVGKIKIDVNSWIEFTKTSIRDP 821  
 DB 761 VFTAPYENKSGRGAEESGIMSKAVEIYIOGKLLKPAVVGKIKIDVNSWIEFTKTSIRDP 821  
 QY 821 CAGPYCDCKRNSDVMDCVILDDGCFILMANHDDYTNQGRFGEIDSLMHLNISVYA 881  
 DB 821 CAGPYCDCKRNSDVMDCVILDDGCFILMANHDDYTNQGRFGEIDSLMHLNISVYA 881  
 QY 881 FNSSTDYQSCBPGAAKPGAGHRSAYVSIADILHIGWMTAAWSILOOFLSLTFPR 941  
 DB 881 FNSSTDYQSCBPGAAKPGAGHRSAYVSIADILHIGWMTAAWSILOOFLSLTFPR 941  
 QY 941 LLEAVEMEDDDFTASISKOSCTITEOTYFFPNDKSKSGVLDCCNCRIFRIVELMTNTL 1001  
 DB 941 LLEAVEMEDDDFTASISKOSCTITEOTYFFPNDKSKSGVLDCCNCRIFRIVELMTNTL 1001  
 QY 1001 IFIWEKSGTCPCPTFRLLIQAEQTSIDGPPCDMWKOPRYRKGPPVPCDNNALBETYTCCG 1061  
 DB 1001 IFIWEKSGTCPCPTFRLLIQAEQTSIDGPPCDMWKOPRYRKGPPVPCDNNALBETYTCCG 1061  
 QY 1062 VS 1063  
 DB 1062 VS 1063  
 QY 1074 VS 1075  
 DB 1074 VS 1075

RESULT 12  
 US-08-223-305C-53

APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
NUMBER OF SPOUNCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEO Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/223.305C  
FILING DATE: April 4, 1994  
APPLICATION DATA:  
APPLICATION NUMBER: 07/868.354  
FILING DATE: April 10, 1992  
APPLICATION DATA:  
APPLICATION NUMBER: US 07/745.206  
FILING DATE: 15-AUG-1991  
APPLICATION DATA:  
APPLICATION NUMBER: US 07/620.250  
FILING DATE: 30-NOV-1990  
APPLICATION DATA:  
APPLICATION NUMBER: US 07/482.384  
FILING DATE: 20-FEB-1990  
APPLICATION DATA:  
APPLICATION NUMBER: US 07/603.751  
FILING DATE: 04-APR-1989  
APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
APPLICATION DATA:  
APPLICATION NUMBER: US 07/176.899  
FILING DATE: 04-APR-1988  
ATTOREY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 52516 (P519739)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEO ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1084 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-223-305C-56

Query Match 97.7%; Score 5475.5; DB 2; Length 1084;  
Best Local Similarity 97.9%; Pred. No. 0;  
Matches 1041; Conservative 6; Mismatches 9; Indels 7; Gaps 1;

QY 1 MAAGCLLALLTLFQSLIGPSSQEPFSAVTIKSMVKMOEDVTLAKTASGVNQLVDI 60  
DB 1 MAAGCLLALLTLFQSLIGPSSQEPFSAVTIKSMVKMOEDVTLAKTASGVNQLVDI 60  
QY 61 YEKYODLVTEFNNAKOLVEIARIDIKILSKRSKALVRLALEAKVOAAHQWREDFASN 120  
DB 61 YEKYODLVTEFNNAKOLVEIARIDIKILSKRSKALVSLALEAKVOAAHQWREDFASN 120

QY 121 EYVYYNADDDLDPEKNDSPPSQRIKPVFIDANFGROISYQHAHVHPTIDYEGSTIVL 180  
DB 121 EYVYYNADDDLDPEKNDSPPSQRIKPVFIEDANFGROISYQHAHVHPTIDYEGSTIVL 180  
QY 181 NELNMTSALDEVFKKRNREDDPSLMQVGSATGLARITPASPWNDSSTPNKIDLYDVR 240  
DB 181 NELNMTSALDEVFKKRNREDDPSLMQVGSATGLARITPASPWNDSSTPNKIDLYDVR 240  
QY 241 RPYWYOGAASPDKMLILVDVSGVGLTKLIRTSVSMLETLSDDDPVNVSANQAD 300  
DB 241 RPYWYOGAASPDKMLILVDVSGVGLTKLIRTSVSMLETLSDDDPVNVSANQAD 300  
QY 301 VSCFQHLVQANRKNKVLKDAVNNITAKGITDYKGSFSAFEOILLNVSRANCKIIML 360  
DB 301 VSCFQHLVQANRKNKVLKDAVNNITAKGITDYKGSFSAFEOILLNVSRANCKIIML 360  
QY 361 FTDGGEERAQELFNKYNKDKKVRVFRFSVGOHNERGPIOMMACENKGYEIPISIAIR 420  
DB 361 FTDGGEERAQELFNKYNKDKKVRVFRFSVGOHNERGPIOMMACENKGYEIPISIAIR 420  
QY 421 INFOEYLDVLGRPMVLADGKAKOVQWTVYLDALDELGLVITGTLPVFNITGONENKTNLK 480  
DB 421 INFOEYLDVLGRPMVLADGKAKOVQWTVYLDALDELGLVITGTLPVFNITGONENKTNLK 480  
QY 481 NOLLIGVGVDSLEDIRLTPRFTLCNGYFFAIDPNGVYLLHPNLQPKPKSQEPVTL 540  
DB 481 NOLLIGVGVDSLEDIRLTPRFTLCNGYFFAIDPNGVYLLHPNLQPKPKSQEPVTL 540  
QY 541 DELDAELENDIKVEIRNKMIDGSEGEKFRFLVSOBERYIDKCNRTYTWTVPNGTDSL 600  
DB 541 DELDAELENDIKVEIRNKMIDGSEGEKFRFLVSOBERYIDKCNRTYTWTVPNGTDSL 600  
QY 601 ALVLPYTSFYIYKAKIETITQARSKKGMKDSFTIKPDNEESGYFPIAPROVCNDLKI 660  
DB 601 ALVLPYTSFYIYKAKIETITQARSKKGMKDSFTIKPDNEESGYFPIAPROVCNDLKI 660  
QY 661 SDNTEFLNFEIDRKTNNPNSCNDLIRVLLDAGFTNELVQYVWSKQNKIKYKAR 720  
DB 661 SDNTEFLNFEIDRKTNNPNSCNDLIRVLLDAGFTNELVQYVWSKQNKIKYKAR 720  
QY 721 FVYTDGGITRYPKKAGNMOENPEYEDSYKSLNDNTVFAFPFKNSGPAVESGI 780  
DB 721 FVYTDGGITRYPKKAGNMOENPEYEDSYKSLNDNTVFAFPFKNSGPAVESGI 780  
QY 781 MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIMENFTKTSIRDPACAGPVCDCKRNSDVMDCVI 840  
DB 781 MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIMENFTKTSIRDPACAGPVCDCKRNSDVMDCVI 840  
QY 841 LDDGFFLIMANHDDYTNOIGRFGELIDPSLMRHLVNI SYVAFNKSXYDQSVCEGAPKQ 900  
DB 841 LDDGFFLIMANHDDYTNOIGRFGELIDPSLMRHLVNI SYVAFNKSXYDQSVCEGAPKQ 900  
QY 901 GAGHRSATVPSTADILIHGMATATAASIIQOFLSLTFPRLEAVEMEDDTFASLSKQ 960  
DB 901 GAGHRSATVPSTADILIHGMATATAASIIQOFLSLTFPRLEAVEMEDDTFASLSKQ 960  
QY 961 SCITEQOTQYFFNDNSKSFSGVLDGNCSTRIFHVKLMNTNLIIFIMWSKGTCCDTRLILI 1020  
DB 961 SCITEQOTQYFFNDNSKSFSGVLDGNCSTRIFHVKLMNTNLIIFIMWSKGTCCDTRLILI 1020  
QY 1021 QAEQTSQGPDPCKVWKOPRRYKKGPDVCFDNNALDEYTDGCGVS 1063  
DB 1021 QAEQTSQGPDPCKVWKOPRRYKKGPDVCFDNNALDEYTDGCGVS 1063  
QY 1063 QAEQTSQGPDPCKVWKOPRRYKKGPDVCFDNNALDEYTDGCGVS 1063  
DB 1063 QAEQTSQGPDPCKVWKOPRRYKKGPDVCFDNNALDEYTDGCGVS 1063

RESULT 11  
US-08-455-543A-53  
Sequence 53; Application US/08455543A  
Patent No. 5792846  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven

? APPLICANT: Ellis, Steven  
 ? APPLICANT: Williams, Mark  
 ? APPLICANT: Feldman, Daniel  
 ? APPLICANT: McCue, Ann  
 ? APPLICANT: Brenner, Robert  
 ? TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
 ? NUMBER OF SEQUENCES: 57  
 ? METHODS  
 ? CORRESPONDENCE ADDRESS:  
 ? ADDRESSEE: Brown, Martin, Haller & McClain  
 ? STREET: 1660 Union Street  
 ? CITY: San Diego  
 ? STATE: California  
 ? COUNTRY: USA  
 ? ZIP: 92101-2926  
 ?  
 ? COMPUTER READABLE FORM:  
 ? MEDIUM TYPE: Diskette  
 ? COMPUTER: IBM Compatible  
 ? OPERATING SYSTEM: DOS  
 ? SOFTWARE: FASTSEQ Version 1.5  
 ? CURRENT APPLICATION DATA:  
 ? APPLICATION NUMBER: US/08/455,543A  
 ? FILING DATE: May 31, 1995  
 ? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: 08/223,305  
 ? FILING DATE: April 4, 1994  
 ? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: 07/868,354  
 ? FILING DATE: April 10, 1992  
 ? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: US 07/745,206  
 ? FILING DATE: 15-AUG-1991  
 ? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: US 07/620,250  
 ? FILING DATE: 30-NOV-1990  
 ? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: US 07/482,384  
 ? FILING DATE: 20-FEB-1990  
 ? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: US 07/603,751  
 ? FILING DATE: 04-APR-1989  
 ? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: WO PCT/US89/01408  
 ? FILING DATE: 04-APR-1989  
 ? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: US 07/176,899  
 ? FILING DATE: 04-APR-1988  
 ? ATTORNEY/AGENT INFORMATION:  
 ? NAME: Seidman, Stephanie L.  
 ? REGISTRATION NUMBER: 33,779  
 ? REFERENCE/DOCKET NUMBER: 6362-52517  
 ? TELECOMMUNICATION INFORMATION:  
 ? TELEPHONE: (619)238-0999  
 ? TELEFAX: (619)238-0062  
 ? INFORMATION FOR SEQ ID NO: 56:  
 ? SEQUENCE CHARACTERISTICS:  
 ? LENGTH: 1084 amino acids  
 ? TYPE: amino acid  
 ? STRANDEDNESS: single  
 ? TOPOLOGY: linear  
 ? MOLECULE TYPE: protein  
 ? FRAGMENT TYPE: internal  
 ? US-08-455-543A-56

Query Match 97.7% Score 5475.5; DB 1; Length 1084;  
 Best Local Similarity 97.98; Pred. No. 0;  
 Matches 1041; Conservative 6; Mismatches 9; Indels 7; Gaps 1;

QY 1 MAACGLATLTITLQSLIGSSQEPSPSAVTIKSWDKMQEDLVTLAKTASGVNOLVDI 60  
 Db 1 MAACGLATLTITLQSLIGSSQEPSPSAVTIKSWDKMQEDLVTLAKTASGVNOLVDI 60  
 QY 61 YEKYQDLTYVEPNNAKOLVEIAARDIEKLISNRKALVRLALEAEKVQAAHQRREDFASN 120

Db 61 YEKYQDLTYVEPNNAKOLVEIAARDIEKLISNRKALVRLALEAEKVQAAHQRREDFASN 120  
 QY 121 EYVYVNAKDDLPBPKNDSEPSORITKPVITDANGROSYOAAVHPTDYESTYVL 180  
 Db 121 EYVYVNAKDDLPBPKNDSEPSORITKPVITDANGROSYOAAVHPTDYESTYVL 180  
 QY 181 NELNMTSALDEVEFKKREEDPSLLMQVEGATGLARYVPASVWNSRTPNKIDYDAR 240  
 Db 181 NELNMTSALDEVEFKKREEDPSLLMQVEGATGLARYVPASVWNSRTPNKIDYDAR 240  
 QY 241 RPWYIQGAASPKDMLILVDVSGSVSGLTLLRTSVSEMLETLSDDEEVNVAFSNAD 300  
 Db 241 RPWYIQGAASPKDMLILVDVSGSVSGLTLLRTSVSEMLETLSDDEEVNVAFSNAD 300  
 QY 301 VSCFOHLVQANRANKVLDKAVNNITAGITTYKKGFSAFEPQLLNVSRANCKITML 360  
 Db 301 VSCFOHLVQANRANKVLDKAVNNITAGITTYKKGFSAFEPQLLNVSRANCKITML 360  
 QY 361 FTDDGEEARQETFAKYNKDKVRFVTFESVGOHNYDRGPIOMACENKGYEIPISGAIR 420  
 Db 361 FTDDGEEARQETFAKYNKDKVRFVTFESVGOHNYDRGPIOMACENKGYEIPISGAIR 420  
 QY 421 INFOEYLDVLAGRPVLAGDKAKOVQWNTVYLDALDELGLVTGTLVPFNTIGONENKNTLK 480  
 Db 421 INFOEYLDVLAGRPVLAGDKAKOVQWNTVYLDALDELGLVTGTLVPFNTIGONENKNTLK 480  
 QY 481 NOLILGVKGVDSLEIDIKLTPRFILCPNGYFAIDPNKYVLLHNLDPKPKSSEPPTL 540  
 Db 481 NOLILGVKGVDSLEIDIKLTPRFILCPNGYFAIDPNKYVLLHNLDPKPKSSEPPTL 540  
 QY 541 DFLDALENDIVETIRNKKMIDGSEGEKPTLVKSQDERYIDKGRRTYTWTPVNCSTDSL 600  
 Db 541 DFLDALENDIVETIRNKKMIDGSEGEKPTLVKSQDERYIDKGRRTYTWTPVNCSTDSL 600  
 QY 601 ALVLPYTSFYIYKAKIETITQARSKKMKDSEFLKPDNFEESGYTEIAPRDYCNDIKI 660  
 Db 601 ALVLPYTSFYIYKAKIETITQARSKKMKDSEFLKPDNFEESGYTEIAPRDYCNDIKI 660  
 QY 661 SDNMTFELNPFNEFIDRKTNNPNSCNTDLINVLADAGTNTLNVYMSKOKINIKYKAR 720  
 Db 661 SDNMTFELNPFNEFIDRKTNNPNSCNTDLINVLADAGTNTLNVYMSKOKINIKYKAR 720  
 QY 721 FVYTDGIRVYPKEAGEWMOENPETYEDSEYKRSIDNDNVYFTAPYRNKSGPAYESGI 780  
 Db 721 FVYTDGIRVYPKEAGEWMOENPETYEDSEYKRSIDNDNVYFTAPYRNKSGPAYESGI 780  
 QY 781 MYSKAVEIYIOGKLLKPAVVGITIDVNSWIENFTYTSIRDPGAGPYCDCKRNSDVMDCVI 840  
 Db 781 MYSKAVEIYIOGKLLKPAVVGITIDVNSWIENFTYTSIRDPGAGPYCDCKRNSDVMDCVI 840  
 QY 841 LDDGGFLMANHDDTYNOIGRFFGEIDPSLMHLNIVSYAANKSYDVOSVCEPAAKQ 900  
 Db 841 LDDGGFLMANHDDTYNOIGRFFGEIDPSLMHLNIVSYAANKSYDVOSVCEPAAKQ 900  
 QY 901 GAGHRSAVYPSIADILHIGWMTAAAMSLIOQFLSLTFPRLLAEVEMEDDFTASLSKQ 960  
 Db 901 GAGHRSAVYPSIADILHIGWMTAAAMSLIOQFLSLTFPRLLAEVEMEDDFTASLSKQ 960  
 QY 961 SCTTEQTOYFFPDNDSKSFSGVLDGNCRKIFVEKIMANTNLIFIVESKGTCCPTRLIL 1020  
 Db 961 SCTTEQTOYFFPDNDSKSFSGVLDGNCRKIFVEKIMANTNLIFIVESKGTCCPTRLIL 1020  
 QY 1021 QAEQTSIDGPNPCDMYKOPRYRKGPVPCPNNALDEYTCGGVYS 1063  
 Db 1021 QAEQTSIDGPNPCDMYKOPRYRKGPVPCPNNALDEYTCGGVYS 1063  
 RESULT 10  
 US-08-223-305C-56  
 ; Sequence 56, Application US/08223305C  
 ; Patent No. 5851824  
 ; GENERAL INFORMATION:

GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/223,305C  
FILING DATE: April 4, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 52516 (P519739)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1086 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-223-305C-54

Query Match 98.0%; Score 5492.5; DB 2; Length 1086;  
Best Local Similarity 98.2%; Pred. No. 0;  
Matches 1044; Conservative 6; Mismatches 8; Indels 5; Gaps 1;

QY 1 MAACGLALITLTFLPSLLIGSSSEPPSAVTIKSWVDKMOEDLVTLAKTASGVNOLVDI 60  
Db 1 MAACGLALITLTFLPSLLIGSSSEPPSAVTIKSWVDKMOEDLVTLAKTASGVNOLVDI 60  
QY 61 YEKYODLTYVEPNNAOLVEIARDEIKLSNRSKALVRLALAEKQVAOHQWREDFASN 120  
|||||

Db 61 YEKYODLTYVEPNNAOLVEIARDEIKLSNRSKALVRLALAEKQVAOHQWREDFASN 120  
QY 121 EYVYVNAKDDLDPERKNDSEPSQRIKPYFIDDPANRGROIYQHAHVHPTDIYEGSTIVL 180  
Db 121 EYVYVNAKDDLDPERKNDSEPSQRIKPYFIDDPANRGROIYQHAHVHPTDIYEGSTIVL 180  
QY 181 NELNMTSALDEVFKKRNREDDPSLMQVFGSATGLARVYPASFWNDSFTPKIDLYDVR 240  
Db 181 NELNMTSALDEVFKKRNREDDPSLMQVFGSATGLARVYPASFWNDSFTPKIDLYDVR 240  
QY 241 RPYITOGAASPKDMLILDVSGSVGLTKLRTSVSEMLETSDDDVNVASFNSNOD 300  
Db 241 RPYITOGAASPKDMLILDVSGSVGLTKLRTSVSEMLETSDDDVNVASFNSNOD 300  
QY 301 VSCFHLVQANRNKKVLDKAVNNITANGIDYKKGSFSAEQLNINVSANCKIIML 360  
Db 301 VSCFHLVQANRNKKVLDKAVNNITANGIDYKKGSFSAEQLNINVSANCKIIML 360  
QY 361 FTDDGGERAOEIFAKYNDKAYVFTFSYGOHNYRGPLOMACENKYYEIPISGAIR 420  
Db 361 FTDDGGERAOEIFAKYNDKAYVFTFSYGOHNYRGPLOMACENKYYEIPISGAIR 420  
QY 421 INTOEYLDVGRPMVLGAKAKOVOMTNYLDALGLVITGTLFVFNITGONENKTNLK 480  
Db 421 INTOEYLDVGRPMVLGAKAKOVOMTNYLDALGLVITGTLFVFNITGONENKTNLK 480  
QY 481 NOLILGVMGVDSLEDIKRLRPRFTLCPNGYFAIDPNGVYLLHBNLOPKNPKSOEPTL 540  
Db 481 NOLILGVMGVDSLEDIKRLRPRFTLCPNGYFAIDPNGVYLLHBNLOPKNPKSOEPTL 540  
QY 541 DFLDALENDIVEIRNKKIIDESEGEKTRTLVKODEXYIDKGRYTWTPVNTDYSL 600  
Db 541 DFLDALENDIVEIRNKKIIDESEGEKTRTLVKODEXYIDKGRYTWTPVNTDYSL 600  
QY 595 536 DFLDALENDIVEIRNKKIIDESEGEKTRTLVKODEXYIDKGRYTWTPVNTDYSL 595  
QY 601 ALVLPYSFYTIKAKIETITQARSKGKMKDSEITLKPDPNSESQYTIAPRDYCNDDKI 660  
Db 601 ALVLPYSFYTIKAKIETITQARSKGKMKDSEITLKPDPNSESQYTIAPRDYCNDDKI 660  
QY 655 596 ALVLPYSFYTIKAKIETITQARSKGKMKDSEITLKPDPNSESQYTIAPRDYCNDDKI 655  
Db 655 596 ALVLPYSFYTIKAKIETITQARSKGKMKDSEITLKPDPNSESQYTIAPRDYCNDDKI 655  
QY 720 661 SDNTEELLNFEIDRKTNNPSCNTDLINRYLLDAGFTNELVONYSKONIKGVAR 720  
Db 720 661 SDNTEELLNFEIDRKTNNPSCNTDLINRYLLDAGFTNELVONYSKONIKGVAR 720  
QY 780 721 FVYTOGTRVYPKRAGEMWQENPEFYEDSFYKRSLDNDNYFTAPYNNKSGPAGYEGSI 780  
Db 780 721 FVYTOGTRVYPKRAGEMWQENPEFYEDSFYKRSLDNDNYFTAPYNNKSGPAGYEGSI 780  
QY 775 716 FVYTOGTRVYPKRAGEMWQENPEFYEDSFYKRSLDNDNYFTAPYNNKSGPAGYEGSI 775  
Db 775 716 FVYTOGTRVYPKRAGEMWQENPEFYEDSFYKRSLDNDNYFTAPYNNKSGPAGYEGSI 775  
QY 840 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPACAGVCCCKRSDVMDCVI 840  
Db 840 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPACAGVCCCKRSDVMDCVI 840  
QY 895 776 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPACAGVCCCKRSDVMDCVI 895  
Db 895 776 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPACAGVCCCKRSDVMDCVI 895  
QY 960 841 LDDGFFLMANHDDYTNOIGREFGETIDPSLMRHLVNISSVAFNKSYDYOSVCEPGAARQ 900  
Db 960 841 LDDGFFLMANHDDYTNOIGREFGETIDPSLMRHLVNISSVAFNKSYDYOSVCEPGAARQ 900  
QY 955 836 LDDGFFLMANHDDYTNOIGREFGETIDPSLMRHLVNISSVAFNKSYDYOSVCEPGAARQ 955  
Db 955 836 LDDGFFLMANHDDYTNOIGREFGETIDPSLMRHLVNISSVAFNKSYDYOSVCEPGAARQ 955  
QY 1020 961 SCITEQTYFFPNDKSKSFSGVLDGNCGRIFFEVKLMTNLTFFIWESEKGTCPCTRLLI 1020  
Db 1020 961 SCITEQTYFFPNDKSKSFSGVLDGNCGRIFFEVKLMTNLTFFIWESEKGTCPCTRLLI 1020  
QY 1015 956 SCTTQTYFFPNDKSKSFSGVLDGNCGRIFFEVKLMTNLTFFIWESEKGTCPCTRLLI 1015  
Db 1015 956 SCTTQTYFFPNDKSKSFSGVLDGNCGRIFFEVKLMTNLTFFIWESEKGTCPCTRLLI 1015  
QY 1063 1021 QAEQTSIDGPPCDMYKQPRYRKGPVDCFDNNALLEDYTDGCGVS 1063  
Db 1063 1021 QAEQTSIDGPPCDMYKQPRYRKGPVDCFDNNALLEDYTDGCGVS 1063

RESULT 9  
US-08-455-543A-56  
; Sequence 56, Application US/08455543A  
; Patent No. 5792846  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael

APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,543A  
FILING DATE: May 31, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/223,305  
FILING DATE: April 4, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-52517  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1086 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-455-543A-54

Query Match 98.0%; Score 5492.5; DB 1; Length 1086;  
Best Local Similarity 98.2%; Pred. No. 0;  
Matches 1044; Conservative 6; Mismatches 8; Indels 5; Gaps 1;

QY 1 MAAGCLATLTLLFOSLLIGPSQSEPPPSAVTIKSWVDKMOEDLVTLAKTAGSVNOLVDI 60  
DB 1 MAAGCLATLTLLFOSLLIGPSSEPPPSAVTIKSWVDKMOEDLVTLAKTAGSVNOLVDI 60

QY 61 YEKYODLYTEPPNNAQVLEIARDEIEKLSNRKALVRLALEAEVQAHHQWREDPASN 120  
DB 61 YEKYODLYTEPPNNAQVLEIARDEIEKLSNRKALVRLALEAEVQAHHQWREDPASN 120  
QY 121 EYVYNAKDLDPEKNDSEPGSQRIKPVFIDDANFGROISYQAAVH1PTDIYEGSTIVL 180  
DB 121 EYVYNAKDLDPEKNDSEPGSQRIKPVFIEDANFGROISYQAAVH1PTDIYEGSTIVL 180  
QY 181 NELNMTSALDEVFKKREEDPSILMQVFGSAGLARIYPASVWDSRPNKIDLYDVR 240  
DB 181 NELNMTSALDEVFKKREEDPSILMQVFGSAGLARIYPASVWDSRPNKIDLYDVR 240  
QY 241 RPYVIGASPKDMLILVSVSGVSGTLKILRTSVSELETLISDDDFVNVASFNSMD 300  
DB 241 RPYVIGASPKDMLILVSVSGVSGTLKILRTSVSELETLISDDDFVNVASFNSMD 300  
QY 301 VSCFHLVQANVRNKKVLDKAVNNITAKGITYDKKGFSAFBOQLNVNSRANCKIIML 360  
DB 301 VSCFHLVQANVRNKKVLDKAVNNITAKGITYDKKGFSAFBOQLNVNSRANCKIIML 360  
QY 361 FTDDGGERAOEIPAKYNNKKYRVTFESVGOHNYDRGPLOHMACGNKGYIEIPSTGAI 420  
DB 361 FTDDGGERAOEIPAKYNNKKYRVTFESVGOHNYDRGPLOHMACGNKGYIEIPSTGAI 420  
QY 421 INTOEYLDVLAGRPVLAGDKAKOVQWNTNYLDALDELGLVITGTLTPVFNITGONENKTNL 480  
DB 421 INTOEYLDVLAGRPVLAGDKAKOVQWNTNYLDALDELGLVITGTLTPVFNITGONENKTNL 480  
QY 481 NOLLIGVGVDSLEDIKRLPRFTLCPNGYFAIDPNGYVLLHPNLOPKNRSGQEPVTL 540  
DB 481 NOLLIGVGVDSLEDIKRLPRFTLCPNGYFAIDPNGYVLLHPNLOPKNRSGQEPVTL 540  
QY 541 DFLDALENDIVETIRNKKMIDSEGEKFTRLVKSODERYIDKGRRTYTPVNGTDYSL 600  
DB 541 DFLDALENDIVETIRNKKMIDSEGEKFTRLVKSODERYIDKGRRTYTPVNGTDYSL 600  
QY 596 ALVLPYSFYIYIKALEETITQARSKKGMKMOSEFLKLDNPEESYTFIARDCNDIKI 655  
DB 596 ALVLPYSFYIYIKALEETITQARSKKGMKMOSEFLKLDNPEESYTFIARDCNDIKI 655  
QY 661 SNNTEFLNNEFTDRKTPNPNPSCNTDLINRVLLDAGFTNELVONVSKOKINIGVKAR 720  
DB 661 SNNTEFLNNEFTDRKTPNPNPSCNTDLINRVLLDAGFTNELVONVSKOKINIGVKAR 720  
QY 715 SDNTEFLNNEFTDRKTPNPNPSCNTDLINRVLLDAGFTNELVONVSKOKINIGVKAR 715  
DB 715 SDNTEFLNNEFTDRKTPNPNPSCNTDLINRVLLDAGFTNELVONVSKOKINIGVKAR 715  
QY 721 FVYTDGGLTRVYPKAGEWMOENPETYDSFKRSLDNDNVFTAPYRNKSGPGAYESGI 780  
DB 721 FVYTDGGLTRVYPKAGEWMOENPETYDSFKRSLDNDNVFTAPYRNKSGPGAYESGI 780  
QY 775 FVYTDGGLTRVYPKAGEWMOENPETYDSFKRSLDNDNVFTAPYRNKSGPGAYESGI 775  
DB 775 FVYTDGGLTRVYPKAGEWMOENPETYDSFKRSLDNDNVFTAPYRNKSGPGAYESGI 775  
QY 781 MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDCAGVPCDCKRNSDVMCVI 840  
DB 781 MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDCAGVPCDCKRNSDVMCVI 840  
QY 841 LDDGGFLMANHDDYTNIGRFGGIDPSLMBHLVNTSVYAFNKSXYDYOSVCEPGAAPQ 900  
DB 841 LDDGGFLMANHDDYTNIGRFGGIDPSLMBHLVNTSVYAFNKSXYDYOSVCEPGAAPQ 900  
QY 895 LDDGGFLMANHDDYTNIGRFGGIDPSLMBHLVNTSVYAFNKSXYDYOSVCEPGAAPQ 895  
DB 895 LDDGGFLMANHDDYTNIGRFGGIDPSLMBHLVNTSVYAFNKSXYDYOSVCEPGAAPQ 895  
QY 901 GAGHSAYVPSIADILHIGWNAATAAASIILOFTLSLFPPLLEAVEHEDDFTASISQ 960  
DB 901 GAGHSAYVPSIADILHIGWNAATAAASIILOFTLSLFPPLLEAVEHEDDFTASISQ 960  
QY 955 GAGHSAYVPSIADILHIGWNAATAAASIILOFTLSLFPPLLEAVEHEDDFTASISQ 955  
DB 955 GAGHSAYVPSIADILHIGWNAATAAASIILOFTLSLFPPLLEAVEHEDDFTASISQ 955  
QY 961 SCITBQTOYFFEDNDSKFSFVLDGNCGRIFHVEKIMNTNLIIFLWESKGTGCPDTRLLI 1020  
DB 961 SCITBQTOYFFEDNDSKFSFVLDGNCGRIFHVEKIMNTNLIIFLWESKGTGCPDTRLLI 1020  
QY 1021 CAEQTSDDGPDQDMYKQRRYRKGPVYCDNNALEDYTDGCVS 1063  
DB 1021 CAEQTSDDGPDQDMYKQRRYRKGPVYCDNNALEDYTDGCVS 1063

RESULT 8  
US-08-223-305C-54  
Sequence 54, Application US/08223305C  
Patent No. 5851824

Db 781 MSAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPGAGPVCDCKRNSDVMDCVI 840  
 QY 841 LDDGFLMANHNDYTNQIGRFFGEIDPSLMRHLVNI SYAENKSYDYOSVCEPGAAPKQ 900  
 Db 841 LDDGFLMANHNDYTNQIGRFFGEIDPSLMRHLVNI SYAENKSYDYOSVCEPGAAPKQ 900  
 QY 901 GAGHRSAYVPSADIILIGMWTAAAMSILQOFLSLTFPRLLLEAVEMEDDFTASLSKQ 960  
 Db 901 GAGHRSAYVPSADIILIGMWTAAAMSILQOFLSLTFPRLLLEAVEMEDDFTASLSKQ 960  
 QY 961 SCITEOTQYFFPDNDKSFSGVLDGNCSTRIFHEKLMNTNLFIWVESKGTCCDTRLLI 1020  
 Db 961 SCITEOTQYFFPDNDKSFSGVLDGNCSTRIFHEKLMNTNLFIWVESKGTCCDTRLLI 1020  
 QY 1021 QAEQTSIDGPNCDMVKQPRYRKGPVCEFNNALEDYTDGCVS 1063  
 Db 1021 QAEQTSIDGPNCDMVKQPRYRKGPVCEFNNALEDYTDGCVS 1063

## RESULT 6

US-09-452-007-4  
 ; Sequence 4, Application US/09452007  
 ; Patent No. 6140485  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Franco, Rodrigo  
 ; APPLICANT: Sun Chen, Ai Ru  
 ; APPLICANT: Suey, David J.  
 ; TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL  
 ; NUMBER OF SEQUENCES: 6  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.  
 ; STREET: Two Millita Drive  
 ; CITY: Lexington  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02173-4799  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/452,007  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/713,118  
 ; FILING DATE: 16-SEP-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Mata, Elizabeth W.  
 ; REGISTRATION NUMBER: 38,236  
 ; REFERENCE/DOCKET NUMBER: ACC96-01  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 617-861-6240  
 ; TELEFAX: 617-861-9540  
 ; INFORMATION FOR SEQ ID NO. 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1091 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-09-452-007-4

Query Match 98.7%; Score 5528; DB 4; Length 1091;  
 Best Local Similarity 98.6%; Pred. No. 0;  
 Matches 1048; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLFLRSLILIGPSSEPPFSAYTIKSWDKMOEDVTLAKTASGVNQIYDI 60  
 Db 1 MAAGCLLALTLFLRSLILIGPSSEPPFSAYTIKSWDKMOEDVTLAKTASGVNQIYDI 60  
 QY 61 YEKYODLYVEFPNNAQOLVEIARDEIKLISRSKALVRLALEAKVOAHOQWREDFASN 120

Db 61 YEKYODLYVEFPNNAQOLVEIARDEIKLISRSKALVRLALEAKVOAHOQWREDFASN 120  
 QY 121 EYVYNAKDDLPKRNSEPGSORIKPEYITDDAENGSOISYQAAVHIPDIYEGSTIVL 180  
 Db 121 EYVYNAKDDLPKRNSEPGSORIKPEYITDDAENGSOISYQAAVHIPDIYEGSTIVL 180  
 QY 181 NELMWTSAIDVEFRKNREDEPSLMOVFSATGLARYPPASPWVDSNRTNKLIDYVRR 240  
 Db 181 NELMWTSAIDVEFRKNREDEPSLMOVFSATGLARYPPASPWVDSNRTNKLIDYVRR 240  
 QY 241 RPWTIOGASPKDMLLVDSVSGVSLTLKILRTSVSEMLETSSDDFVNAVAFSNSAOD 300  
 Db 241 RPWTIOGASPKDMLLVDSVSGVSLTLKILRTSVSEMLETSSDDFVNAVAFSNSAOD 300  
 QY 301 VSCFOHLOAVNRKRVKYLKADAVNNITAKGTIDYKGSFPAEOLANNVSRANCNTIML 360  
 Db 301 VSCFOHLOAVNRKRVKYLKADAVNNITAKGTIDYKGSFPAEOLANNVSRANCNTIML 360  
 QY 361 FTDGGEERAQEIFAKYNDKKRVVFTFVSQOHNYDRGPIDMACENKGYEETIPSGAIR 420  
 Db 361 FTDGGEERAQEIFAKYNDKKRVVFTFVSQOHNYDRGPIDMACENKGYEETIPSGAIR 420  
 QY 421 INTQEYLDVIGRPMVLAGDKAKQYQMTNIVYLDALGLVITGTLPPVFNITGQENKTNLK 480  
 Db 421 INTQEYLDVIGRPMVLAGDKAKQYQMTNIVYLDALGLVITGTLPPVFNITGQENKTNLK 480  
 QY 481 NQILIGVGVSVSLEDIKRLPRFTLCPNCGYFFAIDPNGVLLHPNLOPNPSSOEYVTL 540  
 Db 481 NQILIGVGVSVSLEDIKRLPRFTLCPNCGYFFAIDPNGVLLHPNLOPNPSSOEYVTL 540  
 QY 541 DFLDAELENDIKVEIRKMKMDIGESEKFTPLVKSODERYIDKGNRTYTPVNGTDYSL 600  
 Db 541 DFLDAELENDIKVEIRKMKMDIGESEKFTPLVKSODERYIDKGNRTYTPVNGTDYSL 600  
 QY 601 ALVLPYTSFYIKAKIEETITQASKKGKMKDSETLKPDPNFBESGYTIFAPRDYCDLKI 660  
 Db 601 ALVLPYTSFYIKAKIEETITQASKKGKMKDSETLKPDPNFBESGYTIFAPRDYCDLKI 660  
 QY 661 SDNTEFLNENEFIDKRTPNPNSCNTDLINRYLLDAGFNEIYONVWMSOKNIKGYKAR 720  
 Db 661 SDNTEFLNENEFIDKRTPNPNSCNTDLINRYLLDAGFNEIYONVWMSOKNIKGYKAR 720  
 QY 721 FVVTGIGITRVRYPKEAGENQENPEYEDSEFYKRSIENDNVYFTAPYFNKSGGAEVSGI 780  
 Db 721 FVVTGIGITRVRYPKEAGENQENPEYEDSEFYKRSIENDNVYFTAPYFNKSGGAEVSGI 780  
 QY 781 MSAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPGAGPVCDCKRNSDVMDCVI 840  
 Db 781 MSAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPGAGPVCDCKRNSDVMDCVI 840  
 QY 841 LDDGFLMANHNDYTNQIGRFFGEIDPSLMRHLVNI SYAENKSYDYOSVCEPGAAPKQ 900  
 Db 841 LDDGFLMANHNDYTNQIGRFFGEIDPSLMRHLVNI SYAENKSYDYOSVCEPGAAPKQ 900  
 QY 901 GAGHRSAYVPSADIILIGMWTAAAMSILQOFLSLTFPRLLLEAVEMEDDFTASLSKQ 960  
 Db 901 GAGHRSAYVPSADIILIGMWTAAAMSILQOFLSLTFPRLLLEAVEMEDDFTASLSKQ 960  
 QY 961 SCITEOTQYFFPDNDKSFSGVLDGNCSTRIFHEKLMNTNLFIWVESKGTCCDTRLLI 1020  
 Db 961 SCITEOTQYFFPDNDKSFSGVLDGNCSTRIFHEKLMNTNLFIWVESKGTCCDTRLLI 1020  
 QY 1021 QAEQTSIDGPNCDMVKQPRYRKGPVCEFNNALEDYTDGCVS 1063  
 Db 1021 QAEQTSIDGPNCDMVKQPRYRKGPVCEFNNALEDYTDGCVS 1063

## RESULT 7

US-08-455-543A-54  
 ; Sequence 54, Application US/08455543A  
 ; Patent No. 5792846  
 ; GENERAL INFORMATION:

Query	Match	Best. Local Similarity	Matches 1048	Conservative	Score 5528	DB 3	Length 1091	Mismatches	Indels	Gaps
1	MAAGCLLATLTLFOSLILGSPSSQEPFPSPAAVITISWVDKMDQEDVLTIAKASGVNOLVDI	98.6%	6	9	0	0				
1	MAAGCLLATLTLFOSLILGSPSSQEPFPSPAAVITISWVDKMDQEDVLTIAKASGVNOLVDI	98.6%	6	9	0	0				
61	YEKYODLYVEEPNNAQOLVEIARDIEKILSNRSKALVRLALEAKVOAAHQMRDPASN	98.6%	6	9	0	0				
61	YEKYODLYVEEPNNAQOLVEIARDIEKILSNRSKALVRLALEAKVOAAHQMRDPASN	98.6%	6	9	0	0				
121	EYVYVNAKDDLDPEKNDSEPSQSRIKPAFIEDANFGROIISQHAAVIIPDIYEGSTIYL	98.6%	6	9	0	0				
121	EYVYVNAKDDLDPEKNDSEPSQSRIKPAFIEDANFGROIISQHAAVIIPDIYEGSTIYL	98.6%	6	9	0	0				
181	NEIWNLTSAIDVEFKKREEDPSILMQVEGATGLARVYPASPVWVNSRTPNKIDLYDVR	98.6%	6	9	0	0				
181	NEIWNLTSAIDVEFKKREEDPSILMQVEGATGLARVYPASPVWVNSRTPNKIDLYDVR	98.6%	6	9	0	0				
241	RPWYIGASPKMILLVYSGVSGTLKILRTISVSMLETTSDDPFVWVAFSNSNAD	98.6%	6	9	0	0				
241	RPWYIGASPKMILLVYSGVSGTLKILRTISVSMLETTSDDPFVWVAFSNSNAD	98.6%	6	9	0	0				
301	VSCFOHLVQANVANKKVLKDAVNNITKAGITDYKKGSFAFEDLLNVSANCKMIIML	98.6%	6	9	0	0				
301	VSCFOHLVQANVANKKVLKDAVNNITKAGITDYKKGSFAFEDLLNVSANCKMIIML	98.6%	6	9	0	0				
361	FTPGGGERADEIFAKTKNKKKAVRVTFESVGHANDRGTQIMACENKGYEETPSIGAIR	98.6%	6	9	0	0				
361	FTPGGGERADEIFAKTKNKKKAVRVTFESVGHANDRGTQIMACENKGYEETPSIGAIR	98.6%	6	9	0	0				
361	FTPGGGERADEIFAKTKNKKKAVRVTFESVGHANDRGTQIMACENKGYEETPSIGAIR	98.6%	6	9	0	0				
421	INTQEVLDVYGRPMVLAGDARQAVQWTVVYDADALEGLVINGTLPVNIINGOMENKTNLK	98.6%	6	9	0	0				
421	INTQEVLDVYGRPMVLAGDARQAVQWTVVYDADALEGLVINGTLPVNIINGOMENKTNLK	98.6%	6	9	0	0				
481	NQILILGVMGVDSLEDIKRLPRFTLCPNGYIFALIDNGVYLLHPNLOPKNPKSQEPVTL	98.6%	6	9	0	0				
481	NQILILGVMGVDSLEDIKRLPRFTLCPNGYIFALIDNGVYLLHPNLOPKNPKSQEPVTL	98.6%	6	9	0	0				
541	DELDAELENDIKVEIKNKMIIDGSEKFPRTLVSDQERYIDKCNKRYITMTPVNGDIYSL	98.6%	6	9	0	0				
541	DELDAELENDIKVEIKNKMIIDGSEKFPRTLVSDQERYIDKCNKRYITMTPVNGDIYSL	98.6%	6	9	0	0				
601	ALVLPYTSFYIYIKAKITEETITQARSKKMKMDSETLKDNTFEEGYSFTIAPRYCNDLKI	98.6%	6	9	0	0				
601	ALVLPYTSFYIYIKAKITEETITQARSKKMKMDSETLKDNTFEEGYSFTIAPRYCNDLKI	98.6%	6	9	0	0				
661	SDNNTEPLNFENFIDRKTPNPNPCNTDILINRVLLDAGFTVELYQVWWSQKNIKGYKAR	98.6%	6	9	0	0				
661	SDNNTEPLNFENFIDRKTPNPNPCNTDILINRVLLDAGFTVELYQVWWSQKNIKGYKAR	98.6%	6	9	0	0				
721	FVYVTDGIFTVYVPEKAGENMOENPETYESFARKSLDNDNVYFAPYFNKSGGAATESGI	98.6%	6	9	0	0				
721	FVYVTDGIFTVYVPEKAGENMOENPETYESFARKSLDNDNVYFAPYFNKSGGAATESGI	98.6%	6	9	0	0				
781	MSKAVEITYIQGKLKPAVAVGIKIDVNSMIENFTKTSIRDFCAGPVCDCKRNSDVMDCVI	98.6%	6	9	0	0				
781	MSKAVEITYIQGKLKPAVAVGIKIDVNSMIENFTKTSIRDFCAGPVCDCKRNSDVMDCVI	98.6%	6	9	0	0				



```

Db 61 YEKYQDLTYVEPNNAQRLVEIAARDIEKLSNRKALVSLAEAKVQAAHQWREDFASN 120
Qy 121 EYVYVNAKDDLDPEKNDSPGSGRIKPFVIDANFGROI SYOAAVHIPTDIYEGSTIYL 180
Db 122 EYVYVNAKDDLDPEKNDSPGSGRIKPFVIDANFGROI SYOAAVHIPTDIYEGSTIYL 180
Qy 181 NELNMTSALDEYFKKRNREDPSSLMOVFGSATGLARIYPASPWVNSRTPNKIDLYDVR 240
Db 181 NELNMTSALDEYFKKRNREDPSSLMOVFGSATGLARIYPASPWVNSRTPNKIDLYDVR 240
Qy 241 RPYVIOGAASPKDMLILVDVSGVSGTLTKLIRTSVSEMLETSDDDPVNAFNSNAOD 300
Db 241 RPYVIOGAASPKDMLILVDVSGVSGTLTKLIRTSVSEMLETSDDDPVNAFNSNAOD 300
Qy 301 VSCFOHLVQANVRNKKVYLKDAVNNITAKGITYDYKKGFSFAFEQLNINVSANCKIIML 360
Db 301 VSCFOHLVQANVRNKKVYLKDAVNNITAKGITYDYKKGFSFAFEQLNINVSANCKIIML 360
Qy 361 FTDGEERAQEIFAKYKNDKRVFTFESVGOHNYDRPQIOMMACENKGYEYIPISGAIR 420
Db 361 FTDGEERAQEIFAKYKNDKRVFTFESVGOHNYDRPQIOMMACENKGYEYIPISGAIR 420
Qy 421 INTQETLDVGRPVLAGDKAKOVOMTNYLDALGLVITGTLVFNITGONEKNTMLK 480
Db 421 INTQETLDVGRPVLAGDKAKOVOMTNYLDALGLVITGTLVFNITGONEKNTMLK 480
Qy 481 NQILIGVMGVDSLEDIKLIRPFTLCPCNGYFAIDPNGYVYLHPNLOPKNKSSQEPYTL 540
Db 481 NQILIGVMGVDSLEDIKLIRPFTLCPCNGYFAIDPNGYVYLHPNLOPKNKSSQEPYTL 540
Qy 541 DPLDALENDIYVEIRNKKMIDSESEKTFRLVKSODERYIDKGRITTYTWTPVNGTDSL 600
Db 541 DPLDALENDIYVEIRNKKMIDSESEKTFRLVKSODERYIDKGRITTYTWTPVNGTDSL 600
Qy 601 ALVLPYSFYITKAKIEETITQARSKKGMKDESEKTFRLVKSODERYIDKGRITTYTWTPVNGTDSL 600
Db 601 ALVLPYSFYITKAKIEETITQARSKKGMKDESEKTFRLVKSODERYIDKGRITTYTWTPVNGTDSL 600
Qy 661 SUNNTEFLNFEFIDRKTNNPNSCNTDLINRVLLDAGFTNELVONVYSKONIKGVAR 720
Db 661 SUNNTEFLNFEFIDRKTNNPNSCNTDLINRVLLDAGFTNELVONVYSKONIKGVAR 720
Qy 721 EYVYVNAKDDLDPEKNDSPGSGRIKPFVIDANFGROI SYOAAVHIPTDIYEGSTIYL 180
Db 721 EYVYVNAKDDLDPEKNDSPGSGRIKPFVIDANFGROI SYOAAVHIPTDIYEGSTIYL 180
Qy 781 MYSKAVEIYIOGKLLKPAVVGIIKIDVNSWIEFTKSTIRDPGAGVPCCKRNSDVMDCVI 840
Db 781 MYSKAVEIYIOGKLLKPAVVGIIKIDVNSWIEFTKSTIRDPGAGVPCCKRNSDVMDCVI 840
Qy 841 LDDGGFLMANHDDYTNOIGRPFGEIDPSLMRHLVNI SYVAFNKSVDYOSVCEPGAAPQ 900
Db 841 LDDGGFLMANHDDYTNOIGRPFGEIDPSLMRHLVNI SYVAFNKSVDYOSVCEPGAAPQ 900
Qy 901 GAGHSAVYPSIADLIHGMWATAAAMSLQOFLSLTFPRLLEAVEKEDDFTASLSKQ 960
Db 901 GAGHSAVYPSIADLIHGMWATAAAMSLQOFLSLTFPRLLEAVEKEDDFTASLSKQ 960
Qy 961 SCITTOYOTFFPNDSKSFSGVLDGNCGRIFHEKLMNTNLIETVWESKGCPCOTRLLI 1020
Db 961 SCITTOYOTFFPNDSKSFSGVLDGNCGRIFHEKLMNTNLIETVWESKGCPCOTRLLI 1020
Qy 1021 QAEQTSDDGPCDMVKOPRYRKGPVCFDNNALEDYTDGCGVS 1063
Db 1021 QAEQTSDDGPCDMVKOPRYRKGPVCFDNNALEDYTDGCGVS 1063

```

```

APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: Human Calcium Channel Compositions and
METHODS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,363
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-51506
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0062
TELEFAX: (619)238-0062
INFORMATION FOR SRO ID NO: 25
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-311-363-25

Query Match 98.8%; Score 5532; DB 2; Length 1091;
Best Local Similarly 98.7%; Pred. No. 0;
Matches 1049; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MAACGLALATLTTLROSLLIGPSOEPPEPAAVTIKSWDKMOEDLVTLAKTASGVNOLYDI 60
Db 1 MAACGLALATLTTLROSLLIGPSOEPPEPAAVTIKSWDKMOEDLVTLAKTASGVNOLYDI 60
Qy 61 YEKYQDLTYVEPNNAQRLVEIAARDIEKLSNRKALVSLAEAKVQAAHQWREDFASN 120
Db 61 YEKYQDLTYVEPNNAQRLVEIAARDIEKLSNRKALVSLAEAKVQAAHQWREDFASN 120
Qy 121 EYVYVNAKDDLDPEKNDSPGSGRIKPFVIDANFGROI SYOAAVHIPTDIYEGSTIYL 180
Db 121 EYVYVNAKDDLDPEKNDSPGSGRIKPFVIDANFGROI SYOAAVHIPTDIYEGSTIYL 180
Qy 181 NELNMTSALDEYFKKRNREDPSSLMOVFGSATGLARIYPASPWVNSRTPNKIDLYDVR 240
Db 181 NELNMTSALDEYFKKRNREDPSSLMOVFGSATGLARIYPASPWVNSRTPNKIDLYDVR 240
Qy 241 RPYVIOGAASPKDMLILVDVSGVSGTLTKLIRTSVSEMLETSDDDPVNAFNSNAOD 300
Db 241 RPYVIOGAASPKDMLILVDVSGVSGTLTKLIRTSVSEMLETSDDDPVNAFNSNAOD 300
Qy 301 VSCFOHLVQANVRNKKVYLKDAVNNITAKGITYDYKKGFSFAFEQLNINVSANCKIIML 360
Db 301 VSCFOHLVQANVRNKKVYLKDAVNNITAKGITYDYKKGFSFAFEQLNINVSANCKIIML 360
Qy 361 FTDGEERAQEIFAKYKNDKRVFTFESVGOHNYDRPQIOMMACENKGYEYIPISGAIR 420
Db 361 FTDGEERAQEIFAKYKNDKRVFTFESVGOHNYDRPQIOMMACENKGYEYIPISGAIR 420

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QY 61 YEKYODLYTVEPNNAQOLVEIARDIEKLLSNRSKALVRLALEAEKYQAHOHREDFASN 120
Db 61 YEKYODLYTVEPNNAQOLVEIARDIEKLLSNRSKALVRLALEAEKYQAHOHREDFASN 120
QY 121 EYVYNAKADDLDEKNDSEPGSRIRPVFIIDANFQRQSYQAAVHIPTDIYEGSTIYL 180
Db 121 EYVYNAKADDLDEKNDSEPGSRIRPVFIIDANFQRQSYQAAVHIPTDIYEGSTIYL 180
QY 181 NELNMTSALDEVFKKRRREDDPSLLMOVFSGATGLARYYPASPVNDSSRPNKIDLYDVR 240
Db 181 NELNMTSALDEVFKKRRREDDPSLLMOVFSGATGLARYYPASPVNDSSRPNKIDLYDVR 240
QY 241 RPYVIGGAASPKDMLILVYVSGSVGLTLKIRTSYSEMLETLLSDDDFVNVA SFNSNAOD 300
Db 241 RPYVIGGAASPKDMLILVYVSGSVGLTLKIRTSYSEMLETLLSDDDFVNVA SFNSNAOD 300
QY 301 VSCFOHLVQANVANKKVLKDAVNNITAKGITTQKGFSAFBOGLNYSRANCKIIML 360
Db 301 VSCFOHLVQANVANKKVLKDAVNNITAKGITTQKGFSAFBOGLNYSRANCKIIML 360
QY 361 FTDGERBAOEIPAKYNNKDKKVVFTFESVGOHNYDRGPIOMACENKGYEELPSIGAIR 420
Db 361 FTDGERBAOEIPAKYNNKDKKVVFTFESVGOHNYDRGPIOMACENKGYEELPSIGAIR 420
QY 421 INTQEXYLDVLRPMVLGDKAKOVQWNTNYLDALDELGLVITGTLPEVNTIGONENKTNLK 480
Db 421 INTQEXYLDVLRPMVLGDKAKOVQWNTNYLDALDELGLVITGTLPEVNTIGONENKTNLK 480
QY 481 NQILILVGVDSVLEDIKRLTPFTLCFPGNYFAIDPNGVYLHPVLQPKRNSQEPVTL 540
Db 481 NQILILVGVDSVLEDIKRLTPFTLCFPGNYFAIDPNGVYLHPVLQPKRNSQEPVTL 540
QY 541 DFLDAELNDIKVEIKNNKMDGSEKFTRLVKSODEYR IDKGNNTYMTWPNNGDYSL 600
Db 541 DFLDAELNDIKVEIKNNKMDGSEKFTRLVKSODEYR IDKGNNTYMTWPNNGDYSL 600
QY 601 ALVLPYSEFYIIKAKIETITQARSKKGMKDESETLKPNFESGGYFTAPRDYCNLKI 660
Db 601 ALVLPYSEFYIIKAKIETITQARSKKGMKDESETLKPNFESGGYFTAPRDYCNLKI 660
QY 661 SDNNTFELNFEFIDRKTPNNNSCMTDLINRYLDAGFTTNELVONYMSKOKNIKGVKAR 720
Db 661 SDNNTFELNFEFIDRKTPNNNSCMTDLINRYLDAGFTTNELVONYMSKOKNIKGVKAR 720
QY 721 FVYTDGIGTRVYKKEAGEMNOENPETEYEDSFYKRSIDNINNYFTAYENKSGGAEESGI 780
Db 721 FVYTDGIGTRVYKKEAGEMNOENPETEYEDSFYKRSIDNINNYFTAYENKSGGAEESGI 780
QY 781 MYSKAVEIYIQGKLLKPAVVGIRIDVNSWIENFTKTSIRDPGAGPYCDCKRNSDVMDCVI 840
Db 781 MYSKAVEIYIQGKLLKPAVVGIRIDVNSWIENFTKTSIRDPGAGPYCDCKRNSDVMDCVI 840
QY 841 LDDGGFLMANHDDYTNOIGRFGEGLDPSLMRLVNIAYARNSKSDIYOSVCEPGAAPQ 900
Db 841 LDDGGFLMANHDDYTNOIGRFGEGLDPSLMRLVNIAYARNSKSDIYOSVCEPGAAPQ 900
QY 901 GAGHRASVYPSIADILHIGWMATAAAMSILQOFLSLTFPRLLEAEMEDDPTASLSQ 960
Db 901 GAGHRASVYPSIADILHIGWMATAAAMSILQOFLSLTFPRLLEAEMEDDPTASLSQ 960
QY 961 SCITEQTOYFFDNDSSFSGVLDCGNCSSRI FHEVKLMNTNLI FIMVESKGTGCPDTRLII 1020
Db 961 SCITEQTOYFFDNDSSFSGVLDCGNCSSRI FHEVKLMNTNLI FIMVESKGTGCPDTRLII 1020
QY 1021 QAEQTSDDGPDCDMVQPRYRKGPVDCFDNNALIEDYTDGGSVS 1063
Db 1021 QAEQTSDDGPDCDMVQPRYRKGPVDCFDNNALIEDYTDGGSVS 1063

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RESULT 3  
US-08-223-305C-52  
; Sequence 52, Application US/08223305C

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; Patent No. 5851824
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/223,305C
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 52516 (P519739)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1091 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
; US-08-223-305C-52

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Query Match 98.8%; Score 5532; DB 2; Length 1091;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1049; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
QY 1 MAAGCLLALTLTLOSLLIGPSOEPSPSAVTIKSWDKMOEDLVTLAKTASGVNOLVDI 60
Db 1 MAAGCLLALTLTLOSLLIGPSSEPPPSAVTITSWDKMOEDLVTLAKTASGVNOLVDI 60
QY 61 YEKYODLYTVEPNNAQOLVEIARDIEKLLSNRSKALVRLALEAEKYQAHOHREDFASN 120

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QY 61 YEKYODLYTEBPNNAROLVEIARDIEKLLSNRSKALVRLALEAKVQAAHOMREDFASN 120  
 Db 61 YEKYODLYTEBPNNAROLVEIARDIEKLLSNRSKALVRLALEAKVQAAHOMREDFASN 120  
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 Db 181 NELWMTSLADVEFKKNEDEPSLLMOVFGSAGTGLARYPASPVWNSRTPNKIDLYDVR 240  
 QY 241 RPYWIOGAASPKDMLIIVDSVSGTLLKIRTSVSEMEETLSDDFVWVAFNSNAOD 300  
 Db 241 RPYWIOGAASPKDMLIIVDSVSGTLLKIRTSVSEMEETLSDDFVWVAFNSNAOD 300  
 QY 301 VSCFOHLYOANVRNKKVLDKAVNNITAKGITDYKKGFSFAFEDLLNYSRANCNKIML 360  
 Db 301 VSCFOHLYOANVRNKKVLDKAVNNITAKGITDYKKGFSFAFEDLLNYSRANCNKIML 360  
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 Db 361 FTDOGERAOEIFAKYKKKKVVFVFSVQAHYDRGPIDMACENKGYEIEPSIGAIR 420  
 QY 421 INTQEYLDVGRPMVLADGAKQVMTNVLDALEGLVTGTFLPVFNITGONENKTNLK 480  
 Db 421 INTQEYLDVGRPMVLADGAKQVMTNVLDALEGLVTGTFLPVFNITGONENKTNLK 480  
 QY 481 NOLILGMVGVDSLEDIKRLTPFTLCPNGYFAIDPNGYVLLHPNLOPKNPKSQEPVL 540  
 Db 481 NOLILGMVGVDSLEDIKRLTPFTLCPNGYFAIDPNGYVLLHPNLOPKNPKSQEPVL 540  
 QY 541 DFDAELENDIKVEIRNKMIDGSGEKTPTLVKSDDERYIDKGNNTYWTVPNGTDSL 600  
 Db 541 DFDAELENDIKVEIRNKMIDGSGEKTPTLVKSDDERYIDKGNNTYWTVPNGTDSL 600  
 QY 601 ALVLPYSEFYIKAKIETITQARSKKGMKDETLKPNFEESGYTFIAPRYCNDLKI 660  
 Db 601 ALVLPYSEFYIKAKIETITQARSKKGMKDETLKPNFEESGYTFIAPRYCNDLKI 660  
 QY 661 SDNTEFLNFEEDIRKTPNPNSCNTDLINRYLDAAGTNELVONYMSKOKINIKGVKAR 720  
 Db 661 SDNTEFLNFEEDIRKTPNPNSCNTDLINRYLDAAGTNELVONYMSKOKINIKGVKAR 720  
 QY 721 FVVTDGITRVYPKEAGEMWQENPETEYSPKRSIDNNTYVETAPYKSGPGAYESGI 780  
 Db 721 FVVTDGITRVYPKEAGEMWQENPETEYSPKRSIDNNTYVETAPYKSGPGAYESGI 780  
 QY 781 MYSKAVEIITQGLKPAVVGIIKIDVNSWIENTFTKTSIRDPGAGVDCCKRSDVMDCVI 840  
 Db 781 MYSKAVEIITQGLKPAVVGIIKIDVNSWIENTFTKTSIRDPGAGVDCCKRSDVMDCVI 840  
 QY 841 LDDGGFLMANDDYTNOIGRFFGELIDPSIMRHLNISYAAKNSYDYOSVCEPAAPKQ 900  
 Db 841 LDDGGFLMANDDYTNOIGRFFGELIDPSIMRHLNISYAAKNSYDYOSVCEPAAPKQ 900  
 QY 901 GAGHSASVPSIADLIHIGMATAAWSILOFLLSTFFPRLLEAVEEMDDFTASLSKO 960  
 Db 901 GAGHSASVPSIADLIHIGMATAAWSILOFLLSTFFPRLLEAVEEMDDFTASLSKO 960  
 QY 961 SCITQOTQYFPNDKSKSGVLDGNCGRIFHEVKLANTNLIIFINVESKGTGCPDTRLII 1020  
 Db 961 SCITQOTQYFPNDKSKSGVLDGNCGRIFHEVKLANTNLIIFINVESKGTGCPDTRLII 1020  
 QY 1021 QAEQTSDEGPDPCDMWKQPRYRKRPVPCDNNALJEDYTCGGVS 1063  
 Db 1021 QAEQTSDEGPDPCDMWKQPRYRKRPVPCDNNALJEDYTCGGVS 1063

RESULT 2

US-08-455-543A-52  
 : Sequence 52, Application US/08455543A  
 : Patent No. 5792846

GENERAL INFORMATION:  
 APPLICANT: Harpold, Michael  
 APPLICANT: Ellis, Steven  
 APPLICANT: Williams, Mark  
 APPLICANT: Feldman, Daniel  
 APPLICANT: McCue, Ann  
 APPLICANT: Brenner, Robert  
 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
 NUMBER OF SEQUENCES: 57  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Brown, Martin, Haller & McClain  
 STREET: 1660 Union Street  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92101-2926  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/455,543A  
 FILING DATE: May 31, 1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/223,305  
 FILING DATE: April 4, 1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/868,354  
 FILING DATE: April 10, 1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/745,206  
 FILING DATE: 15-AUG-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/620,250  
 FILING DATE: 30-NOV-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/482,384  
 FILING DATE: 20-FEB-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/603,751  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/US89/01408  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/176,899  
 FILING DATE: 04-APR-1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie L.  
 REGISTRATION NUMBER: 33,779  
 REFERENCE/DOCKET NUMBER: 6362-52517  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619)238-0999  
 TELEFAX: (619)238-0062  
 INFORMATION FOR SEQ ID NO: 52:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1091 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-455-543A-52

Query Match 98.8%; Score 5532; DB 1; Length 1091;  
 Best Local Similarity 98.7%; Pred. No. 0;  
 Matches 1049; Conservative 6; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 MAAGCLLALTLTLFOSLLIGPSSQEPFPPSAVTIKSWDKMOEDLVYLAFTAGSVNOLYDI 60  
 Db 1 MAAGCLLALTLTLFOSLLIGPSSQEPFPPSAVTIKSWDKMOEDLVYLAFTAGSVNOLYDI 60

GenCore version 5.1.3  
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## OM protein - protein search, using sw model

Run on: February 10, 2003, 14:13:55 ; Search time 11.7901 Seconds  
(without alignments)  
2652.785 Million cell updates/sec

Title: US-10-090-827-8

Sequence: 1 MAAGCLLATLTLFQSLILG.....PDVCFDNNALDYDTCGVS 1063

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database :

Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCRTS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5532	98.8	1091	1	US-07-745-206A-25
2	5532	98.8	1091	1	US-08-455-543A-52
3	5532	98.8	1091	2	US-08-223-305C-52
4	5532	98.8	1091	2	US-08-311-363-25
5	5528	98.7	1091	3	US-08-713-118-4
6	5528	98.7	1091	4	US-09-452-007-4
7	5492.5	98.0	1086	1	US-08-455-543A-54
8	5492.5	98.0	1086	2	US-08-223-305C-54
9	5475.5	97.7	1084	1	US-08-455-543A-56
10	5475.5	97.7	1084	2	US-08-223-305C-56
11	5456	97.4	1103	1	US-08-455-543A-53
12	5456	97.4	1103	2	US-08-223-305C-53
13	5436	97.0	1079	1	US-08-455-543A-55
14	5436	97.0	1079	2	US-08-223-305C-55
15	5410.5	96.6	1106	1	US-08-435-675B-5
16	5392.5	96.3	1106	1	US-08-336-257A-8
17	5159.5	92.1	1086	6	5386025-8
18	3025.5	54.0	1145	4	US-09-470-443-2
19	3025.5	54.0	1145	4	US-09-470-443-4
20	3004.5	53.6	1076	4	US-09-470-443-6
21	2563.5	45.8	508	4	US-08-435-675B-6
22	185	3.3	885	3	US-09-074-579-5
23	185	3.3	885	3	US-09-388-774-5
24	164.5	2.9	789	1	US-08-471-033-32
25	164.5	2.9	789	2	US-08-471-044-32
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27	164.5	2.9	789	2	US-08-471-046A-32

28	164.5	2.9	789	2	US-08-470-566B-32	Sequence 32, Appl
29	164.5	2.9	789	2	US-08-838-219B-4	Sequence 4, Appl
30	164.5	2.9	789	2	US-08-469-334-32	Sequence 32, Appl
31	164.5	2.9	789	3	US-09-300-529-32	Sequence 32, Appl
32	164.5	2.9	789	3	US-09-233-336A-4	Sequence 4, Appl
33	164.5	2.9	789	4	US-09-233-752A-4	Sequence 4, Appl
34	164.5	2.9	789	4	US-09-402-036-4	Sequence 4, Appl
35	164.5	2.9	789	4	US-09-904-226-6	Sequence 6, Appl
36	161.5	2.9	746	2	US-08-838-219B-6	Sequence 6, Appl
37	161.5	2.9	746	3	US-09-233-336A-6	Sequence 6, Appl
38	161.5	2.9	746	4	US-09-233-752A-6	Sequence 6, Appl
39	161.5	2.9	746	4	US-09-402-036-6	Sequence 6, Appl
40	161.5	2.9	746	4	US-09-904-226-6	Sequence 6, Appl
41	160.5	2.9	790	4	US-08-960-780-4	Sequence 4, Appl
42	160.5	2.9	790	4	US-09-073-898-4	Sequence 4, Appl
43	160.5	2.9	946	3	US-09-074-579-3	Sequence 3, Appl
44	160.5	2.9	946	4	US-09-388-774-3	Sequence 3, Appl
45	157.5	2.8	789	4	US-08-960-780-6	Sequence 6, Appl

## ALIGNMENTS

RESULT 1  
US-07-745-206A-25  
Sequence 25, Application US/07745206A  
Patent No. 5429921  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: McQue, Ann  
TITLE OF INVENTION: Human Calcium Channel Compositions and  
TITLE OF INVENTION: Methods  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fitch, Even, Tabin & Flannery  
STREET: 135 S. LaSalle  
CITY: Chicago  
STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07745,206A  
FILING DATE: 19910815  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Feder, Scott B  
REFERENCE/DOCKET NUMBER: 51504  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-372-7842  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1091 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-745-206A-25

Query Match 98.8%; Score 5532; DB 1; Length 1091;  
Best Local Similarity 98.7%; Pred. No. 0;  
Matches 1049; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 MAAGCLLATLTLFQSLILGSSQEPFSAVTKSWDKMODLVTLAKTASGVNQLVDI 60  
|||||  
DB 1 MAAGCLLATLTLFQSLILGSSQEPFSAVTKSWDKMODLVTLAKTASGVNQLVDI 60

2000



Db	318	YIYDCLLKVEALISQKNKI	-----	YSNED	34
QY	399	IQMMACENKGYEYIPDSIGAIRINQOEYLDVGRPMVLG	-----	DKAKOV	444
Db	343	INKMYLGGTYVLSTLYNINKIKYNNKKEENRILGL-VIKTGFITTKGIVNNILVHKKKEL	-----		400
QY	445	QMTNYYLDALLEGVITGTPVFE---NTGQENKNTNLKNOLIIG	-----		480
Db	402	NLINSYKFLII-LIIVALEFSVFILLYYTLLSNNEYT---NHIIKICLDITDAIPALPT	-----		451
QY	487	---VMGVDSLEDIKRLTPREFTLPCNGYFEA-----IDPPGYVLVHNPLO-----PKNP	-----		533
Db	458	TLTVGISTAISLKKKFSSTCCCPKINIAQININWVDKIG-TLTENNLOFIIITQNK	-----		511
QY	533	KQEPVYLDLDALEENDIKVEIRNKMIDGESGEKTFPLVKSODERYIDGNRFTYWT	-----		591
Db	517	KNKNMIS-DEFHIK-----EKNTESYIHSKDDNNIHNK	-----		544
QY	593	VAGTGYSLALVLPYTSFYIRAKIETTTQARSKGKKKD-----SETLKPQFE	-----		644
Db	550	-----SIISEYYIKDNMKNLHTSSK-KKSITKERSNPLVOTIKSLCLKDHYIK	-----		596
QY	643	ESGYFIAPRDYCNCDLKTISDNN-TFELN-----FNEF--IDRKTPNNPSCNIDLNRV	-----		693
Db	597	EKKREYYNNNYCNDLHINDTSCSYSLNSETKDAYCEYIDH-----LCD---INK	-----		647
QY	694	LIDAGFTNELVQNVYNSKOKNIKGVARFVYTDGITTVPYKPEAGENQENPEYEDSFYK	-----		753
Db	648	NMDIKSNELMKQYSKNELMGKTIKNEML-----GKYSK	-----		683
QY	754	RLSDNDNVTFAFPAFYNKSGPGAYESGLINYSKAVEIYIOGKLKPAVVG-----IKIDVN	-----		807
Db	682	NEL-----MGKYSKNELMKQYSKNELMGKYSKNELMGKYSKNELMGKTIKNOGVADTN	-----		734
QY	808	SWIENFTKTSIRD-PCAGPVDCCKRNSDVMQV-----ILDDGGFLMANHDYINQIGRF	-----		864
Db	735	IYHMCNDNDYNDPCD---YCNACNNDYTRLEYHNINKNSFNIPPEKKNSYNNISEH	-----		791
QY	863	-----FGELDPSLMRLVNIYSYAF-----NKSY	-----		886
Db	792	IKINYPILFEALACCHTLRSKNNKIMGVDLEILMFNFTNCOMLNNNSFIIEKKKKCSY	-----		851
QY	887	DYQSGCEGAPRKQAGIRSAVYSIADLIHIGMWTAAASIILOQFLSLTFPRILLEAV	-----		946
Db	852	DFQKI---DGDKNIGANDERCHLNN-----NLVSYNIIILKP-----	-----		884
QY	947	EMEDDDFTASLSKOSCTEOTQYFPPDNDKS	-----		977
Db	885	-----EFQSRLOKMSYVYKST-YGNNDNDNN	-----		909
RESULT 15					
ITH2_MESAU					
AC	P97279;	STANDARD;	PRT;	946	AA.
DT	15-JUL-1998	(Rel. 36, Created)			
DT	15-JUL-1998	(Rel. 36, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy chain H2) (HC2).				
GN	ITI12.				
OS	Mesocricetus auratus (Golden hamster).				
OC	Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;				
OC	Mesocricetus.				
OX	NCBI_TaxID=10036;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Liver.				
RX	MEDLINE=97420688; PubMed=9276673;				
RT	Nakatani T., Suzuki Y., Yamamoto T., Sinozawa H.,				
RT	Molecular cloning and sequencing of cDNAs encoding three heavy chain				
RT	precursors of the inter-alpha-trypsin inhibitor in Syrian hamster;				

RA	Enghild J.J.:	Posttranslational modifications of human inter-alpha-inhibitor:	
RT	2."	Identification of glycans and disulfide bridges in heavy chains 1 and 2."	
RL	Biochemistry 37:408-416(1998).		
CC	-1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES.		
CC	-1- SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN.		
CC	BIKUNIN, INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2 AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H3 AND BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.		
CC	-1- PUT: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE.		
CC	-1- MASS SPECTROMETRY: MW=76508; METHOD=MALDI; RANGE=55-702.		
CC	-1- SIMILARITY: BELONGS TO THE ITH FAMILY.		
CC	-1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb.ch/announce/or_send_an_email_to_license@isb-sib.ch">http://www.isb.ch/announce/or_send_an_email_to_license@isb-sib.ch</a> ).		
CC	-----		
DR	EMBL; X07173; CAA30160.1; ALT_SEQ.		
DR	EMBL; M18193; AAA60558.1; -.		
DR	EMBL; M33033; AAA59195.1; -.		
DR	PIR; S00346; IYH02.		
DR	PIR; B34245; B34245.		
DR	GlycoSuiteDB: P19823; -.		
DR	Genew; HGNC:6167; ITH2.		
DR	MIM; 146640; -.		
DR	InterPro: IPR002035; VWFA_A.		
DR	Pfam: PF00092; vwa; 1.		
DR	SMART: SM00327; VMA; 1.		
DR	PROSITE; PS50234; VWFA: 1.		
KW	Serine protease inhibitor; Repeat; Signal; Multigene family;		
KW	Glycoprotein.		
FT	SIGNAL	1	18
FT	PROPEP	19	54
FT	CHAIN	55	702
FT			
FT	PROPEP	703	946
FT	DOMAIN	308	468
FT	DISULFID	261	264
FT	DISULFID	650	651
FT	CARBOHYD	118	118
FT			
FT	CARBOHYD	666	666
FT			
FT	CARBOHYD	671	671
FT	CARBOHYD	673	673
FT			
FT	CARBOHYD	675	675
FT			
FT	CARBOHYD	691	691
FT			
FT	MOD_RES	282	282
FT	MOD_RES	283	283
FT	BINDING	702	702
FT	CONFLICT	374	374
FT	CONFLICT	674	674
FT	CONFLICT	705	705
FT	CONFLICT	729	729
FT	CONFLICT	731	731
FT	SEQUENCE	946 AA;	106436 MW; 1478CF358F3BA776 CRC64;

Query Match Similarity	2.8%	Score 155.5	DB 1	Length 946
Best Local Similarity	19.8%	Pred. No. 0.12		
Matches 134	Conservative 106	Mismatches 249	Indels 189	Gaps 31

QY	33	IKSWDKMEDLVTTAKTASGVNQLVDIYEKYODLYEVPNNAROLVE-----	80
		: : : : :           : : : : :     : : :	
Db	26	LSEFVD--YEDLVEL---APGKFLVLAENRRYORSL---PQSEBMEAEVDQTLTSYKV	77
		: : : : :           : : : : :     : : :	
QY	81	-----IAARDIEKLNRKALVRLALEAKYQAAHQMKREDAASN-----	120
		: : : : :           : : : : :     : : :	
Db	78	QSTITSRMAATMTLOSQKVVNNSPOPNVVEVDQIPKGA-----FISNFSMTVDGKTFRRS	131
		: : : : :           : : : : :     : : :	
QY	121	-----EYVYVYAK-----DDLDPEKDNSE-----PGSORIKPFIFIDANPGRQ	158
		: : : : :           : : : : :     : : :	
Db	132	IKETVGRALRYAQRARAKKTAGLVSSALDDMFENFTEVNVLPKAKVQFELHYDEYKWKRL	191
		: : : : :           : : : : :     : : :	
QY	159	ISYOH-----AAVHIPDIYEGSTIVLMELNMTSALD-----EVPKRNBE-----	199
		: : : : :           : : : : :     : : :	
Db	192	GSVEHRIYLOPGRLAHLEVDVWVLEPQGLRPLHVPDPFEGHFGDGVPIVSKGQAKHVP	251
		: : : : :           : : : : :     : : :	
QY	200	DPSLMQVRESAIGLARYPASPWNDSRTPKIDLYVRRP-----WYIOGAA	249
		: : : : :           : : : : :     : : :	
Db	252	KPIVAAQ-----RIPCSCR--ETAVDGEVLVDYVKREKAGELVFNCGFVAFRA	300
		: : : : :           : : : : :     : : :	
QY	250	S-----PKDMLILVDVSGVSGITLKLIRTSVSEMLETTLSDDDFVNVASFNSAADVSC	303
		: : : : :           : : : : :     : : :	
Db	301	PDNLDLPFKHILFLVIDVSGSMGVKMKQVTEVMKTIIDDLAEDHSEVIDFQNIIR--TW	358
		: : : : :           : : : : :     : : :	
QY	304	FQHLVQANVRNKKVYLKDAVNNITFANGITDYKKGP---SFAEQLLNVNSRANCKIML	360
		: : : : :           : : : : :     : : :	
Db	359	RNDLISATKQVADAKRYIEKIQPSGGININALLRALFIINEANNNGILDPNSVSILIL	418
		: : : : :           : : : : :     : : :	
QY	361	FTDS---GGERAQELFAKYNKDKVRFTEFSVQG--HYHDSGRPIOMACENKG-----	408
		: : : : :           : : : : :     : : :	
Db	419	VSDDPVPGVLGKLSIQKQVKNKENDONLSLSLGGFVDYDPLKRLSNENHGGIAORLYG	478
		: : : : :           : : : : :     : : :	
QY	409	-----YYEYI--PSIGAIRIN--TOEYIDLV-----GRPMYIAG--DKAKO	443
		: : : : :           : : : : :     : : :	
Db	479	NQDTSQKKFKNYQVSTPLLRNVQFNPHYTSVTDYQNNFNHFGSGEIVYAGFPDAK	537
		: : : : :           : : : : :     : : :	
QY	444	VQWTVNYLDALEGLVITGTLPEVFNITGONENKTNLAKQILLGVAGVDSLEDI---KR	499
		: : : : :           : : : : :     : : :	
Db	538	-----LDQIE--SVYTA-----TSANQOLFLEFLAOMDLODFLSKDKH	574
		: : : : :           : : : : :     : : :	
QY	500	LTPREFICPGVGEAIDPNGVYLHPNLQPKPKQDEPVLDFDALENDIKVETIRNKK	559
		: : : : :           : : : : :     : : :	
Db	575	ADDPFTR-KIMAYLTIN---QLAERSIAP--TAAAKRIRITSILOMSLDHIIYTPPLISLV	629
		: : : : :           : : : : :     : : :	
QY	560	IDGSGEKTFRTLVKSOD	577
		: : : : :           : : : : :     : : :	
Db	630	IENAGDERMLADAPQD	647
		: : : : :           : : : : :     : : :	

RESULT 14
ATX1_PLAFA
ID ATX1_PLAFA STANDARD; PRT; 1956 AA.
AC 004956;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, last sequence update)
DT 16-OCT-2001 (Rel. 40, last annotation update)
DE Probable cation-transporting ATPase 1 (EC 3.6.3.-).
OS Plasmodium falciparum.
OC Eukaryotes; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxId=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=T9/96;
RX MEDLINE=93132070; PubMed=8421054;
RA Krishna S., Cowan G., Meade J.C., Wells R.A., Stringer J.R.,
RA Robson K.J.;
RT "A family of cation ATPase-like molecules from Plasmodium
RT falciparum".;





RA Niehaus F., Frey B., Antankian G.;  
 RT "Cloning and characterisation of a thermostable alpha-DNA polymerase  
 from the hyperthermophilic archaeon Thermococcus sp. TY.";  
 RL Gene 204:153-158(1997).  
 CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate -> N diphosphate  
 + (DNA)(N).  
 CC -1- PTM: THIS PROTEIN UNDERGOES A PROTEIN SELF SPLICING THAT INVOLVES  
 A POST-TRANSLATIONAL EXCISION OF THE THREE INTERVENING REGION  
 (INTEINS) FOLLOWED BY PEPTIDE LIGATION.  
 CC -1- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL: Y13030; CAA73475.1; .  
 DR HSSP: P56689; 1TGO.  
 DR InterPro: IPR002064; DNA\_pol\_B.  
 DR InterPro: IPR003586; Hedgehog\_hinc.  
 DR InterPro: IPR003587; Hedgehog\_hinc.  
 DR InterPro: IPR002203; Intein.  
 DR InterPro: IPR004042; Intein\_endonuc.  
 DR InterPro: IPR004578; Pol2.  
 DR Pfam: PF00136; DNA\_pol\_B\_4.  
 DR Pfam: PF03104; DNA\_pol\_B\_exo; 1.  
 DR PRINTS: PR00379; INTEIN.  
 DR SMART: SM00303; HincC; 3.  
 DR SMART: SM00306; HincN; 3.  
 DR SMART: SM00486; PolBc; 1.  
 DR TIGRFA: TIGR00592; pol2; 2.  
 DR PROSITE: PS00116; DNA\_POLYMERASE\_B; FALSE\_NEG.  
 DR PROSITE: PS00818; INTEIN\_C\_TER; 3.  
 DR PROSITE: PS00819; INTEIN\_ENDONUCLEASE; 2.  
 DR PROSITE: PS00817; INTEIN\_N\_TER; 3.  
 KW Transferase; DNA-directed DNA polymerase; DNA replication;  
 KW DNA-binding; Hydrolyase; Endonuclease; Autocatalytic cleavage;  
 KW Protein splicing.  
 FT CHAIN 1 409 DNA POLYMERASE, 1ST PART (POTENTIAL).  
 FT CHAIN 410 769 INTEIN I.  
 FT CHAIN 770 855 DNA POLYMERASE, 2ND PART (POTENTIAL).  
 FT CHAIN 856 1392 INTEIN II.  
 FT CHAIN 1393 1441 DNA POLYMERASE, 3RD PART (POTENTIAL).  
 FT CHAIN 1442 1598 INTEIN III.  
 FT CHAIN 1599 1829 DNA POLYMERASE, 4TH PART (POTENTIAL).  
 SQ SEQUENCE 1829 AA; 211875 MW; A11348BC57EB9CB3 CRC64;  
 Query Match 2.9%; Score 162; DB 1; Length 1829;  
 Best Local Similarity 20.8%; Pred. No. 0.13;  
 Matches 178; Conservative 101; Mismatches 294; Indels 284; Gaps 42;  
 QY 16 SLILGSSQEPSPS-----AVITKSW-----DKMOEDLVTLA 48  
 DB 229 TLLIGDKHPEKPIHRMGDSFAVEIKGRIHFDLPFVARTINLPYTLAEAVYEAVALGKT 288  
 QY 49 KTFASGVNOLVDIYEKYODI-----YTFEPNNAQLVEIAARDIEKLSRSKALVALAE 103  
 DB 289 KSLTGAEEETALWEIESKKAQYASWE--DNAATEL-----GKEPPEARE 334  
 QY 104 AEKVAQAOWREDPAS--NEVVY-----NAKDDLDPEKNDEPGSORIKPFI----- 150  
 DB 335 LAKLIGQSVWDYSRSTGLVEMYLRLVAVERNELAPNKPDEERYRRRLRTYIGGYKE 394  
 QY 151 DDANFGROISTOHAAYHPTD--IYEGSTV---LNEFMTSAIDVEYKKNREDEPSL 203  
 DB 395 PERGIMENIAYDFRCH-PADTRKVIYKGGIYINISDYKEDYILGIDG----- 441  
 QY 204 LMGVFSATGILARYYPASWVNSR---TPN-KIDLYDVRRRPWPYIQGASPKDMLIWD 259  
 DB 442 -WQ--RVKWKVHYEGKLININGLCKTPNKHVPVTEENDROTRI-----RSLAKSF 491

QY 260 VEGSVSGTLKIRTSVEEMLETISDDDEVNAVSPNSN----- 297  
 DB 492 LSGKKG---KITTKL-----FEKIAFEKKKPEEELIGELSGILLABGT 537  
 QY 298 -AQVSCF-----OHLVQANV-RNKKVLKDAY-----NNITAKG----- 329  
 DB 538 LKDIIEYDSSRGKRISHQYRVETTEIGENKEILLERYLFDMFGIRPSVKKKGDPTA 597  
 QY 330 -ITPKKGFSPAPOLLNVANSRANCKIIMLFDGGEERAOELPAKYNCKDKVRVPTF 387  
 DB 536 IKITTAKKAVYLQIEELK-NIESLYAPAVLRGF-----BRDAVNRKIRSTIYVT- 647  
 QY 388 SVGOHNVGRPIQWACENKGY---YFIPSGAIRINTQEVLDVGPWVLADDAKKQV 444  
 DB 648 -QGTNNKKKIDIVAKLDSGLPIPSRYKYKTIENKELTKHILLETGHD----- 695  
 QY 445 QMTNVLDALEGLVITGTLPEVNTIGNE-----NKTNLKNOLLGVMGVDSLE 495  
 DB 636 -----GLITFQTLVGFISSKNEALEKAEVRENNRKLKNSFYMLSTFEVSSE 743  
 QY 456 DIKRLTPRFTLCPNGYIYAIIDPNCVLLHPMLQKPNKPSQEPVLDLDALENDIKVEI 555  
 DB 744 YKGEVYDLTLEGMPYPA---NG-ILTHNSLYPSIIVTN-VSPDTLIER----- 789  
 QY 556 RNKMIDGSEGEKFTLVKSODERYIDKGNRTYTPVNGDYSLALVLPYSFYIKAK 615  
 DB 790 -----GCANYDAPVIG--YFCKADFG-----FIPSI 815  
 QY 616 IETITQARSKKKKKMSETLKPDEESGY-----TFIAPRDYCNLKDLSNDNTE 666  
 DB 816 IGEITTRQEIKKKK--ATIDPIEKMLDYRORAVKLLANSILPNEW---LPIIENGVEV 870  
 QY 667 FLNNEFIDR-----KTPNPNSCOTDILNVLVLDAGTNLNVNYSKQNIIGVAPF 721  
 DB 871 KFKVIGETIDRYMEQKQKRVTDTEVLE--VDNIFAFSL-NKSKSEIKKVAL- 924  
 QY 722 VTTDGITRYYPKEAGE 738  
 DB 925 -----IHKYKGEAYE 935  
 RESULT 12  
 Y103-SYNY3  
 ID Y103-SYNY3 STANDARD; PRT; 420 AA.  
 AC 055874;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Hypothetical protein s110103.  
 GN SL0103.  
 OS Synechocystis sp. (strain PCC 6803).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.  
 OX NCBI-TaxID=1148;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=96127529; PubMed=8590279;  
 RA Kaneo T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,  
 Sugitara M., Tabata S.;  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb  
 region from map positions 648 to 924 of the genome.";  
 RL DNA Res. 2:153-166(1995).  
 CC -1- SIMILARITY: TO E. COLI YPKF.  
 CC -1- SIMILARITY: CONTAINS 1 WMPA DOMAIN.  
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Db 133 YANVRRLKQGLPPDAVRVEIYVPSMDI--KDKQSIAPSKPIPFAMRYELA--- 187  
 QY 219 PASPVWNSRSTPNKIDLYVRRRPWYIQGAASPKDMLIVDVGSG--VSGTLTKLRTSVS 277  
 Db 188 PA-PW-NEGRITLLKVDILAKDKRSELPAS---NLVFLIDTSGSMISERPLIOSSIK 241  
 QY 278 EMLETISDDDFVAVASFSNADVSCFOHLYOAVNRKKVLKDAVNNTAKGITDYKGF 337  
 Db 242 LTVKLEFREDNDIAIYVADSRIA-----LPSISGSHKKEINAAIDDAEGSTNGAGL 296  
 QY 338 SFAPFOLLVYNSRANCKNIIMFLTDG-----GEERAOEIFAKYNNKKKRVVFFSGQ 391  
 Db 297 ELAYQOAT-GRIGGIN-ILLATDGFNVGIDPKSTESKVKQRESGVTLSTFGVN 354  
 QY 392 HNYDRCPIDMAACENKGYEYIPISGAIRINTOEYLDVGRPMVL--AGDKAKOYQ---- 445  
 Db 355 SNVNEAMVRIADVGNNGNSYIDTIS---EAQXVLNSMRMLTVAKDKVAAQIEFNPA 410  
 QY 446 WNVYLDALDELGVITGILPVENITGQNEKNTLNKQILGVAGVD-VSLEDI---KRLT 501  
 Db 411 WTEY---KQIGYE-----KROLREHFHNDNDVADGIGAKHIT 447  
 QY 502 PRFTLCPNGYFAIDPNGVYLLHPNLQPKNPKSOE 536  
 Db 448 LFEFLINGQKASIDKRLRA--PDNKLAKSKDKE 480

RESULT 10  
 ITH3\_MESAU STANDARD: PRT: 886 AA.  
 AC P97280:  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Inter-alpha-trypsin inhibitor heavy chain H3 precursor (ITI heavy chain H3) (H3).  
 DE ITH3.  
 GN Mesocricetus auratus (Golden hamster).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 OX NCBI\_TaxID=10036;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver.  
 RA MEDLINE=97420688; PubMed=9276673;  
 RA Nakatani T., Suzuki Y., Yamamoto T., Sinozara H.;  
 RT "Molecular cloning and sequencing of cDNAs encoding three heavy-chain precursors of the inter-alpha-trypsin inhibitor in Syrian hamster: implications for the evolution of the inter-alpha-trypsin inhibitor heavy chain family.";  
 RT J. Biochem. 122:71-82(1997).  
 RL (2)  
 RN SEQUENCE OF 31-50; 446-472 AND 504-523, AND SUBUNITS.  
 RP TISSUE=Plasma;  
 RC MEDLINE=97018241; PubMed=8864857;  
 RA Yamamoto T., Yamamoto K., Sinozara H.;  
 RT "Inter-alpha-trypsin inhibitor and its related proteins in Syrian hamster urine and plasma.";  
 RL J. Biochem. 120:145-152(1996).  
 CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY SIMILARITY).  
 CC -1- SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN, BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2 AND BIKUNIN. INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND BIKUNIN. AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.  
 CC -1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN

CC 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE ITH FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 WFPA DOMAIN.  
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 CC EMBL: D89287; BAA13940.1; -  
 DR InterPro: IPR002035; WVF\_A.  
 DR Pfam: PF00092; WVF\_1.  
 DR SMART: SM00327; WVF\_1.  
 DR PROSITE: PS0234; WVF\_1.  
 KW Serine protease inhibitor; Repeat; Signal; Multigene family;  
 KM Glycoprotein.  
 FT SIGNAL 1 18  
 FT PROPEP 19 30  
 FT CHAIN 31 646  
 FT PROPEP 647 886  
 FT DOMAIN 279 439  
 FT CARBOHYD 88 88  
 FT CARBOHYD 577 577  
 FT BINDING 646 646  
 FT SEQUENCE 886 AA; 99018 MW; AC0594C6852576B8 CRC64;  
 SQ  
 Query Match 3.0%; Score 166; DB 1; Length 886;  
 Best Local Similarity 23.2%; Pred. No. 0.026; Indels 51; Gaps 11;  
 Matches 66; Conservative 57; Mismatches 111;  
 QY 202 SLNQVFGSATGLARYYPASPVWNSRT-PNKID-----LYDVRRP-PWYIOGA-- 248  
 Db 208 SALTKSPGKGGKHHVSPS---LDQKSCPTGDSILNGLDFTIYVYNNRSPGNQVYNG 264  
 QY 249 -----ASPKMLLVDSVSGSGTLTKLRTSVSEMLETISDDDFVAVASFSN 296  
 Db 265 YFVHFAPDGLPVVPRKIVIVIDISGSMGRKIQGTRVALKILDDMKDDYINFLTST 324  
 QY 297 NAQDVSCFOHLYOAVNRKKVYLKDAVNNTAKGITDYKGFAPQQLN---YVNSA 352  
 Db 325 GV--TTMKDLDVQATPRANLEARTPVASISDQGTNINDGLRGIMLTDAREQHTVPER 382  
 QY 353 NCNKTIMLFTDG-----GEERAOEIFAKYNNKKKRVVFFTSVG--OHNYDRGPIOMACENK 407  
 Db 383 STSIIIML-TDGDANNGESRPERKIOERVRAKICGRPLVNLGFGNNLNFLETALLENH 441  
 QY 408 GYVEIPISGAIRINTOEYLDVGRPMVLAGDKAKOYQNTNYLD 452  
 Db 442 GVARRIEDSDANLDQGFEEYVAPPL-----TNEVE 475  
 RESULT 11  
 DPOL\_THEST STANDARD: PRT: 1829 AA.  
 AC 033845:  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE DNA polymerase (EC 2.7.7.7).  
 GN POL.  
 OS Thermococcus sp. (strain TY).  
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
 OC Thermococcus.  
 OX NCBI\_TaxID=110163;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98094267; PubMed=9434178;

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CC EMBL: X83231; CAA58233.1; -
DR InterPro: IPR002035; VWF_A.
DR Pfam: PF00092; Vwf; 1.
DR SMART: SM00327; VWA; 1.
DR PROSITE: PS50234; VWF_A; 1.
KW Serine protease inhibitor; Repeat; signal; Multigene family;
KM Glycoprotein.
FT SIGNAL 1 21 POTENTIAL.
FT PROPEP 22 33 BY SIMILARITY.
FT CHAIN 34 647 INTER-ALPHA-TRIPSPIN INHIBITOR HEAVY CHAIN
FT PROPEP 648 887 BY SIMILARITY.
FT DOMAIN 282 442 VWF_A.
FT CAROHD 91 91 N-LINKED (GLCNAc... ) (POTENTIAL).
FT CAROHD 580 580 N-LINKED (GLCNAc... ) (POTENTIAL).
FT BINDING 647 647 CHONDROITIN 4-SULFATE, CROSS-LINK SITE
FT BINDING 647 647 (BY SIMILARITY).
SQ SEQUENCE 887 AA; 99097 MW; 399F0FF96D514096 CRC64;

Query Match 3.3%; Score 183.5; DB 1; Length 887;
Best Local Similarity 18.4%; Pred. No. 0.0024; Indels 271; Gaps 37;
Matches 172; Conservative 139; Mismatches 353;

QY 27 PPSAVTIKSVDRKMOEDVLTAKTAGVNOQVDIYKYQDLYTVBPNNARQLVEIARDI 86
DB 101 YGGSVKEKVAOKYOKKAVSOGKTAG---LYKASGRKLEKFTVGVNAAGSKVIFELTY 156
QY 87 EKLSNRKALVRLAEKVAOAHOMRD---FASNEVYVNAKDDLDPEKNDSEPSQ 143
DB 157 EELL-KRNGKYEMLKQVOPKQVRFELDAHIFEPQISMDA----- 199
QY 144 RIKPVEIDANRGROISYQHAANHPTDIEGSTIVLNLNMTSALDEYFKKRNREDPSL 203
DB 200 -----DASF-----ITNDL-LGSALTKSF----- 217
QY 204 LMQVGSATGLARYYPASPMVDSRT-PNKID-----LYDYRRP-----WY 244
DB 218 -----SGKKGHVFRPSLDQRCPCPTSLDNGDFTIYDVNRSPNGVQVNGYF 269
QY 245 I-----QG-AASPKMLIVDVSQSGITLKLIRTSVSEMLETSDDDFVNAFNSNA 298
DB 270 VHEFAPQGLPVYPKNIAFIVDVSQSGIRKIQOTREALKILDDMEELYLFILFSTGV 329
QY 299 QDVSCFOHLYOAVNRKATKLVANNITAKGIDTKYKGSFAFEOILANTVSRAN----- 353
DB 330 --TTWMDHLYKATPALEEARAFVKNIIRDMSMTNINDGLRGIEML--NKAREDHLYPE 384
QY 354 -CNKIIMLETDG---GEERAOEIFAKYKDKKRVYFTFSVG-QHNYDRGPIQWACENK 407
DB 385 RSTSLIYMLTLDGANTGESRPERKIQENRNNAIRGKPEPLYNLGFNNLNTNPLESLALENH 444
QY 408 GYYEELPSIGAIRINQVELDIVLGRPMVLAGKAKOVQNTNYLALLEGIVITGTLPLVF 467
DB 445 GEARRIYEDSDASLQLOGEYEEVANPL-----TNVELEYENA-----IL 485
QY 468 NITGQENKTNLKNQILVVMGVDSLEDIKRLTPFTLCPGYVYAIIDPNGYVLLPML 527
DB 486 DILRNYSPPHYDSSELIVAGRLVDRVND-----PKAVYKGGALN----- 526
QY 528 QPANPKSQEPVTLIDDALENDIKVEIRNKMIDGESGKTF-----RTLYKSQDERYI 581
DB 527 ---DLTFEEVDKEMDAALK-----RQGYIFGDYIERLMAVYLITIEOLLERKNKARD 576
QY 582 DKGNRTYMTPVNGTYSILA--LVLPYSPYYIKAKIEFTITQARSKKCKMDSF---L 636
DB 577 EKENTY-----AALELSLYHFVPLTSMVYTKPEDNEQTAIDKPEBAISATAYL 631
QY 637 KPDNFESEGYETIAPDYCNDLKISDNTEELLNF---NEFTDRKTPNNPSCNTDILNV 693
DB 632 TSOQSSHSPIYY-----DGDPIFIQVPGKMDTICFNIDKPGVGLSLIDGP 679
QY 694 LLDAGFTNELLVONYWSKQKNIKGVKARFVYTDGKITRVYPKRAGENWQENPETYEDSYK 753

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DB 680 VTGIAYTGQIT-----GEKGNASSRTGKT----- 704
QY 754 RSLDNDNVYFTAPYFNKSGPGAYESGIMVSKAVEITYOGKILKPAVVGIRKIDVNSMIENF 813
DB 705 -----YEGFLGIGANAMDFRIVYTEKIIILN-----GDALSTFSSMLDLY 744
QY 814 TKTSIRPCAGPYCDCKRNSDVMDCVILDDG-GFLLMAN-----HDDYTNQIGRFG 864
DB 745 TVTQ-----TGLSTYINRKNMV--VSFEDGISFVILVHVMKKHPVHQDFLG-----FY 792
QY 865 EIDPSLRHLVNSIVAFNKSVDYQSV-CEPGAAP 898
DB 793 VVDSHRMSAQTHGLIGQFQPFDFKVPEDVRGSDP 827

RESULT 9
YFBK_ECOLI STANDARD; PRT; 575 AA.
AC P76481;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein yfbk.
GN YFBK OR B2270.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
  Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
  Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
  Mau B., Shao Y.;
  "The complete genome sequence of Escherichia coli K-12.";
  Science 277:1453-1474(1997).
RL -1 SIMILARITY: TO SYNECHOCYSTIS PCC 6803 SLR0103.
CC -1 SIMILARITY: COMTAINS 1 VWF_A DOMAIN.
CC
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CC
CC EMBL: AE000317; AAC75330.1; -
DR EcoGene: EG14095; yfbk.
DR InterPro: IPR002035; VWF_A.
DR Pfam: PF00092; Vwf; 1.
DR SMART: SM00327; VWA; 1.
DR PROSITE: PS50234; VWF_A; 1.
KW Hypothetical protein; Complete proteome.
FT DOMAIN 216 394 VWF_A.
SQ SEQUENCE 575 AA; 63634 MW; 7BB6A1A77A2BE11 CRC64;

Query Match 3.0%; Score 168.5; DB 1; Length 575;
Best Local Similarity 21.6%; Pred. No. 0.0098;
Matches 111; Conservative 94; Mismatches 205; Indels 105; Gaps 24;

QY 71 EPNNAARQLVEIARIDIEKLSNRKALVRLAEKVAOAHQWREDEPASNEVYVYNNAKDD 130
DB 22 QPENKESQOQSPSTTEQOVLAAQQAIAK---EAPQSAHA---AKALAAQCEYQOYSKQA 75
QY 131 LDPEKND-----SEPGSRIKPVITDANFGROISYQHA---VHIPTDI 172
DB 76 LQGRIGQAPTPARAKAKATHIANPGTARYQOF---DDNPYKQVAVNPANLAFSDVDYDGS 132
QY 173 YEGSTIVINE-----LNMTSALDEYFKKRNREDPSLIMQVFSATGLARYI 218

```

RP SEQUENCE OF 631-647, AND CROSS-LINKAGE SITE TO BIKUNIN.  
 RX MEDLINE=91093267; PubMed=1898736;  
 RA Enghild J.J., Salvesen G., Hefte S.A., Thøgersen I.B.,  
 RA Rutherford S., Pizzo S.V.,  
 RT Chondroitin 4-sulfate covalently cross-links the chains of the  
 RT human blood protein pre-alpha-inhibitor \*;  
 RL J. Biol. Chem. 266:747-751(1991).  
 CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A  
 CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,  
 CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE  
 CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE  
 CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES.  
 CC -1- SUBUNIT: I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM  
 CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,  
 CC BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-1) IS COMPOSED OF H1, H2  
 CC AND BIKUNIN. INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND  
 CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-1) OF H3 AND BIKUNIN.  
 CC -1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN  
 CC 4-SULFATE BRIDGE TO THEIR C-TERMINAL ASPARTATE.  
 CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 WFMA DOMAIN.  
 CC -----  
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 CC -----  
 DR EMBL: X67055; CAA47439.1;  
 DR EMBL: X14690; CAA32821.1;  
 DR Genbank: HGNC:6168; ITIH3.  
 DR MIM: 146650;  
 DR InterPro: IPR002035; VWF\_A.  
 DR Pfam: PF00092; vwa; 1.  
 DR SMART: SM00327; VWA; 1.  
 DR PROSITE: PS00234; VWA; 1.  
 DR Serine protease inhibitor; Repeat; Signal; Multigene family;  
 KW Glycoprotein.  
 FT SIGNAL 1 17 POTENTIAL.  
 FT PROPEP 18 30  
 FT CHAIN 31 647 INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN  
 FT H3.  
 FT PROPEP 648 885  
 FT DOMAIN 278 438 WFMA.  
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 576 576 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT BINDING 647 647 CHONDROITIN 4-SULFATE, CROSS-LINK SITE.  
 FT CONFLICT 344 344 R -> K (IN REF. 2).  
 FT CONFLICT 357 357 N -> G (IN REF. 2).  
 FT CONFLICT 846 846 Q -> H (IN REF. 2).  
 SO SEQUENCE 885 AA; 99121 MW; B638568F5E4A1B CRC64;  
 Query Match 3.3%; Score 185; DB 1; Length 885;  
 Best Local Similarity 21.3%; Pred. No. 0.0019;  
 Matches 137; Conservative 113; Mismatches 243; Indels 150; Gaps 36;  
 QY 45 VLAHTASGVQVQDIYKYODLTVEPNNAKRLVETIARDIEKLKRSKALVLALEA 104  
 DB 77 VLPKTAITITFTLTIT-----DGVVY-PGVNKE-KEVAKKQYKAVSOGKTAGL----- 123  
 QY 105 EKVQAAMHQRDF-----ASNEVYVYNAKDDLPEDKNDSEPSORIKPFIDANFGR 157  
 DB 124 --VNASGRKLEKFTVSVVAVAGSVTFELLYEELKKHKKGYEYKLVOP-----K 172  
 QY 158 QISQHAHVAHPTDIYESTIVLNLMTSALDEVFKKKNREEDSLLMQVFGSA-----T 212  
 DB 173 QL-VKHFIEV--DIFEPQGI-----SMLD-----AASFTINDLLGSLTKSFS 214  
 QY 213 GLARYYPASPMVNSRT-PNKID-----LVDVRRP-----WTI-----QG- 247  
 DB 215 GKKGHVSKPFLDOORSCPTCTDSLNLGMDFTTYDVNRESPGVNVQVNGYVFHFAPQGL 274

QY 248 AASPDMILNDVSGVSGLTFLKIRTSVSEMLETLSDDDFVNVAFSNADVSCF-OH 306  
 DB 275 PVYPRKVAFFVIDISGSMAGRKLEQTKREALRLIDEMKREDLNLFTLSG---DVSTKEH 331  
 QY 307 LVQANVRKKVYKADAVNNITAKGITDYKGFSPAEQOLLNVSR-----ANCKITML 360  
 DB 332 LVQAPENMLQEARFTVVKSMEDKGMTININDGLRGISML---NKAREHRIPERSTIVIM 388  
 QY 361 FTDG-----GEERAOEIFAKYK--DKRYVFTFSVGVGNDRGIOMACNKKIYIEP 414  
 DB 369 LTDSGANVSGESPEKIQENNVNNAIGKPLYNLQFG--NNLWYNFLNNALNHNQFARIY 447  
 QY 415 SIGAIRINTQETLDYGRPVYLAGDKAKOVQNTVNYLDAL-----LGLVITGTL 465  
 DB 448 EDSADLQLOGFEEYEVANPL-LTGEMEYPE--NAIDLTQNTQYHFDGSEIYVACRLV 504  
 QY 466 VENTIGQENKNTNK-----NQLIGVWGVDVSLIEDIKRLPTFLCPNGYFAIDPN-- 518  
 DB 505 DEDM---NSFRADYKGGCATNDL---TETEVDKMEK-----ALQERDYIFG---NYI 550  
 QY 519 ---GYVLLHFNLPK---NPKSOEPTLDLDELNDIKVEIRNMKIDGSEKTFRT 571  
 DB 551 ERLMAYILTEQLLEKRRKKAHEEKENLTARALDLSLKYHFTVPLTSMVTKPE----- 603  
 QY 572 LVKSODERYI-DKGNRYTWTVPV-GDYSLALVLPYSEFYI 612  
 DB 604 --DNEDERAIADKPEDAEATPVSPAMSYLTSYPPQNPYYIV 644  
 RESULT 8  
 ITIH3\_RAT  
 ID ITIH3\_RAT STANDARD; PRT; 887 AA.  
 AC Q63416;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Inter-alpha-trypsin inhibitor heavy chain H3 precursor (ITI heavy  
 DE chain H3).  
 GN ITIH3.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI-TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Sprague-Dawley; TISSUE-Liver;  
 RA Blom A., Fries E.;  
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A  
 CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,  
 CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE  
 CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE  
 CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY  
 CC SIMILARITY).  
 CC -1- SUBUNIT: I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM  
 CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,  
 CC BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-1) IS COMPOSED OF H1, H2  
 CC AND BIKUNIN. INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND  
 CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-1) OF H3 AND BIKUNIN.  
 CC -1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN  
 CC 4-SULFATE BRIDGE TO THEIR C-TERMINAL ASPARTATE (BY  
 CC SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 WFMA DOMAIN.  
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UN36.CABEL
ID UN36.CABEL STANDARD; PRT: 734 AA.
AC P34374;
DT 01-FEB-1994 (Rel. 28, Created)
DE 01-FEB-1994 (Rel. 28, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein unc-36.
GN UNC-36 OR UNC-72 OR C50C3.11.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromodorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Betts M.,
RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., De Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Lathrop P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
RA Sims M., Smailson N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Wainstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RL elegans."
RL Nature 368:33-38(1994).
CC -1- SIMILARITY: TO CALCIUM CHANNEL ALPHA-2B SUBUNIT.
CC -1- SIMILARITY: CONTAINS 1 VFMA DOMAIN.
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CC -----
DR EMBL: L14433; AAA27969.1;
DR PIR: S44617; S44617.
DR WormPep: C50C3.11; CE00117.
DR InterPro: IPR004010; Cache.
DR InterPro: IPR002035; VFMA_A.
DR Pfam: PF00092; vma: 1.
DR Pfam: PF02743; Cache: 1.
DR SMART: SM00327; VMA: 1.
DR PROSITE: PS50234; VFMA: 1.
KM Ionic channel; Ion transport; Voltage-gated channel; Calcium channel;
KM Glycoprotein.
FT DOMAIN 250 435 VFMA.
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 476 476 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 514 514 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 734 AA; 85034 MW; CCFB78C8DEE4B71F CRC64;

Query Match 10.98; Score 611; DB 1; Length 734;
Best Local Similarity 26.35; Pred. No. 6; te-29;
Matches 179; Conservative 127; Mismatches 261; Indels 108; Gaps 19;

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OY 157 ROISYOAHAHPIPTDIYEGSTIVLNLMTSALDEVEFKKREDEPSLQVGSATGLAR 216
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 156 LPTSSVSAVHIPTPLDRNEDLRLKIDW-SDIDAYRRNRRETRKLAQLCSEAGYR 214
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 217 YTPASPVV-DNSRTPNKIDLDYRRRPWTYOGAASPKMLIVDVGSGVGLTKILRTS 275
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 215 YTPAASVFWNQ--DEHLDFDPCRNTEWYINSATNSKNVILMLDMSGSMICORVEAKOT 272
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 276 VSEMLFTLSDDDFVNVAFFNSNA--QDVSCFQHLVQAVNRKKVLDKAVNNITAKGTD 332
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 273 TEALLETLSNDYFNMTSTSKNFTLLDGGNGTLQATMRNKKALRRRMDYQSGKAE 332
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 333 YKGFSEAFEPOLINYN-----VRANCKIMLEFTDGERAEIPEAKNKKRVVTF 387
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 333 YKALPLAEFVLLDINNCGDNRNGACENVIMLTGARNAKKIDPMADKRVVTF 392
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 388 SVGOHNTDRGPDIOMACENKGYIEIPSGALINTOEYL---DYLGRPWLADGRAKO 443
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 393 LVDEDAIDFNEVREMAKNNGYVHVAANADVDEKIHRYIRMSRVYGRHYESGOLS-- 450
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 444 VQMTNYLDALELGL--VITGLPEFNITGONENKTN----- 478
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 451 -WMTGYREKLYLPREIFAEVPTITNOSFAVNNKASRRKIRLQSEARSRAFTVTSY 509
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 479 --LKNOLILGVMGVSLDIDKRLTPFTLCPNGYFAIDPNGVYLLHPNLOPKNP--- 532
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 510 PVIYETFMGVAVNIPLFEVAAKSHPNIGSKSYFMLDONGFVTHQLRPIDFTY 569
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 533 KSEPTVTLPLD-----ALENDIVEIRNKIDGE 563
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 570 HKQNNYMDLLEVGONONVRSSQSAVSDLVCEGANYAECDLKRRAVKMIIDCD 629
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 564 SGKRTFTLYKSODERY---IDK---GNRTYTWPTGDSVSLVLTPTSYFYIKAKI 616
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 630 NSD-----VQGLDVLYATFELDRIYVPTNTTYAEICINANFVLGLAVAKGDIYRVK- 682
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 617 EETITQARSKKGRMK 631
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 683 -----QKKYDFGRVK 692
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
ID ITH3_MOUSE STANDARD; PRT: 886 AA.
AC 061704;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inter-alpha-trypsin inhibitor heavy chain H3 precursor (ITI heavy
DE chain H3).
DE ITH3.
GN ITH3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6N; TISSUE=Liver;
RX MEDLINE=95194326; PubMed=7534067;
RA Chan P., Risler J.-L., Raguenez G., Sallier J.-P.;
RT "The three heavy-chain precursors for the inter-alpha-inhibitor
RT family in mouse: new members of the multicopper oxidase protein group
RT with differential transcription in liver and brain."
RL Biochem. J. 306:505-512(1995).
CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SPERM OR AS A
CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN.
CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
CC SIMILARITY).
CC -1- SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
CC BIKONIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2

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RESULT 4
YL9_CAEEL          STANDARD:      PRT: 1205 AA.
ID YL9_CAEEL
AC P34372:
DT 01-FEB-1994 (Rel. 28, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein C50C3.9 in chromosome III precursor.
GN C50C3.9.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Felodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=94150718; PubMed=7906398;
RX Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kersey J., Kirsten J., Lalister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
RA Sims M., Smailton N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaughan M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RT Nature 368:32-38(1994).
RL [2]
RP REVISIONS.
RA Waterston R.;
RL Submitted (Aug-2001) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 WFA DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL: L14433; AAA27971.2; -.
DR PIR: S44619; S44619.
DR WormPep: C50C3.9; CE24860.
DR InterPro: IPR02035; WFA.
DR InterPro: IPR004010; Cache.
DR Pfam: PF00092; wfa; 1.
DR Pfam: PF02743; Cache; 1.
DR SMART: SM00327; WFA; 1.
DR Hypothetical protein; Signal.
KW Hypothetical protein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 1205
FT DOMAIN 250 435
FT SEQUENCE 1205 AA; 139339 MW; 79A2P96C052BF91C CRC64;
Query Match 13.5%; Score 754; DB 1; Length 1205;
Best Local Similarity 23.8%; Pred. No. 3.8e-37;
Matches 284; Conservative 206; Mismatches 475; Indels 230; Gaps 42;
OY 47 LAKTASGVQVLDYIEKYDDLVTEPNNAKRLVETARIEKILSRKAL--VRLALEA 104
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 36 MEYTSKISHETTLKONRYKEVEEQFDRALSKSRHIEDYLYKRSQFAVKARISLEA 95
OY 105 EKVOAHQREDFASNEVYVYNAKDDLDPEK--NDSEPSGSRILP-----VFIDANF-G 156
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 96 RSVRNDSTVNDQSKSFIFPMGAKQGDGTITYESNHCLKRLKVNTEKFNLTQNNFYTT 155
OY 157 ROISYQAAVHIPTDIEGSTITVNLNMTSALDEVFKNRREDPSLLMQVEGSATGLAR 216

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DB 156 LPTSSVSAVAHPIPLYDRNEDLLRKIDW--SDIAYRTNREETKDLAFLQFCEAGYMR 214
OY 217 YYPASPWV-DNSRTPNNIDLDVRRRPVYLOGAASPMDLILVDVSGSGGLTKLIRTS 275
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 215 YYPASWFWMDNQ--DEHLDLFCRNTETMYINSATNSKNVILMDSSMLGQREYAKOT 272
OY 276 VSEMLETISDDDFVNAVSFNSNA--ODVSCFOILVQANRKNKVLDAVNNITAKGTD 332
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 273 TEALLETLSHNDYINIMFSGNTFLDGCNTGNLLDQATRNKALKRKMDTYQSEKAE 332
OY 333 YKKGSEFAEQLLVN-----VSRANCKIIMFTDGEERPADEIFAKYKKDKRVYTF 387
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 333 YEKALPLAFSVLLDINNCGDNNRGACENVIMLTIDAPNAYKKIKFDMYNAADKKVFYTF 392
OY 388 SVGQHNDRGPIQWACENKGYEIEISGIRINTQEYL---DVGGRMVLADGAKO 443
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 393 LVGDEALDENFVREMACNNRGVNVANMADVDEKIHHTYIRMSRVVGRYKESGOLS-- 450
OY 444 VQMTNVYLDALDELGL--VITGLPVNITGQNEKNTN----- 478
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 451 -WMTGVYERLYLDRPELFAEPVPIITNOSFAYNMKASRRKIRIQKSEASRMPTVTVSY 509
OY 479 --LNQQLIGVGVDSLEDIKRLTPRTLCPNGYFAIDPNGVYLLHPNLQKRP--- 532
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 510 PVIWETFMGYAAVNIPLTEVAQKSHPNATGSKSYFPMIDQNGFVMTHPDLRPDPFTKY 569
OY 533 KSGEFTVLDFD-----AELFNITKYEIRKIMIDGE 563
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 570 HKQNYNNMDLLELVGQNVNRRSQKQAVSDLVCEGANYAECDVLDLRRAVRMMIIDD 639
OY 564 SGEKTFRTLVKSDERY---IDK---GNRTYTWTPYNGTDYSLATLPTYSFYIRAKI 616
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 630 NSD-----VOODVLYATELLDVRYPQNTNYAECINHANFVGLAVAGDDYRV--- 679
OY 617 EETITQARKKGGKKKDESETLKPDNFEESGYTFIAPRDYC--NDIKISDNTE-FLNFNE 673
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 680 -----YKQKKYDDEGRVYKMDWMDGDKRMRLHPHMYCEFLNDTIDMSKEAEIYAOQ 721
OY 674 FIDR-KTPNNNSCWTDILNRYLDAGFTNELVQVYNSKQKNIK--VKARFVYTDGDT 729
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 732 MSDSGKAPLCEYRRNIVKELLDMEATSNLIDS-WTOFQFMKNLILHAFATPSGMI 790
OY 730 RYVP-----KEAGENMOE-----NPEYEDSFYRS--- 755
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 791 RYNNLTLDYVYIDPYMSIFEHIGHLISIEHAQSYNHFITDLNRKSTDYRRAARMK 850
OY 756 -----LDNDVYFTAPYFNKSGPAGESGIMSKAVE-IYIQKLLKPAVVGIKIDVNS 808
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 851 DTIMEDVSNNSKIYKSETQLTGYLGNENLIMLQAFKATY-----LDKAVLGV---S 900
OY 809 WLENPTKTSIRDPGAPVCCCKRNSDWDVCIILDDGFFLLMANHDYV-----NOT 859
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 901 GFE--FAYDHVVDYMAEH--GCPASDDRKCYLLDEHAHYVFFSNDNDISTYEDLYGKRI 957
OY 860 GRFGEIDPSLMRLVNISVYAFNKS-----DYQVSCERGAPKQAGHRSAYPSIA 913
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 958 SOYFGGLNRINQARM---ALLVENKFTYKLTLYTDNQAVCAEKAYTSSGNRLRPFTYIFR 1014
OY 914 DILHGMWATAAAMSIIQOFLLSLTFPRLLEAVEMEDDFTASLSKOS-----CTEOTY 969
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1015 FLMOFTFNFMVLAQISGGFLIMPLNIOFTEA-----YASPHETGTDVYPCPKQSSFY 1067
OY 970 FFDNDSKSFSGV--LDCN-----CSRIFHEKMLNPLILFIMV-ESGTCRPCD 1015
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1068 FSNKDGKRRPGTTHLVNKRSEPRCKMNKASVMEASFDVGNLVLVWWTITQDASENCY 1127
OY 1016 TRLILOAEQTSDDGPPDCDMVK-----OPRYKGPDVCF--DNNALEDYDTC 1059
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1128 DESCSMHTISNQVFPGRPEYVKNBEETCEBENKRRKADVCTSIDDDSENERRC 1182

```

RESULT 5



RP SEQUENCE OF 961-975; 992-1000 AND 1033-1050.  
 RX MEDLINE=9036835; PubMed=2168391;  
 RA de Jongh K.S., Warner C., Caterall W.A.;  
 RT "Subunits of purified calcium channels. Alpha 2 and delta are encoded  
 by the same gene."  
 RL J. Biol. Chem. 265:14738-14741(1990).  
 CC -1- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN  
 EXCITATION-CONTRACTION COUPLING.  
 CC -1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:  
 ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS  
 HETERODIMERS THAT ARE DISULFIDE-LINKED.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE  
 SPLICING.  
 CC -1- TISSUE SPECIFICITY: SKELETAL MUSCLE.  
 CC -1- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM  
 A PRECURSOR FORM.  
 CC -1- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.  
 CC -1- SIMILARITY: CONTAINS 1 WFPA DOMAIN.  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL: M21948; AAA91562.1;  
 DR PIR: S10579; CRRBA2;  
 DR Interpro: IPR004010; Cache.  
 DR Interpro: IPR002035; VWF\_A.  
 DR Pfam: PF00092; vwa: 1.  
 DR Pfam: PF02743; Cache: 1.  
 DR SMART: SM00327; vwa: 1.  
 DR PROSITE: PS0234; VWF\_A; 1.  
 DR Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;  
 KW Calcium channel; Glycoprotein; Phosphorylation; Signal;  
 KW Alternative splicing.  
 FT SIGNAL 1 26  
 FT CHAIN 27 960  
 FT CHAIN 961 1106  
 FT TRANSMEM 448 471  
 FT TRANSMEM 921 945  
 FT TRANSMEM 1082 1101  
 FT DOMAIN 255 432  
 FT CARBOHYD 94 94  
 FT CARBOHYD 138 138  
 FT CARBOHYD 186 186  
 FT CARBOHYD 326 326  
 FT CARBOHYD 350 350  
 FT CARBOHYD 477 477  
 FT CARBOHYD 606 606  
 FT CARBOHYD 615 615  
 FT CARBOHYD 678 678  
 FT CARBOHYD 784 784  
 FT CARBOHYD 827 827  
 FT CARBOHYD 891 891  
 FT CARBOHYD 898 898  
 FT CARBOHYD 988 988  
 FT CARBOHYD 1001 1001  
 FT MOD. RES 503 503  
 FT MOD. RES 848 848  
 FT SEQUENCE 1106 AA: 125042 MW: B00DE7F3C877B618 CRC64;  
 Query Match 96.5%; Score 5405.5; DB 1; Length 1106;  
 Best local Similarity 95.4%; Pred. No. 2,5e-314;  
 Matches 1035; Conservative 11; Mismatches 10; Indels 29; Gaps 4;

QY 59 DIYEKQDLYTEPPNAROLVETIARDIEKLNSNSKALVRLAEKVOAAHQRDEFA 118  
 DB 61 DIYEKQDLYTEPPNAROLVETIARDIEKLNSNSKALVRLAEKVOAAHQRDEFA 120  
 QY 119 SNEVYNNKDDDDPEKNSEPSORIKRPFIDDAFNGQISYQAAHHPIDIEGSI 178  
 DB 121 SNEVYNNKDDDDPEKNSEPSORIKRPFIDDAFNGQISYQAAHHPIDIEGSI 180  
 QY 179 VNELNMTSALDEVEFKNREEDPSLLMQVGSATGLARYPPASPMWDSRPNKIDLDV 238  
 DB 181 VNELNMTSALDEVEFKNREEDPSLLMQVGSATGLARYPPASPMWDSRPNKIDLDV 240  
 QY 239 RRRPWYIQGAAPKMDLLVVDVSGVSGTLKLTIRTSVSEMLETSDDDPVVASFNSA 298  
 DB 241 RRRPWYIQGAAPKMDLLVVDVSGVSGTLKLTIRTSVSEMLETSDDDPVVASFNSA 300  
 QY 299 QDVSCFOHLYOANVRNKKVLDKAVNNITKGTIDKGFSPFEOILNYSRACNKKI 358  
 DB 301 QDVSCFOHLYOANVRNKKVLDKAVNNITKGTIDKGFSPFEOILNYSRACNKKI 360  
 QY 359 MFTDGEERAOEIFAKYNNKDKRVFFSVGOHNYDGRPIOMMACENKGYEIPISGA 418  
 DB 361 MFTDGEERAOEIFAKYNNKDKRVFFSVGOHNYDGRPIOMMACENKGYEIPISGA 420  
 QY 419 IRIHQEYLDVIGRPVYLAGDAKOVNTNYLDLLEGLVITGTLVPVFNITGONENKTN 478  
 DB 421 IRIHQEYLDVIGRPVYLAGDAKOVNTNYLDLLEGLVITGTLVPVFNITGONENKTN 480  
 QY 479 LKNQILLGVAGVDSLEDEIKRLTPRTLCPNGYEAIIDPNGVILHPLMOCK----- 530  
 DB 481 LKNQILLGVAGVDSLEDEIKRLTPRTLCPNGYEAIIDPNGVILHPLMOCK----- 540  
 QY 531 -----NPKSQEPVTLDFDAELENDIKVEIRNKMIDEGSEKTFRTVKSODER 579  
 DB 541 INLKRKRPVQNPQKQEPVTLDFDAELENDIKVEIRNKMIDEGSEKTFRTVKSODER 600  
 QY 580 YIDKGNRTYTPVNVCTDY-SIALVLPYSTRYIAKIEFTTQARSKKMKKQSETLKP 638  
 DB 601 YIDKGNRTYTPVNVCTDY-SIALVLPYSTRYIAKIEFTTQARSKKMKKQSETLKP 653  
 QY 639 DNEESGTYFIAPRYCNDLKISDNTTEFLNENFDRKTPNNPSCNTDLINRVLLDAG 698  
 DB 654 DNEESGTYFIAPRYCNDLKISDNTTEFLNENFDRKTPNNPSCNTDLINRVLLDAG 713  
 QY 699 FTNELVQNTWSKQNKIKGVKARFVVTIDGITRVYPKEAGENMOENPETYEDSFYKRSIDN 758  
 DB 714 FTNELVQNTWSKQNKIKGVKARFVVTIDGITRVYPKEAGENMOENPETYEDSFYKRSIDN 773  
 QY 759 DNYVTAFYFNKSGGAEISGIMSKAVEIYIOGKLKPAVVGIRKIDVNSWIEFTYTSI 818  
 DB 774 DNYVTAFYFNKSGGAEISGIMSKAVEIYIOGKLKPAVVGIRKIDVNSWIEFTYTSI 833  
 QY 819 RDPGAPVDCCKRNSDAMDVCYILDDGGFLMAHHDDYVNOIGREFGELDSLMHNLNIS 878  
 DB 834 RDPGAPVDCCKRNSDAMDVCYILDDGGFLMAHHDDYVNOIGREFGELDSLMHNLNIS 893  
 QY 879 VYAFKSYDYOSVCEPGAAPKQAGHRSAYVSIADILHIGMATAAAMSILQOFLSLT 938  
 DB 894 VYAFKSYDYOSVCEPGAAPKQAGHRSAYVSIADILHIGMATAAAMSILQOFLSLT 953  
 QY 939 FPRILEAEMDDDDPTASMSKOSCTTEOTYFFPNDKSFSGVLDGCGNSIFHYEKLAM 998  
 DB 954 FPRILEAEMDDDDPTASMSKOSCTTEOTYFFPNDKSFSGVLDGCGNSIFHYEKLAM 1013  
 QY 999 TNLIFINVESKGTCPDTRILLIOAEQTSDDGDPDMDYKQPYRKGPPVPCDNNALDEYTD 1058  
 DB 1014 TNLIFINVESKGTCPDTRILLIOAEQTSDDGDPDMDYKQPYRKGPPVPCDNNALDEYTD 1073  
 QY 1059 CGGVS 1063  
 DB 1074 CGGVS 1078



Query Match	98.8%	Score 5532	DB 1	Length 1091
Best Local Similarity	98.7%	Pred. No. 0		
Matches 1049	Conservative	6	Mismatches	8
			Indels	0
			Caps	0

QY	1	MAAGCLLATLTLTFLFOSLLIGSPSSQGEFFPSAVYIKSNVDMKQEDLVTLAKTASGVNQLYDI	60
Db	1	MAAGCLLATLTLTFLFOSLLIGSPSSSEFFPSAVYIKSNVDMKQEDLVTLAKTASGVNQLYDI	60
QY	61	YERYQDLYTVEPNNAQOLVEIARADIEKLISNSRKALVRLALAEVQAQHOHREDFASN	120
Db	61	YERYQDLYTVEPNNAQOLVEIARADIEKLISNSRKALVRLALAEVQAQHOHREDFASN	120
QY	121	EYVYVYAKXDLDPEKNDSPSGSORIKPVYITDANFGROISYQAAVHIPTDIEGSTITVL	180
Db	121	EYVYVYAKXDLDPEKNDSPSGSORIKPVYITDANFGROISYQAAVHIPTDIEGSTITVL	180
QY	181	NELNMTSALDEVYKKNRREDPSLLMQVEGSATGLRYYASVWVONSRRPNKIDLYDPR	240
Db	181	NELNMTSALDEVYKKNRREDPSLLMQVEGSATGLRYYASVWVONSRRPNKIDLYDPR	240
QY	241	RPMVYIQGAASPRDMLLDVYSGVSGGLTLKLIRISVSEMLTETLSDDDPVYVNASFNSNQD	300
Db	241	RPMVYIQGAASPRDMLLDVYSGVSGGLTLKLIRISVSEMLTETLSDDDPVYVNASFNSNQD	300
QY	301	VSCFQHLVQANRNKVKYLKDAVNNITTAGITDYYKKGSFAPQOLLNVVSRANCKITML	360
Db	301	VSCFQHLVQANRNKVKYLKDAVNNITTAGITDYYKKGSFAPQOLLNVVSRANCKITML	360
QY	361	FTDGEERAAQETFAKYNKDKKRVFTFSVGQHNTRDGRPIOMMAGENKGYEIEIPISGAIR	420
Db	361	FTDGEERAAQETFAKYNKDKKRVFTFSVGQHNTRDGRPIOMMAGENKGYEIEIPISGAIR	420
QY	421	INTQGEYLVVLGSPVTLADDKAKQOVMYVYIDALELGLVITGTLPEVNIITGQENENKTNLAK	480
Db	421	INTQGEYLVVLGSPVTLADDKAKQOVMYVYIDALELGLVITGTLPEVNIITQGFENKTYLAK	480
QY	481	NOLILGVNGVDVSLIEDIKRLTPRFLCPNGYGFADIDPGYVYLHPNLQPKPKSOEPVTL	540
Db	481	NOLILGVNGVDVSLIEDIKRLTPRFLCPNGYGFADIDPGYVYLHPNLQPKPKSOEPVTL	540
QY	541	DLFLAELENDIKVFLRNKMDIGESGERTFRLVKSQDERITDKGNRTYTWTPVNGTDSL	600
Db	541	DLFLAELENDIKVFLRNKMDIGESGERTFRLVKSQDERITDKGNRTYTWTPVNGTDSL	600
QY	601	ALVLPYTSFYVYIKAKIETITQARSKKGKMDSFTLKPDPNEESGYFIFIAPRDVCNDLKI	660
Db	601	ALVLPYTSFYVYIKAKIETITQARSKKGKMDSFTLKPDPNEESGYFIFIAPRDVCNDLKI	660

RESULT 2	TD	STANDARD;	PRT; 1091 AA.
'CIC2_RAT			
AC	CIC2_RAT		
AC	PIG290;		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta subunits precursor.		
GN	CACNA2D1 OR CACNL2A OR CCHL2A.		
OS	Rattus norvegicus (Rat)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RR	[1]		
RP	SEQUENCE FROM N.A.		
RA	MEDLINE=92228762; PubMed=1314383;		
RA	Kim H.L., Kim H., Lee P., King R.G., Chin H.;		
RT	"Rat brain expresses an alternatively spliced form of the		
RT	dihydropyridine-sensitive L-type calcium channel alpha 2 subunit.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 89:3251-3255(1992).		
CC	-1- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN		
CC	EXCITATION-CONTRACTION COUPLING.		
CC	-1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:		
CC	ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS		
CC	HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE		
CC	SPlicing.		
CC	-1- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM		
CC	A PRECURSOR FORM (BY SIMILARITY).		
CC	-1- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.		
CC	-1- SIMILARITY: CONTAINS 1 WMPA DOMAIN.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).		
CC	-----		
CC	EMBL; M86621; AAA41088.1; -.		

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 10, 2003, 14:13:50 ; Search time 9.75229 Seconds  
(without alignments)  
4520.920 Million cell updates/sec

Title: US-10-090-827-8

Perfect score: 5602  
Sequence: 1 MAACGLALITLITLFOSLILG.....PDVCFDNNALDYTDGCVS 1063

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : SWISSPROT\_40:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5532	98.8	1091	CIC2_HUMAN	P54289 homo sapien
2	5420	96.8	1091	CIC2_RAT	P54290 rattus norv
3	5405.5	96.5	1106	CIC2_RABIT	P13806 oryctolagus
4	754	13.5	1205	YLJ9_CAEEL	P34372 caenorhabdi
5	611	10.9	734	UN36_CAEEL	P34374 caenorhabdi
6	196.5	3.5	886	ITR3_MOUSE	Q61704 mus musculi
7	185	3.3	885	ITR3_HUMAN	Q06033 homo sapien
8	183.5	3.3	887	ITR3_RAT	Q63416 rattus norv
9	168.5	3.0	575	YPRK_FCOLI	P76481 escherichia
10	166	3.0	886	ITR3_MESAU	P97480 mesocricetu
11	162	2.9	1829	DPOL_THEST	Q33845 thermococcu
12	160.5	2.9	420	YI03_SYNY3	Q55874 synechocyst
13	155.5	2.8	946	ITR2_HUMAN	P19823 homo sapien
14	155	2.8	1956	ATY1_PLAFA	Q04956 plasmodium
15	153	2.7	946	ITR2_MESAU	P97479 mesocricetu
16	149.5	2.7	654	MCPC_BACSU	P54576 bacillus su
17	149.5	2.7	921	ITR1_PIOTM	P79263 sus scrofa
18	147	2.6	1087	XYNX_CLOTM	P38535 clostridium
19	144.5	2.6	929	CALC_NOTVI	Q91145 notophthalm
20	144	2.6	930	ITR4_HUMAN	Q14624 h inter-ailp
21	143.5	2.6	935	ITR2_PIG	Q02668 sus scrofa
22	142	2.5	964	DPOL_CBEPV	P30319 choristoneu
23	142	2.5	3063	CALC_HUMAN	Q99119 homo sapien
24	141.5	2.5	946	ITR2_MOUSE	Q61703 mus musculi
25	141	2.5	1290	BXCI_CLOBO	P18640 clostridium
26	140.5	2.5	764	PAG_BACAN	P13423 bacillus an
27	140	2.5	1180	C4A8_BACCTI	P16480 bacillus th
28	138.5	2.5	382	YLJ0_CAEEL	P34373 caenorhabdi
29	137.5	2.5	862	MOTS_BORBU	Q51737 borrelia bu
30	137	2.4	3305	APLP_MANSE	Q25490 manduca sex
31	136	2.4	697	YE97_SCHPO	Q13773 schizosacch
32	134	2.4	1251	RBP2_PLAIVB	Q00799 plasmodium
33	133	2.4	1169	SMC_METUA	Q59037 methanococc

34	132	2.4	984	HYSA_STRAG	Q53591 streptococc
35	132	2.4	1875	MLP1_YEAST	Q02455 saccharomyc
36	131.5	2.3	1487	BLM_DROME	Q9vg18 drosophila
37	131.5	2.3	3712	IMA_DROME	Q00174 drosophila
38	131	2.3	1513	STU1_YEAST	P38198 saccharomyc
39	131	2.3	2710	TOXA_CLODI	P16154 clostridium
40	131	2.3	3119	CALC_MOUSE	Q60847 mus musculi
41	130.5	2.3	1323	ADRI_YEAST	P07248 saccharomyc
42	129.5	2.3	1254	UBPC_YEAST	P39538 saccharomyc
43	128.5	2.3	547	SYM_BUCAI	P57210 buchnera ap
44	128	2.3	1658	YME7_YEAST	Q03661 saccharomyc
45	127.5	2.3	1176	SLAP_BACSH	P38537 bacillus sp

## ALIGNMENTS

RESULT 1  
CIC2\_HUMAN STANDARD; PRT; 1091 AA.  
ID CIC2\_HUMAN  
AC P54289;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta  
DE subunits precursor.  
GN CACNA2D1 OR CACNA12A OR CCHL2A.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92110010; PubMed=1309651;  
RA Williams M.E., Feldman D.H., McCue A.F., Brenner R.,  
RA Velliclebi G., Ellis S.B., Harpold M.M.;  
RT "Structure and functional expression of alpha 1, alpha 2, and beta  
RT subunits of a novel human neuronal calcium channel subtype.";  
RL Neuron 8:71-84(1992).  
CC -1- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN  
CC EXCITATION-CONTRACTION COUPLING.  
CC -1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:  
CC ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS  
CC HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- TISSUE SPECIFICITY: CENTRAL NERVOUS SYSTEM, SKELETAL MUSCLE AND  
CC AORTA TISSUES.  
CC -1- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM  
CC A PRECURSOR FORM (BY SIMILARITY).  
CC -1- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.  
CC -1- SIMILARITY: CONTAINS 1 VMPA DOMAIN.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC -----  
CC EMBL: M76559; AAA51903.1;  
CC Genew: HGNC:1399; CACNA2D1.  
CC MIM: 114204;  
DR InterPro: IPR004010; Cache.  
DR InterPro: IPR002035; VWF\_A.  
DR Pfam: PF00092; VWA; 1.  
DR Pfam: PF02743; Cache; 1.  
DR SMART: SM00327; VWA; 1.  
DR PROSITE: PS50234; VMPA; 1.  
KW Ionic channel. Transmembrane. Ion transport. Voltage-gated channel.  
KW Calcium channel. Glycoprotein. Phosphorylation. Signal.  
FT SIGNAL 1 24  
FT CHAIN 25 944 L-TYPE CALCIUM CHANNEL ALPHA-2 SUBUNIT

```

Db 41 PLNLGLVLDHSGMDGPLETVKSAALGLIDLEDDDLVIAADHRAKIV-----IENQ 95
QY 311 NVNRKKVLKDAVNNITANGITDYKGFAPFOLLNVNVRANKNIIMLEPTDGEERAO 370
Db 96 QVRNGAALAKAIEERLAKAGTAIDELKLGIOEAKGEBDEV---HIFLITDGENEHD 152
QY 371 E-----IFAKYKKKVRVFTFSGOHNTRDGPDIOMACENKNG---YYEIDPSIGAIRINTQ 424
Db 153 NDRLCKLGTASDYKLTIVHTLGFSDH--WNOVDLEAIAASQGSLSYEINPS--EALHTFRQ 210
QY 425 EYLDVGRPVVLADKAKOYQWNTVYDALELG---LVITGLTPVNNITGONKNTNK 480
Db 211 LF-----QRRSNVGLTNAHL--LEELAPQAHAI--VKPAQVSPETMDLT-VQ 254
QY 481 NOLLIGVGVVSLIEDIKRLTPRETLCPNGYFAIDPNGYVLLHPNLQPKPKSQE-----536
Db 255 NQGAIEEVRGDDMTDERV-----LLNLNYLDQLLEPGHVGIVGOYRYPDASGQNTL 309
QY 537 ----PVLDFDALENDIVEIRNKMIDEGSEKT--FRTLVKSQDERIDKGNRTYTW 590
Db 310 SDPLPLITQ--VQYQYQSTVOVESITLTLAKYRQTOIAETKLKAGDRQGAATVMTAAK 368
QY 591 TPVNGIDYSLALVPTYSFYIRAKIETITQARSKKGGKKMDETLKP 638
Db 369 TALQMGDKNGATILQTNV---TRLQSGEDLSEGDRTKTRVSKTTLQ 413

RESULT 15
140884
cytoxin L - Clostridium sordellii
C:Species: Clostridium sordellii
C:Date: 16-Aug-1996 #sequence-revision 16-Aug-1996 #text-change 15-Oct-1999
R:Green, G.A.; Schue, V.; Montell, H.
Gene 161, 57-61, 1995
A:Title: Cloning and characterization of the cytoxin L-encoding gene of Clostridium sordellii
A:Reference number: 140884; MID:95369733; PMID:7642137
A:Accession: 140884
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2364 <RES>
A:Cross-references: EMBL:X82638; NID:91000694; PID:CA557959.1; PID:91000695
C:Superfamily: cpl repeat homology
C:Keywords: cytoxin

```

Query Match 2.9% Score 160.5; DB 2; Length 2364;  
 Best Local Similarity 18.0%; Pred. No. 0.68;  
 Matches 219; Conservative 142; Mismatches 346; Indels 513; Gaps 58;

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QY 6 LIALTLTLPQSLIGSSQEPFPAVTKSWDKMOEDLVTLAKTASGVNOLVD-----59
Db 1066 IMAVNLTAATAIV-----TSNALGIASGSIL--LVPLAGISAGIPSLVNNELLILQ 1114
QY 60 ----IYEQDLYVEPNANQV-----ETIARDIEKLKSNKALVRLALAE 105
Db 1115 DKATKVIDYFKHISLAETEGAFLLDKLIMPDDLVLEID--FNNSITLTKCEIMRA 1172
QY 106 KYOAAHOWRED---FASNEVYV-----YNA--KDDLDPER-----135
Db 1173 EGSGHTLDDIDHFFSSPSITYRKPMWLSYDVNLKKEKIDFSDMLVLPNAPNRVGY 1232
QY 136 ----NDSEPGSORIKP-----VFIDANFGR-QISYOHAAVHIPTD 171
Db 1233 EMGWTPGRFSLNDSTKILDRIRHIEGQFYWRYPAFADALITLTKRKYEDTIVRIMD 1292
QY 172 IYEGSTIVLNNMTSALDEYFKKREDPSILMOVFSATGLARYYPASPVVNSRTPN 231
Db 1293 GNTKRSFYV-----PVITTEQIRKN-----LSYSFYS--GGSYSLSISPMNM-----1333
QY 232 KIDLVDVRRRPVYIOGAASPKDMLILVDVSGVSGTLKLRISVSEMLLETLSDDDPVNV 291
Db 1334 -IDLNLVENDTM-----VIDVNVVKNITTESDEIOKGELIENI-----1371

```

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QY 292 ASFNSNAQDVSCQHLYQAVNRKKVYLKDAVNNITAK---GITDYKGFAPFOLLNVN 348
Db 1372 ----LSKLIIEEDNKIT---LNNHTINPYGDINESNRFSLFSLIEDIN 1413
QY 349 ----VSRA-----MCKRIMLETD-----GGEERAOEIFA-----KYN- 377
Db 1414 IIEIDVSKSYKILLSGNCKMIENSDDIOCKIDHIGNGEHOKTIPSYIDNETKNG 1473
QY 378 ---KDKKRVFTFSGOHNTRDGPDIOMACENKNGYEEIPSGAIRINTQEYLDVGRPM 434
Db 1474 FIDYSKKEGLFAEFSNESIIRN--IYMPDSNNLFTYSSKDLKDIRIINK-----GVK 1525
QY 435 VLAGDKAQ-----VQWNTVYDALELGIVITGTLPEVNNITGONKNTNL 479
Db 1526 LLIGNFKDKMAKVSLSFTIEDNTIKLNGVILDE-----NGVAOILKFNNAKSAINT 1578
QY 480 KNOILLGVGVVSLIEDIKRLTPRETLCPNGYFAIDPNGYVLLHPNLQPKPKSQEPT 539
Db 1579 SNLMMFLSINIK-----NIFYNNLDPRNIEFILDTNF-----1611
QY 540 LDFLALENDIKVETRNKMIDEGSEKTFRPLVKSQDERIDKGNRTYTWTPVNGTDYS 599
Db 1612 ----IISGNSISQFE-LIDCKDN-----1631
QY 600 LALVLPYTSFYIRAKIETITQARSKKGGKKMDETLKPDNEESGYTFIAPROYCDNLK 659
Db 1632 ---IQP--FYINKIKET-----STLVGNKQN--LIVBSYHLDD--1666
QY 660 ISDNNTEFLNFE---FIDR--KTPNNSCNTDLIN-----RYLLDAGF 699
Db 1667 -SGNISSTVINSQKLYGLIDRYVKNVILAPLYTDEINIPYKPNICEVEIILDANY 1725
QY 700 TNE-----LVQNYW-----SKQNIKGVKARFVVTGCTIRVYPKEAGE 738
Db 1726 INEKTANNINDISTYVWDNGSDIILIANSEEDNQPVKIRFV-----NVEKSTAA 1778
QY 739 ----NMOENDE-----TYEDSFYKR-----SLDNNYVETAFENKSGPGA 775
Db 1779 DKLSFNSDKQDVSVKLIITFSLAAYSDFDEYFGLVSLDND-----FYIINSFGN 1831
QY 776 YESGIMSKAVEIYIQKL--LKP---AVVGI-KIDVNSIENFTKTSIRDPGAGPYCD 828
Db 1832 MVSGL-----IYINDSLYFKPKPKNNLITGFTTIDGNKYFDPKSG-----AASI--1877
QY 829 CKRNSDVMDCVILDDGGFLMANHDDYTN-----QIG-----RFF--GEIDPSLMR 872
Db 1878 ----GEITIDGKDYTFNKGILQVGVINTSDGLKYFAPAGTLDENLEG 1921
QY 873 HLVIN-----SVYAFNKSVDYQSVCEPGCAAPKQAGHRSAYVPSIADILHIGMWATA 924
Db 1922 ESNVFTGKLNIDGRIYFEDNY-----RAA 1946
QY 925 AAMSILQGFLLSTFFRPLEAVEMEDDFTASLSKQSCITEQIOYFENDSKSFSFGVLD 984
Db 1947 VEMKLD-----DETYFNPKTGEALKGHQT 1973
QY 985 GNCGRIFHVEKLMNTNLIPI 1004
Db 1974 GDNKYFFDDNGIMQTFIT 1993

```

Search completed: February 10, 2003, 14:22:02  
 Job time : 29.2324 secs

## RESULT 12

JC5576

Inter-alpha-trypsin inhibitor heavy chain 3 - golden hamster

C:Species: Mesocricetus auratus (golden hamster)

C:Date: 23-Sep-1997 #sequence\_revision 23-Sep-1997 #text\_change 17-Mar-1999

C:Accession: J05576; PC4486

R:Nakatani, T.; Suzuki, Y.; Yamamoto, T.; Sinochara, H.

J. Biochem. 122, 71-82, 1997

A:Title: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precursors

in inhibitor heavy chain family. C5574; M01D:97420688; PMID:9276673

A:Reference number: JC5576

A:Accession: JC5576

A:Molecule type: mRNA

A:Cross-references: DDBJ:D89287

A:Experimental source: liver

A:Accession: PC4486

A:Molecule type: protein

A:Residues: 34-53;449-475;509-526 &lt;NA2&gt;

C:Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3 were

that the complexes play important role for pancreatic cancer.

C:Superfamily: inter-alpha-trypsin inhibitor complex component II

F:236-239,664-865/Disulfide bonds: #status predicted

Query Match 3.0%; Score 166; DB 2; Length 889;

Best Local Similarity 23.2%; Pred. No. 0.068;

Matches 66; Conservative 57; Mismatches 111; Indels 51; Gaps 11;

QY 202 SLIMVFGATGLARYPPSPWVDSRT-PNKID-----LDVRRR-FWYIGA-- 248

Db 211 SALTFSFGKGVSEKPS--LDQORSCPTDLSLNGDFTIYDVNESPQVQVNG 267

QY 249 -----ASPKDMLVDSVSGSLTLKLRISVSEMLETLSDDDVFNVSFNS 296

Db 268 YFHFAPAGLPVPKPNIVYIDISSMAGRKIQOTRVALKLTIDMKDDYINLFEST 327

QY 297 NADVSCFOHLVQANVRNKKVLDVANNITAKGIDYKGFSPFQOLN----YVNSRA 352

Db 328 GV--TWKDSLVQATPANLEARTFVRSISDQMTNINGLGIMLTDARQHTVPER 385

QY 353 NCKKIIMLPDGC-----GERAOFIFAKYNDKKVRFVFTSVG-QHNYDGPLOMWCENK 407

Db 386 STSIITML-TDGDANTGESPEKIQENVRKALIGRPPLYNLGNLNTNLETALLENH 444

QY 408 GYVEIPISGIRINTQEVLDVGRPMVLGDKAKQVMTNVL 452

Db 445 GVARRIYEDSANLQLOGFVEYVANPLL-----TNVEVE 478

## RESULT 13

F64688

protease (BC 3.4.-.-) - Helicobacter pylori (strain 26695)

C:Species: Helicobacter pylori

C:Date: 09-Aug-1997 #sequence\_revision 15-Aug-1997 #text\_change 29-Sep-1999

C:Accession: F64688

R:Tombl, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Frieschmann, R.D.

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodok, A.; McKen-

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.

Nature 388, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karik, P.D.; Smith, H.O.; Fraser, C.

A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A:Reference number: A64520; M01D:97394467; PMID:9252185

A:Accession: F64688

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-459 &lt;TOM&gt;

A:Cross-references: GB:AE000636; GB:AE000511; NID:g2314517; PIDN:AD08394.1; PID:g231452

C:Genetics:

A:Start codon: GTG

C:Superfamily: carboxyl-terminal processing proteinase

C:Keywords: hydrolase

Query Match 2.9%; Score 165; DB 2; Length 459;

Best Local Similarity 22.2%; Pred. No. 0.027;

Matches 138; Conservative 69; Mismatches 198; Indels 216; Gaps 30;

QY 6 LLATLTLFLOSLIGSPSPFPSPATIKSMVNMQEDLTTLKTASGV-----NOLY 58

Db 3 LLITKRLFKLLAVSLAVSLHGEVEKRPVPRVKKDPOLA--AKRVAFSRFSNVYS 60

QY 59 DYERKODLYTVEPNMAROLVEIARDIEKLSNRKALVLLAEKVAOHOMREDA 118

Db 61 EIEKKYVDKISIS-----EIMTKALEGLLSMLD-----AHS----- 91

QY 119 SNEVYYNAKDDLPEDKNDSPGSRKIPFIDANGROISYQAHVHIPTDIESTI 178

Db 92 ----AYLN-----EKFKK-----FOAQTEGFGGLITGVKRGCVLT 125

QY 179 VLNELNMTSAL-----DEYFKRREDDPSILMQVGSATGLARYPPSPWVDSRTNP 231

Db 126 VIALEGPATKAGVKSQDNLKINNE-----STLSMSIDDAINLRGKPKTP----- 173

QY 232 KIDLYVRRRPWYIQAASPKDML--ILVDVSGSVGLTLKLRISVSEMLETLSDDDFV 289

Db 174 -IQITVVRKN-----EPKPLVFNIIRDI-----IKLPSVYVKIKIKET--PYLYV 214

QY 290 NVASFNSNAQDVSCFOHLVQANVRNKKVLDVANNITAKGIDYKGFSPF----- 341

Db 215 RVSGDKKVTK-SVLEGL-KANPRAKGLVDLRGN--PGGLNQAVGLSNLFKEGYLV 270

QY 342 -----POLNLYNVRAN-----CNKIIIMLPTDGEERAOEIFAKYNDKKVRFVFTSVG 390

Db 271 QKGRKKEENLEY--KANGRAPYTNLPYLVNNGSASASTVAGLQDHKRAVY--IG 324

QY 391 QHNTRDGPLOMWCENKGYEIPISGIRINTQEVLDVGRPMVLGDKAKQVMTN 450

Db 325 ETEFGKGVOMLDPVKNK-----EAKIKITARYYLPSSGR-----TIQAGIT 366

QY 451 IDALELGLVITGTLPEVNTGONENKTNLKNQGLIGVGVDSLEDIKRLRPFTLCPNG 510

Db 367 PDI--VIYGRKVP-----ENKKEFKLE-----ADLKH----- 392

QY 511 YFFAIDPNGVYLH-----PNIQPKRKSQBPVTLDFLAELNDIKVEIRNKMIDE-- 563

Db 393 -----HLEQELKKIDKTPNSKE-----ADKDKNEEKEIYPPKMIINDIQ 433

QY 564 -----SGEKFTPLVKSODER 579

Db 434 IKTALDSLKTSVDEKMDK 454

## RESULT 14

S76691

hypothetical protein - Synechocystis sp. (strain PCC 6803)

C:Species: Synechocystis sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 08-Oct-1999

C:Accession: S76691

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,

O.K.; Okumura, S.; Shimizu, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yea

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys

S.

A:Reference number: S74322; M01D:97061201; PMID:8905231

A:Accession: S76691

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-420 &lt;KAN&gt;

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Genetics:

Query Match 2.9%; Score 160.5; DB 2; Length 420;

Best Local Similarity 21.1%; Pred. No. 0.044;

Matches 86; Conservative 86; Mismatches 181; Indels 55; Gaps 16;

QY 251 PKDMLIVDVSSVSGTLKLRISVSEMLETLSDDDFVNVSFNSNAQDVSCFOHLVQA 310

A:Reference number: A96900; MUID:21359325; PMID:21359325  
 A:Accession: D97033  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1819 <KUR>  
 A:Cross-references: GB:AE001437; PIDN:AAK79055.1; PID:g15023996; GSPDB:GN00168  
 A:Experimental source: Clostridium acetobutylicum ATCC824  
 C:Genetics:  
 A:Gene: CAC1081

Query Match 3.0%; Score 170.5; DB 2; Length 1819;  
 Best Local Similarity 18.8%; Pred. No. 0.11;  
 Matches 194; Conservative 153; Mismatches 334; Indels 351; Gaps 53;

```

QY 24 QEPSPSVITKSVNKKQEDL-VTLAKTASGVNQLVD-----IYEKYODLYTVEPNNA 75
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 133 EQQIKNARTSKG-ADLTKDEIGTTIANTSDIKGIFDRMTKGTAVVSDYQFLITQVNSN 191
QY 76 RLVEIARDEIKLSRSKALV-----RLALEKVOAAHOMREDFASNEVYVYNA 127
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 192 N-----LQDINSMLTGRYALISKILSTVDKITTAVSNINNDHESDFTALQI--YNY 243
QY 128 KDLDEPEKND-----SEPGSORIKPFVFD-----DA-----NFGF-OISYOH-A 164
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 244 QEDLVPLNENISAANKKSGDSLSSSEINIVAKDSLSKLDALERINLGGCTIDYHFTG 303
QY 165 AVHIIPDIYGSTIYVNLMTWISALDEVEKKNR--EDPSLLMQV--FGSATGLARYPA 220
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 304 AAVVDENNEEDVANGMANGKW-----FERNNAIEINSIYVPLSRINSGBSTADYDA 356
QY 221 --SPWVDSKTPN-----KIDLYVRRRPWTQCA 248
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 357 IQVDGVDNNDIKSVIAEKKOLKGNLNIIEIKSAVEEYKTVLDFYLIRK-----GT 411
QY 249 ASKRD--MLLDVVS--GSVSGD-----TLKLRTSVSEMLETSLD-----DD 287
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 412 AKVSDYNAIGLGVEDNTDMNELLKNDIKTLKQININSIISKLNINAGTDPD 471
QY 288 FNVVAFSNSAODVSCF-----QHLVQAVNR--NKKVLDVANNITAK----- 328
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 472 YTHL-NISSYTDNISFTIDDIKTAKQANGSGLNKGIKIDSVNSLSKLSAMDRIINAGSA 530
QY 329 GITDYK---KGFSAFEOLUNYVNSRANCKIIMLFTGGEGEROELPAKYNK----- 378
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 531 ALDDYVLGLIEGTSNDLTFVNNQVKGSKCTIDELKTVSD--ALKLDSINKVNGDA 588
QY 379 --DKKRV--FTSVQGHNTDRPIOMACENKGY--YEIPISG--AIRIN----- 422
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 589 TYDDYIKIGIVIKIEVYYNG-----VFKGKNYFLEELKVGIMIAVVRISTENIKNG 643
QY 423 -----TOEYLDVLRPVLADGKAKOV-----QNTNYL 451
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 644 VGSVEDFTAGTGYTEENIKIKINKYIIEGGDASPEAISNITTEVNVETIOSLKRSSQV 703
QY 452 ---DALEGLVITGTLPVFNITGN-----ENKTLNKLQNLIGVAGVDSLEDIR 499
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 704 TAEDVKSIGLST-----VTEENISYIMDRVKNYYSKELLEVAIIKEEYIER 755
QY 500 LPPFRLTPNGYFAI-----DPNGYVLHPNLOPKNPKSOEPTLDFLDALEND 550
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 756 IMCGATYADYEIKVGTGVSNTSINDYV-----KSGNLTTRBELAKI--D 802
QY 551 IKVE-----IRNKMIDGESGEKTFR-----TLVKSODERYIDKNRITWTVPVGT 596
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 803 VIEIGTQSAHADVIGRVNIGEANISDFEFGITIVVNSFIQYVDHLKDKDKTTIDAI 862
QY 597 DYSLALVLPYTSFYITAKIETITQANSKKGKMKDSETLKPDNFEEGYTFIAPROYCN 656
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 863 KAAYVFEVGOYSIY-----EELN-----KGTATL-----DIYN 890
QY 657 DKLISDNTEFLNNEFIDRKTPNPNPCNTDLNRYVLLDAGFTNELVONWMSOKINKG 716
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 891 SLGIGVTTENTITYINLNKISSYFNAS--DIOTKY-----NALISVGYEEINKG 940

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QY 717 VKARFVVTDOGITRYVPKKEAGENMOENPETYEDSFYKRSNDNDNYFTAPYFNKSGPGAY 776
DB 941 EATVDVYTSIGITGV-----TKENIIFINTYIKE--GQY 972
QY 777 ESGIMVSKAVEI-----YIO---GKLKPAVVGKIDVNSMINFTTSIRDCACPV 826
DB 973 FDLTSLKSSVEVLEEKYEAVKITSCK--AVVG-----DYTKVGIKDYEENI 1018
QY 827 CDCKRNSDVMDC 838
DB 1019 AVYINLMDLQNC 1030

```

## RESULT 11

Hypothetical protein b2270 - Escherichia coli (strain K-12)  
 C:Species: Escherichia coli  
 C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002  
 C:Accession: D64998  
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;  
 A.: Rose, D.J.; Mau, B.; Shao, Y.  
 A:Title: The complete genome sequence of Escherichia coli K-12.  
 A:Reference number: A64720; MUID:97426617; PMID:9278503  
 A:Accession: D64998  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-575 <BLAT>  
 A:Cross-references: GB:AE000317; GB:U00096; NID:g1788605; PIDN:AAK75330.1; PID:g17886  
 A:Experimental source: strain K-12, substrain M61655

Query Match 3.0%; Score 168.5; DB 2; Length 575;  
 Best Local Similarity 21.6%; Pred. No. 0.024;  
 Matches 111; Conservative 94; Mismatches 205; Indels 105; Gaps 24;

```

QY 71 PENNARQLVEIARDEIKLSNRSKALVRLALEKVOAAHOMREDFASNEVYVYNAKDD 130
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 22 QPENKSGQQQPSPTTEGQVLAQQAIAK--EADQSA--AKALAQDEVQYISDKQA 75
QY 131 LDPEKND-----SEPGSORIKPFVITDANEGRQISYHAA--VHIPTDI 172
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 76 LQRIQEPPTARAARAKAKATHIANGTARVQOF--DDNPVKQVQAQPLATFSLDVTGS 132
QY 173 YEGSTIVNE-----LNTSALDEVEKKNREDEPSLLMQVGSATGLARY 218
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 133 YANVRRELNGQLLPPDAVRYEELVYVFPSPWDI--KDKOSTPASKRPIPPAMRYELA-- 187
QY 219 PASTPVDNSKTPNKKIDLYVRRRPWYIQGAASPKDMLLVDSGS--VSGTLKLRTSVS 277
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 188 PA-PW-NEORFLKYVDILAKRKSEELPAS--NLVFLIDTSGSMISDERLPLIQSSLK 241
QY 278 EMLFTLSDDEPVNVAASNSNAODVSCFQHLVQAVNRKKVYLKDAVNNITAKGITDYKGF 337
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 242 LVLVELKQDNIATVYTAGSRIA-----LPSISGSKRAINAISLIDEGSTNGAGL 296
QY 338 SFAEOLINYNVSRANCKIIMLFTDG-----GEERAQEIFKYNKDKVRVFTSVQ 391
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 297 ELAYQAQTK--GFIKGGINR--ILATDGDENVGIDDPKRSISMKRKORESVTLSTGVGN 354
QY 392 HNHYRGPIOMACENKGYEIPISGAIIRNTQEDYLDVLRPVL--AGDKAKOV----- 445
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 355 SNNEAMAVRIADVGNNSYSIDTLS---EAQKVLNSEKRMQLITVAKOVKQAIFENNA 410
QY 446 WTNYVIDALEGLVITGTLPVFNITGNENKTLNKLQNLIGVAGV--VSLEDI--KRLT 501
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 411 WYREY---RQIGF-----KQRLREHFNNDNVADIGACKHIT 447
QY 502 PFTLCPNGYFAIDPNGYVLHPNLOPKNPKSOE 536
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 448 LLEFELTNGOKASIDKLRYA--PDNKLAKSKDKTKE 480

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Oy 796 KPAVVGKIDVNSMIEKTKSTINDPCAG 824  
 Db 1016 NQAVPPIQLLEVYDKIDDDT-----SPLAG 1039

## RESULT 9

Inter-alpha-trypsin inhibitor heavy chain 3 precursor - human  
 N:Alternate names: HC3; Inter-alpha-trypsin inhibitor chain H3; pre-alpha-inhibitor heavy chain H3  
 C:Species: Homo sapiens (man)  
 C:Date: 03-May-1994 #sequence-revision 20-Feb-1995 #text-change 04-Feb-2000  
 C:Accession: S30350; S34123; S02141; D34245; A39079; S50133; B53642; A59167  
 R:Bourguignon, J.; Diarra-Mehrpour, M.; Thiberville, L.; Bost, F.; Sesbouee, R.; Martin, Eur. J. Biochem. 212, 771-776, 1993  
 A:Title: Human pre-alpha-trypsin inhibitor precursor heavy chain cDNA and deduced amino acid sequence  
 A:Reference number: S30350; MUID:93215656; PMID:7681778  
 A:Accession: S30350  
 A:Molecule type: mRNA  
 A:Residues: 1-885 <BOU1>  
 A:Cross-references: EMBL:X67055; NID:9288562  
 R:Bourguignon, J.  
 Submitted to the EMBL Data Library, June 1992  
 A:Reference number: S34123  
 A:Accession: S34123  
 A:Molecule type: mRNA  
 A:Residues: 1-310, 'K', 312-343, 'R', 345-885 <BOU2>  
 A:Cross-references: EMBL:X67055; NID:9288562; PDB:CAA47439.1; PID:9288563  
 R:Diarra-Mehrpour, M.; Bourguignon, J.; Sesbouee, R.; Mattei, M.G.; Passage, E.; Saller, Eur. J. Biochem. 179, 147-154, 1989  
 A:Title: Human plasma inter-alpha-trypsin inhibitor is encoded by four genes on three chromosomes  
 A:Reference number: S02141; MUID:89137072; PMID:2465147  
 A:Accession: S02141  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 341-356, 'G', 358-845, 'H', 847-885 <DIA1>  
 A:Cross-references: EMBL:X14690; NID:935464; PDB:CAA32821.1; PID:935465  
 R:Englind, J.J.; Thøgersen, I.B.; Plazzo, S.V.; Salvesen, G.  
 J. Biol. Chem. 264, 15975-15981, 1989  
 A:Title: Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-alpha-trypsin inhibitor  
 A:Reference number: A92736; MUID:89380192; PMID:2476436  
 A:Accession: D34245  
 A:Molecule type: protein  
 A:Residues: 30-49 <ENG1>  
 R:Englind, J.J.; Salvesen, G.; Hefta, S.A.; Thøgersen, I.B.; Rutherford, S.; Plazzo, S.V.  
 J. Biol. Chem. 266, 747-751, 1991  
 A:Title: Chondroitin 4-sulfate covalently cross-links the chains of the human blood protein inter-alpha-trypsin inhibitor  
 A:Reference number: A39079; MUID:91093267; PMID:1898736  
 A:Accession: A39079  
 A:Molecule type: protein  
 A:Residues: 631-647 <ENG2>  
 R:Diarra-Mehrpour, M.; Bourguignon, J.; Sarafan, N.; Bost, F.; Sesbouee, R.; Muschio-Bot Biochim. Biophys. Acta 1219, 551-554, 1994  
 A:Title: Tandem orientation of the inter-alpha-trypsin inhibitor heavy chain H1 and H3 genes  
 A:Reference number: S50132; MUID:95002176; PMID:7522574  
 A:Accession: S50133  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-27 <DIA2>  
 A:Cross-references: EMBL:X75318  
 R:Wislowski, H.G.; Burgess, M.H.; Oppenheim, J.D.; Vilcek, J.  
 Biochemistry 33, 7423-7429, 1994  
 A:Title: TSG-6, an arthritis-associated hyaluronan binding protein, forms a stable complex with inter-alpha-trypsin inhibitor  
 A:Reference number: A53642; MUID:94271799; PMID:7516184  
 A:Accession: B53642  
 A:Molecule type: protein  
 A:Residues: 30-34, 'X' <WIS>  
 R:Jessen, T.E.; Faarvang, K.L.; Ploug, M.  
 FEBS Lett. 230, 195-200, 1988  
 A:Title: Carbohydrate as covalent crosslink in human inter-alpha-trypsin inhibitor: a novel crosslink  
 A:Reference number: S02431; MUID:88167187; PMID:2450785  
 A:Accession: A59167  
 A:Molecule type: protein  
 A:Residues: 30-32, 'GEKROAVDT' <JES>

C:Comment: As pre-alpha-inhibitor, this protein is covalently cross-linked by chondroitin C:Genetics:  
 A:Gene: GDB:ITIH3  
 A:Cross-references: GDB:120109; OMIM:146650  
 A:Map position: 3p13-3p12  
 C:Superfamily: Inter-alpha-trypsin inhibitor complex component II  
 C:Keywords: chondroitin sulfate proteoglycan; glycoprotein; heterodimer; proteinase I  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-29/Domain: propeptide #status predicted <PRO>  
 F:30-647/Product: inter-alpha-trypsin inhibitor heavy chain 3 #status experimental <M>  
 F:648-885/Domain: carboxyl-terminal propeptide #status predicted <CPT>  
 F:87,576/Binding site: carboxylate (Asn) (covalent) #status predicted  
 F:647/Modified site: chondroitin sulfate ester carboxyl end (Asp) (in mature form) #s

Query Match 3.4% Score 188; DB 2; Length 885;  
 Best Local Similarity 21.5% Pred. No. 0.0032;  
 Matches 138; Conservative 112; Mismatches 243; Indels 150; Gaps 36;

Oy 45 VTLAKTAGVNOVLVDYKDYQDYLYVEPNARQVETIARDIEKLISNSKALVRLALDA 104  
 Db 77 VELPKTAFITNFLETL-----DGVTV-PCNVKE-KEVAKQYKAVSOGKTAGL----- 123  
 Oy 105 EKVOAAGQWEDF-----ASNEVYVYNAKDDLPEDKNSRSGRIKPFVIDANPGR 157  
 Db 124 --VNASGRKLEKFTVSVNVAAGSKVTFELTYEELKRHKGYMTYKQV-----K 172  
 Oy 158 QISYQAAVHLPDIYEGSTIVLELNMVTSALDVEFKNEEDPSILMOYFSA-----T 212  
 Db 173 QL-VKHEIEIV--DIFEPQI-----SMLD-----AASFTINDLLGSLATKFSFS 214  
 Oy 213 GLARYPASPVWDSRF-PNKID-----LYDARRP-----WT-----QG- 247  
 Db 215 GKKGVSFKFSILDQRCSPCTDSILNGDEFTIYDVNRSPGNVOIVNGVFHFPAPQGL 274  
 Oy 248 AASPDKMLIVDVSGVSGLTILKLRFSVEMLETTSDDDFVNVASPSNAQVSGF-QH 306  
 Db 275 PVYKRNVAFYDIDSGMAGRLEPQTKALRILEDMDQEDYLNITLFSG--DYSTWKEH 331  
 Oy 307 LVQANVRKVKLVKDAVNNITAKGITYDKKGFSAEQLNVNSR-----ANCKMILM 360  
 Db 332 LVQATPENVLQAKTFKFSVMEKDKGWTINDGLRIGISM--NKAKEHRIRPERSTVISIM 388  
 Oy 361 FTDG-----GERRADIFAKYK--DKYRVTFESVGHNDYDRGIDOMACENKGYEIP 414  
 Db 389 LTDDGANVGESEPRKIDENVRNATIGKFPVNLGFG--NNLNVNLENNALNENGFARIT 447  
 Oy 415 SIGAIRITQGYLDVLAGPVLADKAKQVQWTVNYDALE-----LGIYITGLP 465  
 Db 448 EDSADLDLQGFYEVANPL-LTGVEMEYFE--NAIDLQNTQYHFDGSEIYVAGRLV 504  
 Oy 466 VENTIGQENKTNLK-----NQLLGWGVDSLEIDIKLRPTLCPNGYFPAIDPN-- 518  
 Db 505 DEDM--NSFADVYGHGATNDL--FTTEVDKEMEK-----ALDERDITF--NYI 550  
 Oy 519 ----GYVLLHNTLQPK--NPKSOEPTVLDPLDALENDIVKEIRNMKIDSEGEKFTFT 571  
 Db 551 ERLMAVLTIEOLLERKNAHGEKKNLTARALDLSLKHFTVPLTSMVYKPE----- 603  
 Oy 572 LVKSODERYI-DKGNRTYTWTPVN-GTDYSIALVLPYFSFYI 612  
 Db 604 --DNEDERAIADKPEDAEATPVSPAMSYLTSYQPPQRYTV 644  
 RESULT 10  
 D97033  
 uncharacterized protein, probably surface-located [Imported] - Clostridium acetobutylicum  
 C:Species: Clostridium acetobutylicum  
 C:Date: 14-Sep-2001 #sequence-revision 14-Sep-2001 #text-change 14-Sep-2001  
 C:Accession: D97033  
 R:Noelling, J.; Breton, G.; Ometchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L.  
 J. Bacteriol. 183, 4823-4838, 2001  
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium



Db 174 QL-VRH--FEIDAHIFEPQGI-----SMLD-----AEASFITNDLGSALTKSFS 215  
 QY 213 GLAIVYASPMVDNSRT-PMKID-----LYDVRRP-----WYI-----QG- 247  
 Db 216 GKKHVSFKPSLDQASCPCCTDLSLNGDFTIYDVVRESPPNVQIYNGCYFHFAPQGL 275  
 QY 248 AASPKDLILVDVSGSYGLTKLIRTSVSEMLETSDDOFVAVAFNSNAOVSCPO-H 306  
 Db 276 PVPKNIYEFIVDVSIGSGSKRIQOTREALKLITLDYKEDYLNFIEST--DVTWKDH 332  
 QY 307 LVQAVNKKVLDVAVNITAKGITDYKGFSAFEOLLNYSRAN-----CNKTIIM 360  
 Db 333 LVQATPAALKEAKTFVKNIHQSMTNINDGLKIGIML--NKARDHYPERKSTSIITM 389  
 QY 361 FTGG-----GEERAOEIFAKNK--DKKAVYFTSVGOHNTDRGPIDMACENKGYEYEP 414  
 Db 390 LITGDANTGSRPEKIQEYVNRNAGKGFPLYNIGFG--NMLNMYFLETLLENHGLARIRY 448  
 QY 415 SIGAIRINDEYDVLGRPVVLADGKAKQVOMTNYVLDALGLVITGTLPPVNTIGOMF 474  
 Db 449 EDDANLQLOGFVEYVANPL-----TNVEYEPENA-----ITDLTRNSY 489  
 QY 475 NKTNLKNOLLGVGVDSLEDIKRLTPRTLCPPNGYFAIDPNGYVLLHPNLQPKPKS 534  
 Db 490 PHFYDSEIYVAGRLVDRMNDN-----FKADYKCHGALN-----DLTF 527  
 QY 535 QEPVTLDFDALENDIKYKIRKMDGESGEK--TFRLVKSODERYIDKGNRYTTWTP 592  
 Db 528 TEVEVMEEDALK-----EOGYTEGDIYERLMAVYLIEQLERKKNKAKDDEKENIT- 579  
 QY 593 VNGTDVSLA--LVLPYSEYIYAKIEFTITQARSKKGMKQSEI-----LKPDNFEESG 645  
 Db 580 AEALDLSLHYFTPLTSNVVYTKPEDENOGTSLADNAGEAEAFETITMFLTTQSSOSP 639  
 QY 646 YFTIAPRDYCNLDKISDNTEFLNFEFIDKRTPNPSCNTDLINRYLLDAGFTNELVO 705  
 Db 640 YYYV-----DGGPHFIQI-----PGKNDISCFENIDKPGVLRILIQ 676  
 QY 706 NWSKQKNIKGVKARFVYVDGKITRYPRKEAGENNOENETEDSFYKSLDNDNYVTA 765  
 Db 677 D-----PVT--GIT-VTGOIID-----KKS--MASSRTGK 702  
 QY 766 PYFNSGPGAYESGIMVSKAVEIYQKLLKPAVVGIKIDVNSMIENFTKTSIRPOCAP 825  
 Db 703 TYFGKLGITNAMDFRVEVTEKILIG-----TGAELSTSWLDYTYVO-----TGL 750  
 QY 826 VQDCKRNSVYMCVILIDG-GFLMAN-----HDDYTNQIGRFGEIDPSLMRHLVN 876  
 Db 751 SVTINKKKMMV--VSFGDISIFVILHGWKKHPVHODFLG-----FYVDSHRMSAQTH 803  
 QY 877 ISVYAFNKSYDQSY-CEPGANP 898  
 Db 804 GLLGQFQFQFDFKVFGRGSDP 826

## RESULT 8

C68880

hypothetical protein yycC [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C.Species: Lactococcus lactis subsp. lactis

C.Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001

C.Accession: C68880

R.Biotin, A.; Winker, P.; Manger, S.; Jallion, O.; Malarne, K.; Weissenbach, J.; Ehrlich

A.Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss

A.Reference number: A86625; MUID:21235186; PMID:11337471

A.Accession: C68880

A.Status: Preliminary

A.Molecule type: DNA

A.Residues: 1-1450 <STO>

A.Cross-references: GB:AE005176; PID:912725093; PIDN:AAK06141.1; GSPDB:GN00146

C.Genetics:

A:Gene: yycC

Query Match 3.4%; Score 190.5; DB 2; Length 1450;  
 Best Local Similarity 19.4%; Pred. No. 0.005;  
 Matches 203; Conservative 148; Mismatches 339; Indels 339; Gaps 51;  
 QY 37 YKMOEDVLTAKTASGVNOLVDIYKYODLYTEBPNNAROLVELAARDIER-----L 89  
 Db 69 IKTEENDKELKLFSPGNOPIEIE--NESWTLKKNY-----IISDFKENGKLYL 120  
 QY 90 LNSKALVRLALEKXQAAHQR--EDFA-----SNEYVYNA 127  
 Db 121 RANNSTISLNTLQDAKLIENDQVISEDILAKKESTIFSLYIPENNAKDSKEDKNNT 180  
 QY 128 KDDLPEKNDSEPSQRIKP--VFIDANFRQISTYQAAVH----- 167  
 Db 181 EEVLNNESSQEEVTSQKLKDSQLAFSYSNFGIKASFIDLQNTENISPEYRQDETGISP 240  
 QY 168 ----IPTDIYEGSTIVLNLMTSALDEVFKKREEDBSILMOYFGSATGLARYYPASPW 223  
 Db 241 NMSWIP--GNTTVVNHQGNSEF-----SSQMDGVNSMN--GEATNLNENGYIEYAG 287  
 QY 224 VDN-----SRTPNKIDLY-DVRRRPWYIQGAASPKDMLLVDSVSGSLTLK 270  
 Db 268 VANNPVPALKRYAKETETPGLYDYLVNRCN--VQNDIKPVDIVLVDMSGSMQAKET 344  
 QY 271 LIRTSVSEMLETLSD--DEVNV--ASFNSNAODVSCFOHVOANVRNKKVYLDK-----A 321  
 Db 345 AVRGVSDPFLSTIQNTAVADYVNVGIVGSSPGNVYVAGSGLIYVPI--DKVSESHVKS 402  
 QY 322 VNNITA--KGIITYKKKFSFAEQLNYSRANCKIIMLFDGGEERAQEIFARYNK 378  
 Db 403 INQALAPQSGTETQLGRKTEML--EODSDNCKMMLMTDG--VPFSPKYNS 455  
 QY 379 DKVVR--VFESVGOHNTDRG--PIQ--WMAENKGYEYI--PSGARITQOE 425  
 Db 456 ASKVNVNLYIGSFASRDRPENTSKIOSPYVKIINGNSNIEIKDWTAAULGEAEISKOE 515  
 QY 426 YLDVGRPMVLAD-----KAKOVOMTNYVLDALGLVITGTLPPVNTIGONE 474  
 Db 516 ISEIHTLGIQNGDSYLSGEEVKSRTSLATGLYQDANSAN-----DITDYK 565  
 QY 475 NKTN--LNQOLLGVMGVDSLEDIK----- 498  
 Db 566 NOANVLSRENTTNGLLDPLGAQFEYKDTKFEITSGEDSIDNLPYKINEKLEISN 625  
 QY 499 -----RLTPRTLCPPNGYFAIDPNGYVLLHPNLQPKPKSO----- 535  
 Db 626 LINGKNOEQVQIHQYKRLNTEEDPKTNYIOM--NGETTLPPN--GSNPNKYNFGVPSA 681  
 QY 536 --EPVTLDFDALENDIKYKIRKMDGE--SGEKTFFRLVKSODERYIDKGNRY 588  
 Db 682 KSSGINLTLEKOWLANSENIPENVELLIGRRSAQISSDWTKYTLAKDDE----- 731  
 QY 589 TWTPVNGTDVSLAVLPTYS-----FYIYKAKI-----EETITQARSKK 629  
 Db 732 -WR-----SQLENLKYSLIGEEPIYETKDEVLNSETYDITIGEDTITIANIEK 783  
 QY 630 MKQSETLKPNDFESGGYFTIAPRDYCN--DLKISDNTEFL--LNENE--PIDKRT 679  
 Db 784 IOLIKTSNHNDNEPLSEVEFVLKNSQGEEDKATYNEGEGELFPEKRLNNGEEOQLHEIKS 843  
 QY 680 PNN-----PSCNTD-----LINRYLLDAGFTNEL--VONYWSKQKNI 714  
 Db 844 PGLHLEGPWKIKTEFENGQPIIVYDQIADLDEHYNKFMSLITNDINVEEF--RMS 899  
 QY 715 KGVARFVVT--DGIITRVYKPA--GENQENP-----EYEDSPFK 753  
 Db 900 VTIDKRAVDSEBKIDGAVFNLVQIESVDLTLQKLEITNNLLPGLVALQESVSPNGY 959  
 QY 754 RSLDNDNYVETA-----PYFNKSGGAVESGIMVSKAV--ETIYQKLL 795  
 Db 960 R--DDEVHFFRVKFNQSIYVAGSEGIDIPFLDENSG--KNGLYVLNBEENGDLHLTLIFY 1015

```

RESULT 6
T18770
probable calcium channel protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T18770; T25249
R: Sulston, J.
submitted to the EMBL Data Library, June 1995
A: Reference number: Z19019
A: Accession: T18770
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: DNA
A: Residues: 1-1148 <W12>
A: Cross-references: EMBL:249907; PIDN:CAA90091.1; GSPDB:GN00020; CESP:T24F1.6
A: Experimental source: clone B0491
R: Chui, C.
submitted to the EMBL Data Library, June 1995
A: Reference number: Z20004
A: Accession: T25249
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: DNA
A: Residues: 1-1148 <W12>
A: Cross-references: EMBL:249912; PIDN:CAA90141.1; GSPDB:GN00020; CESP:T24F1.6
A: Experimental source: clone T24F1
C: Genetics:
A: Gene: CESP:T24F1.6
A: Map position: 2
A: Intons: 91/2; 131/3; 170/3; 283/1; 322/2; 410/3; 487/1; 563/1; 602/3; 654/3; 683/3;
Query Match 10.3%; Score 579.5; DB 2; Length 1148;
Best Local Similarity 21.7%; Pred. No. 1.5e-26;
Matches 251; Conservative 214; Mismatches 424; Indels 269; Gaps 48;
QY 37 VDKMOEDVTLA-----KTASGVNOLVIEKYQDLYVEPNNAQVLEIARDI 86
DB 99 VDIIEEPASIAQFASANILDFEFOSRFSLOVEFEKIKEDAEKLRVATEHL 158
QY 87 EKLINSKRALVRLALEAEKVOAHQWREDFASNEVYVYNAKDLDPEKNDSPGSOR-- 144
DB 159 DRLVTRNVYDLKLIASSAEASAVF-----DEYDQAVAVYQADKRCE 201
QY 145 --IKPVEIDANFGROIISYOH---AAVHIPDIYEGSTIVLNLNMTSA--LDEVEKKNR 197
DB 202 AYMKKNESMHFVSNK-VEHNSKSGIHIVESYQCDPRVARDPDMGTGKHEKTSMDNK 260
QY 198 EEDPSILMOYFGSATGLARYPASPVVDNRTPKIDLYVRRRPYIQASAPKMLIL 257
DB 261 EKAPEMOHQYIGYSGILTRMYPRRW-KVEPTPTIDLFDRPRRPWFVNAESVPKDIVFL 319
QY 258 VDVSGSVGLTKLIRTSVSEMLETSDDFVNVASFNNAOD-VSCFOH-LVQANVRNK 315
DB 320 LDISSGSKGPTMLIKITMMATILSTLSPNDYFEGVYVNNHFNPLISANTPMPATTSNK 379
QY 316 KVLDAVNNTAKGITDYKGFSPFQOL--LNTVNS-----RANCKTIMLETDGEE 367
DB 380 KVFEEELGMELEKQQAFAFAPLRKSLDYLKGNLDSNQSGLADYRSECHKLLIIFTDGVD 439
QY 368 RAQEI-----FAKYKDKKVVYFTSVQHNTRDGP-OMACAEKGGYVYIPISGAIRIN 422
DB 440 WPHOIIDEEFQTRNSE-LIRIFGSMG-YGTSLILPLOOYAKASHGYSSEIDSIIMDKPQ 497
QY 423 TOEIVDVIAGPMVLAKGRK-----QVQMTVNYIDALEGLVITGTLTFVFNITGQNN 475
DB 498 SRTIQNTLSQ---VRGELKGTNAEKREPSMTQIYMETOGTGPVITSLPIL-----TSE 549
QY 476 KTNLKNOLLIGVGVDSLEDIKRLPRFTLCPNGYFAIDPNCYVLLHPNLQ-PKNPK- 533
DB 550 QIRVRDQKAGVVAIDISIKFEKTHP--TSSEQMTGYIDNNGMLIYHPOLQIPKTEVH 607
QY 534 -----SQEPY-----TLDDLEALENDIVEI 555
DB 608 CVRSACYDAQOVOKAGSGLRVHYGFSDEVRVRLVGLIDSIPTLDWYDLEGSTAIRDL 667

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QY 556 RNKMIDGSGEKTPTLYKSDERYIDKGNRTYTWTVPVNGDYSLAV--LPTYSFYIK 613
DB 668 RR-----RITTKCYEEAIKDNSKEYHCSHKSDPFLVLYNNIQLTYYTDD 715
QY 614 AKIEFTTQ-----ARSKGKKMSDETLKPDNFEESGYTAPRDYC--NDLKISDN 663
DB 716 SVQELGLTDNKLVPFYPYRDVQGWKIDVYAAHBRFRV--WSDISEKEICAQDDMRIPRA 773
QY 664 NTEFLINNEFLDKRTPNPNPCNTDLIRVLLDAGFTVELYQNTWSKOKNKGVKAPFY 723
DB 774 FTKGGSWTQSWPKSDIDHTTC-----LLAQYPENASVPHVYNS-----FVR 815
QY 724 TDCGITRYVPKAGEWMOENPEYEDSPYKRSLLDNVYFAPFNKSGPAYESGIWVS 783
DB 816 TRSKLTATFPYCCSHDMAKVNKKPDEL-KLTNDNDV-----QFSNR-----SESLIIT 864
QY 784 KAVEIYIOGKLLKPAVAVGIKIDVN--SWIENFTKTSIRDCAGPYCDCKRNSD-----V 835
DB 865 RTIADYDNRL---AVGTOEMKENFDDQYFDFNET-----RONPDKICRK 906
QY 836 MDCVLLDGGGFLMANHDDYTNQIGRFGELDPSLMRLVNI SYAFNKSTDYQVCE-P 894
DB 907 QCSITTRNGHVIASAHARPAHLAKF---DPQLFESLVVNVSTNSMTVEQSECKAK 962
QY 895 GAAPQAGAGHRAVYVSTADILHIGMAVTA--AMSILOFLLSLTFPRLLEAVEMEDDD 952
DB 963 RVAP-----WSSAPGSSILIRYVTSL-----ERLAKTS 992
QY 953 FTASLSKOSCIETOQYEFNDNSKFSGLVDCGNC-SRIFFVEKLMNTLFIWESKGT 1011
DB 993 FPNRLLESALTLDVADQPSMTGNTCTFOKIKPFERCFFMFFHYRMTLNTTK-QLDGTGMS 1051
QY 1012 C-----PCDTRLLIQAEQTSQDPP-----CMVNRQPRYRKBPVQCFD 1049
DB 1052 CSRYAKLYPVPTTSLIILADACQYRPRKRIESEPRKLEKQDV-HSHARRPD----- 1106
QY 1050 NNALED-----YTDC 1059
DB 1107 --ALNDWKITDLOKKNHYDC 1122

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RESULT 7
S54355
Inter-alpha-trypsin inhibitor heavy chain 3 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 04-Feb-2000
C:Accession: S54355
R: Chan, P.; Risler, J.L.; Raguenez, G.; Salier, J.P.
Biochem. J. 306, 505-512, 1995
A: Title: The three heavy-chain precursors for the inter-alpha-inhibitor family in mou
A: Reference number: S54353; MUID:95194326; PMID:7534067
A: Accession: S54355
A: Status: preliminary; nucleic acid sequence not shown
A: Molecule type: mRNA
A: Residues: 1-886 <CHA>
A: Cross-references: EMBL:X70393; NID:6695635; PIDN:CAA49843.1; PID:6695636
C: Superfamily: Inter-alpha-trypsin inhibitor complex component II
Query Match 3.5%; Score 196.5; DB 2; Length 886;
Best Local Similarity 20.5%; Pred. No. 0.00099;
Matches 189; Conservative 142; Mismatches 349; Indels 243; Gaps 46;
QY 45 VTLKTAGSVNOLVDYEKYQDLYVEPNNAQVLEIARDTEKLLNSRKALVLALEA 104
DB 78 VELPKTAFTNTTLTI-----DGVTY-PEGVKE-KEVAQKQYEKAVSOGKTAGL----- 124
QY 105 EKVOAHHQWREDF-----ASNEVYVYNAKDLDPEKNDSPGSORIKPVFIDANFGR 157
DB 125 --VKASGRLEKFTVSVNVAAGSKVTFELTYELLKRNKGKYEMLKYO-----K 173
QY 158 QISTQAAVHIPDIDYEGSTIVLNLNMTSALDEVFKKREDDPSLMOVFSA-----T 212

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Db 14 ASALLA-TALLAALGADVRSQOIPLSV-VKLMSAFGEGLKSTIAARYSSQILLQKKK 71
Qy 63 KYODLYTEPNNAQOLYEIAARDIKELLSNRKALVRLALEAEKQVQAHOHREDFASNEV 122
Db 72 EYKQVVAIEIDGLOLVKAKIMEEFHKSSEAVRLVEAAEHLKHEPDADI---QY 128
Qy 123 VYNNAK---DOLDPEKNDESPQSORIKPVFIDANFGROISYQAAVH1PTDIYEGSTIYL 180
Db 129 EYFNVLNERDKDGNFELGKEFI-LAPNDHFNNLPVNISLSDVQPTMNNKNDPAIV 186
Qy 181 NELNMTLSALDEVFKKNNREDEPSLLMQVGSATGLARYTPASHWVNDNSTRPKIDLYDVR 240
Db 187 NCVYSESILNKVFYDNFPRDPSLLMQVGSAGFROYPGIKWBPDE---NGVAFADCRN 243
Qy 241 RFWYIOGAAPKMDLILVDVSGVSGTLTKLIRTSVSEMLETISDDDFVNVAFNSNQD 300
Db 244 RMYIOAATSPRDVYILVDVSGSMKGLITAKQTVSSILDTLDDDFNITITNEELIY 303
Qy 301 VS-CFO-HLVQANVRNKKVLDKAVNNITAKITDYKKGSPAFQOLLNVNYSRAN-CNK 356
Db 304 VEPCLNGTLVQADRTNKHFEHLDKLFAKIGMLDIALNEAFNITLSDFNHTGGGSIQ 363
Qy 357 IIMLPTDGEERAEIIFAKYN-KDKKVVTFEFSVGOHNYDGPQIOMACENKGYETEPS 415
Db 364 AIMLITDCAVDITITFAKYMPPDKKVFITYLIGREAFADNLKMWACAKGFEPTQIST 423
Qy 416 IGARINTQEXYLDVIGRPMVLADGKAKOVQNTNYLD-----ALEGLVY--TGTL 464
Db 424 LADQVENMEYLVLSRKYI--DQEHVYVTFEAVISTLPQAKIADDOGLVMTIYAM 481
Qy 465 PVFNITGNEKNTLNKOLLIGWGVVSLDRIKRLPRFTLCNGYFAIDPNGVYLH 524
Db 482 FVFS---KONETSKG-ILGYYVGTDPVPELKITIPKYLIGHYAFALTNGYILTH 536
Qy 525 PNLQF---KNKSOEP--VTLDFLDALENDIKVEIRKMLDGESEKTEPTLTKSODER 579
Db 537 PELRLYBEGKKRRKPNSSVDSLEVEDRDY-LRANMNRKTKG--FSMEVK---K 589
Qy 580 YIDKGNRT-----YWTVPNGTDSLALVPT-YSEYIKAK--IBETITQANSKKGM 630
Db 590 TVDGKRVLYMTINDYIIDIKGTPESLGVALSRRGHKVFPGNVTIEGL----- 639
Qy 631 KDSFLKDNDEESGYFIAPROCYN-DLKSDMNTFELNENFIDRKTPNPNPSCMTL 689
Db 640 -----HDLHPDVSLADEMSYCTNDLPEHRHLSQLAIKLYLGKKEP-LIQCCKEL 690
Qy 690 INRYLLDAGFTNELVQNWVS-----KOKNIKGYKARFVVDGITGVYV----- 733
Db 691 IOEVLFLDA-VVSAPLEAVWISLANKSENSKGYEVAFLGRTGLSKINLEFGAEQLTNQ 749
Qy 734 ---KENGEMQENPETYEDSYKSLDN--DNYVTFAPY---FNKSGPGAYESGIVNSKA 785
Db 750 DFLKAGKENJFNADHPELWYRRABEQIAGSFVYSIPFSGTGVKS-----NVVTASTS 803
Qy 786 VEITYOGLKLPAYVGIKIDVNSWIENTFTKTSIRDPGAPVCOCKRSDVMDCYIIDCG 845
Db 804 IQLDERKSPVAIVGIOMKLEFFORKEFWTASROCASLDGKCSISCODEVTNCLIDNNG 863
Qy 846 FLMANHDDYTNIGREFGEIDPSLMRHLVNIYYAFNKSADYOSVCEPAAPROGAGR 905
Db 864 FILVS--EDYT--QTGDFEGVEGAVNMKLLTMSFKRITLYDQAMK---ANKESDSA 917
Qy 906 SAYPSTADLIHIGWMAATAAMSLQOFLSLTFPRLLEAVEMEDDFTASLSK---Q 960
Db 918 HGLLDYKAFEL-----SAKWMITELVYLVEF---NLCSMWHSMTAKAKIKOTLE 967
Qy 961 SCITEOTQYFEDNDKSFSGVLDGNCGRIFHYEKLNTNLIIFMYSKTCGCDT---R 1017
Db 968 PCDEYFAFVSEKRIKETGNIACEDCSKSFVIOQIPSSMLFNVYDS--SCLESVAPI 1025
Qy 1018 LLIQABQTSDBPDCPMVKOPRRYKKGPDVCFDNNALDYDTCGVS 1063

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Db 1026 TMADIETRYNESLCKERLKAOKIRRPESCHGFHPEENARECGAS 1071
RESULT 5
S44617
C5003.11 protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #extl_change 30-Jun-2001
R:Favell, A.D.
Submitted to the EMBL Data Library, May 1993
A:Description: Sequence of the C. elegans cosmid C5003.
A:Reference number: S44627
A:Accession: S44617
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-734 <FAV>
A:Cross-references: EMBL:114433; NID:g289649; PID:g289650
C:Genetics:
A:Introns: 24/2; 87/3; 175/1; 259/1; 290/3; 346/3; 460/3; 538/3
Query Match 10.9%; Score 611; DB 2; Length 734;
Best Local Similarity 26.5%; Pred. No. 9, 6e-29;
Matches 179; Conservative 127; Mismatches 261; Indels 108; Gaps 19;
Qy 47 LAKTASGVNOLVDIYERYODLYTEPNNAQOLYEIAARDIKELLSNRKAL--VRLALEA 104
Db 36 MKTEFSLSHETILKONYEKLEVEEDQFPAELKSKKHRIEDLYLKVSOPATKATLSLA 95
Qy 105 EKVQAAHOREDFASNEVYNNAKDLDPERK-NDSEPSQRIKP-----VFIDANF-G 156
Db 96 RSYRNDSTVNDPQSKSEIRFMSAKGNDGTITYESHNLRLKLVNETKSPNLQANFTY 155
Qy 157 RQSYQAAVHIPTDYEESTIYLNELNMTSALDEVFKKNNREDEPSLLMQVGSATGLAR 216
Db 156 LPTSSVSAVHIPTPLDYDRNEDLRLKIDW-SDIDAVYRNRETKDLAQOLCSEAGYMR 214
Qy 217 YYPASPVV-DNSRTPKIDLYDVRRRPWTQGAAPKMDLILVDVSGVSGTLTKLIRTS 275
Db 215 YYPAAAFWQNDQ--DEHDLDFDCRNTEWITNSATNKNVLMIDHSGSLMGORYEYAKOT 272
Qy 276 VSEMLTSLDDDFVNVAFSNSNA---QDVSCFOHLVQANVRNKKVLDKAVNNITAKGTD 332
Db 273 TEALILETSHNDYFNIMFTSKNTFLDGCNGTNGILLQATMRNKKALKRMDITYQSGRAE 332
Qy 333 YKGFSPAFQOLLNLYN-----VSANCNKIIMLFTDGEERAEIIFAKYNKDKYRVTFE 387
Db 333 YKALPLAFSVLIDINNCGDNNRGACENVIMLITDGADNAYKRTFDMYNAKRVRFTE 392
Qy 388 SVGOHNYDRGPQIOMACENKGYEYELPSIGAIRINTQEYL---DVLGRPVYLAGDKAQ 443
Db 393 LVGDEAIDFNEVEEMACNNRGYVHVANMADYDEKHHIIRMSRYVGHGHYESOLS-- 450
Qy 444 VQNTNYLDALEGL--VITGLPVPNTTGQNDENKTN-----ALENDIKVEIRNKNIDG 478
Db 451 -WMTGYREKLYLPREIAPAEVPITNOSFAVMNKAASRRKIRLOKSEARSHFTVYSY 509
Qy 479 --LKNOLLIGVMDVDSLDIRKLRPRFTLCNGYFAIDPBGVYLHFNLPKRP----- 532
Db 510 PLYVNETFPGVAVNIPLLEVAKSHPANIGSKSTFEMLDQGFVWTHQPLRIDPFTKY 569
Qy 533 KSGEPVTLDFD-----ALENDIKVEIRNKNIDG 563
Db 570 HKQNYNMMDLLELEVQONVRSQSAVSDLVCEGSANVACEVDLKRKAVRKMIIDC 629
Qy 564 SGKRTFTLVKSDERY---IDK---GNRTYTWVPNGTDSLALVLPYTSFYIYAKI 616
Db 630 NSD-----VQOILDVYATELLDRYYPQTNTYVABCINHNVLGLAAVAKGDYRVVK- 682
Qy 617 EETITQARSKKGMK 631
Db 683 -----QKRYDFGRVK 692

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Db 1020 MOAEOISDGPDPDVKOPRRYKGPVCFDNNVLEDYTCGVS 1063

# RESULT 3

CHRM2

Calcium channel protein alpha-2 chain precursor - rabbit

N:Alternate names: dihydropyridine-binding protein, 140K

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 31-Mar-1992 #sequence,revision 31-Mar-1992 #text\_change 22-Jun-1999

C:Accession: S10579; A39518; A33409

R:Ellis, S.B.; Williams, M.E.; Ways, N.R.; Brenner, R.; Sharp, A.H.; Leung, A.T.; Campbell, S.E.; 1661-1664, 1988

A:Title: Sequence and expression of mRNAs encoding the alpha(1) and alpha(2) subunits of

A:Reference number: S10579; MUID:88336904; PMID:2458626

A:Accession: S10579

A:Molecule type: mRNA

A:Residues: 1-1106 <ELL>

A:Cross-references: EMBL:M21948; NID:g164762; PIDN:AAA81562.1; PID:g164763

A:Note: 57-Asn, 106-Lys, and deletion of 620-Ser were also found

R:Jay, S.D.; Sharp, A.H.; Kahn, S.D.; Vedyick, T.S.; Harpold, M.M.; Campbell, K.P.

J. Biol. Chem. 266, 3287-3293, 1991

A:Title: Structural characterization of the dihydropyridine-sensitive calcium channel al

A:Reference number: A39518; MUID:91131638; PMID:1847144

A:Accession: A39518

A:Molecule type: Protein

A:Residues: 961-973 <JAY>

A:Note: this sequence represents the amino end of a glycosylated peptide that appears at

at the amino end and identical molecular weights (17k) following deglycosylation

R:Hamilton, S.L.; Hawkes, M.J.; Brush, K.; Cook, R.

Biochemistry 28, 7820-7828, 1989

A:Title: Subunit composition of the purified dihydropyridine binding protein from skelet

A:Reference number: A33409; MUID:90122765; PMID:2558713

A:Accession: A33409

A:Status: preliminary

A:Molecule type: protein

A:Residues: 27-44, S',46-47 <HAM>

C:Superfamily: calcium channel alpha-2 chain

C:Keywords: calcium; disulfide bond; glycoprotein; ion channel; membrane protein; phosph

F.1-26/Domain: signal sequence #status predicted <SIG>

F.27-1106/Product: calcium channel alpha-2 chain #status predicted <MAT>

F.94,138,186,326,350,470,477,606,615,678,697,784,827,891,898,988,1001,1081/Binding site:

Query Match 96.5%; Score 5405.5; DB 1; Length 1106;

Best Local Similarity 95.4%; Pred. No. 2.7e-316;

Matches 1035; Conservative 11; Mismatches 10; Indels 29; Gaps 4;

1 MAAGCLATLTLFOS--LLIGPSSEPPSAVTIKSWDKMOEDLVLTAKTASGVNOLY 58

1 MAAGPLATLTLMOQMLLIGPSSEPPSAVTIKSWDKMOEDLVLTAKTASGVHOLY 60

59 DIYEKYQDLYTEPPNAROLVEIAADIEKLNSKALVRLALEAKYQAAHOMREDA 118

61 DIYEKYQDLYTEPPNAROLVEIAADIEKLNSKALVRLALEAKYQAAHOMREDA 120

119 SNEVYVYNAKDDLPKNDSEPGSQRIKVEPIDANFGQISYQAAVHIPDIYEGSTI 178

121 SNEVYVYNAKDDLPKNDSEPGSQRIKVEPIDANFGQISYQAAVHIPDIYEGSTI 180

179 VLNELMWTASALDEVFKKNEDEPSILMOVFGSATGLARYPPSPWVDNRTNKKIDLYY 238

181 VLNELMWTASALDEVFKKNEDEPSILMOVFGSATGLARYPPSPWVDNRTNKKIDLYY 240

239 RRRPWTIOGAASPKDMLIIVDVGSGVGLTLKIRTSVEMLETTSDDDFVWVASFNSNA 298

241 RRRPWTIOGAASPKDMLIIVDVGSGVGLTLKIRTSVEMLETTSDDDFVWVASFNSNA 300

301 QDVSCFOHLVQAVNRKKYLKDAVNNITAKGITDYKKGSFAFEQLLNVNSRANCKII 360

299 QDVSCFOHLVQAVNRKKYLKDAVNNITAKGITDYKKGSFAFEQLLNVNSRANCKII 358

359 MLTDSGGERAQBIFAKYKNDKVRVFTFSVGOHNYDRGPIDQMACEKNGYVEIPSTGA 418

361 MLTDSGGERAQBIFAKYKNDKVRVFTFSVGOHNYDRGPIDQMACEKNGYVEIPSTGA 420

QY 419 IRLNTEYLDLGRPMVLADKAKOYQWNVYLDALGLVITGTLPEVNTIGQENKTN 478

Db 421 IRLNTEYLDLGRPMVLADKAKOYQWNVYLDALGLVITGTLPEVNTIGQENKTN 480

QY 479 LKNOLLIGWGVDSLEIDKRLPRFLCPNGYFFAIDPBGVYLLHPNLOPKDIGVIGPT 530

Db 481 LKNOLLIGWGVDSLEIDKRLPRFLCPNGYFFAIDPBGVYLLHPNLOPKDIGVIGPT 540

QY 531 -----NPKSQEPVLDLDALENDIVEIRNKKMIDSESGEPTLVKSODER 579

Db 541 INLKRPNVONPKSQEPVLDLDALENDIVEIRNKKMIDSESGEPTLVKSODER 600

QY 580 YIDKGNRTYTWTPVNGTDY-SLALVLPPTYFYIKAKIEETIQOASRKKMKDSETLAP 638

Db 601 YIDKGNRTYTWTPVNGTDYSSALVLPPTYFYIKAKIEETIQOARY-----SETLAP 653

QY 639 DNFESGTYFLAPDYONDKISDNNEFLNREPIFRDKTPNNPSCNDLIRVLLDAG 698

Db 654 DNFESGTYFLAPDYOSDLKPSDNNEFLNREPIFRDKTPNNPSCNDLIRVLLDAG 713

QY 699 FTNELVONYSKOKNIGKARFVYTDGTRVYPKAGEENMOENPEYEDSEYKRSIDN 758

Db 714 FTNELVONYSKOKNIGKARFVYTDGTRVYPKAGEENMOENPEYEDSEYKRSIDN 773

QY 759 DNYVETAPYFNKSGPAYESGIMVSKAVEITYOGKLLKPAVVGIKIDVNSWIEPFTKSI 818

Db 774 DNYVETAPYFNKSGPAYESGIMVSKAVEITYOGKLLKPAVVGIKIDVNSWIEPFTKSI 833

QY 819 RDPGAPYCDCKRSDVDCVYLLDDGFLMANHDDVTNIOGRFGIDISLRHVNIS 878

Db 834 RDPGAPYCDCKRSDVDCVYLLDDGFLMANHDDVTNIOGRFGIDISLRHVNIS 893

QY 879 VYAFNKSVDYQVCEPAGAPKOGAGHRSAYPSIADLIHIGMATAAAGSILLOFLLST 938

Db 894 VYAFNKSVDYQVCEPAGAPKOGAGHRSAYPSIADLIHIGMATAAAGSILLOFLLST 953

QY 939 FPRLLAEVEMDDFTASLSKQSCITBOYFFPDNDSKFSGVLDGCGNSRIFHVEKLM 998

Db 954 FPRLLAEVEMDDFTASLSKQSCITBOYFFPDNDSKFSGVLDGCGNSRIFHVEKLM 1013

QY 999 TNLFIWESGTCPCOTRILIOAEQTSDDGPPCDMWKOPRRYKGPVCFDNNVLEDYTD 1058

Db 1014 TNLFIWESGTCPCOTRILIOAEQTSDDGPPCDMWKOPRRYKGPVCFDNNVLEDYTD 1073

QY 1059 CGVS 1063

Db 1074 CGVS 1078

RESULT 4

30256

calcium channel alpha-2-delta-C chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 22-Oct-1999 #sequence,revision 22-Oct-1999 #text\_change 20-Jun-2000

C:Accession: T30256

R:Klugbauer, N.; Lacinova, L.; Marais, E.; Hobom, M.; Hofmann, F.

J. Neurosci. 19, 648-691, 1999

A:Title: Molecular diversity of the calcium channel alpha2delta subunit.

A:Reference number: 220794

A:Accession: T30256

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1091 <KLU>

A:Cross-references: EMBL:AJ010949; PIDN:CAA09423.1

C:Experimental source: brain

C:Superfamily: calcium channel alpha-2 chain

Query Match 20.4%; Score 1145.5; DB 2; Length 1091;

Best Local Similarity 28.6%; Pred. No. 1.5e-60;

Matches 322; Conservative 234; Mismatches 437; Indels 133; Gaps 40;

3 ACCLLATLTLFOSLLIGPSSEPPSAVTIKSWDKMOEDLVLTAKTASGVNOLYDI 62

Db 301 VSCFOHLVQANRNNKVLKDAVNNITAKGIDTYKKGFSFAEQLLNNTVSRANCKIIML 360  
 QY 361 FTDDGGERAOEIFAKYNNKDKVRVFTFSVGOHNDRGPIOMMACENKGYEIPISGAIR 420  
 Db 361 FTDDGGERAOEIFAKYNNKDKVRVFTFSVGOHNDRGPIOMMACENKGYEIPISGAIR 420  
 QY 421 INTQGYLVLGPRMVLADGKAKOVMTNVLDALEGLVITGTLPEVNTIGQFENKTNLK 480  
 Db 421 INTQGYLVLGPRMVLADGKAKOVMTNVLDALEGLVITGTLPEVNTIGQFENKTNLK 480  
 QY 481 NOLLIGVGVDSLEDIKRLTPRTFLCPNGYFAIDPNGYVLLHPNLOPKPKSOEPTVL 540  
 Db 481 NOLLIGVGVDSLEDIKRLTPRTFLCPNGYFAIDPNGYVLLHPNLOPKPKSOEPTVL 540  
 QY 541 DFLDALENDIKVEIRNNKMDIGSEGEKTFRLVKSODERYIDKGNRTYTWPVNGTDSL 600  
 Db 541 DFLDALENDIKVEIRNNKMDIGSEGEKTFRLVKSODERYIDKGNRTYTWPVNGTDSL 600  
 QY 601 ALVLPYTSFYIYKAKIEETITQARSKKGMKDSFTLKPDNFEEGTYFIAPRDYCNLDKI 660  
 Db 601 ALVLPYTSFYIYKAKIEETITQARSKKGMKDSFTLKPDNFEEGTYFIAPRDYCNLDKI 660  
 QY 661 SDNTEFLNFEIDKRTPNPNSCNTDLINRVLLDAGFTNELVQNTWSKOKNIKGYKAR 720  
 Db 661 SDNTEFLNFEIDKRTPNPNSCNTDLINRVLLDAGFTNELVQNTWSKOKNIKGYKAR 720  
 QY 721 FVVTDDGITRYPKEAGENNQENPEYEDSFYKRSILDNDNYVTPAPYFNKSGCAVESGI 780  
 Db 721 FVVTDDGITRYPKEAGENNQENPEYEDSFYKRSILDNDNYVTPAPYFNKSGCAVESGI 780  
 QY 781 MVSRAVEIYIOGKLKPAVVGIKIDVNSWIENFTKTSIRPCAGPVDCCKRNSDVMDCVI 840  
 Db 781 MVSRAVEIYIOGKLKPAVVGIKIDVNSWIENFTKTSIRPCAGPVDCCKRNSDVMDCVI 840  
 QY 841 LDGGEFLMANHNDYTNQIGRFGELIDPSCMLRHVNISYAFNKSYDYOSVCEPGAAPKQ 900  
 Db 841 LDGGEFLMANHNDYTNQIGRFGELIDPSCMLRHVNISYAFNKSYDYOSVCEPGAAPKQ 900  
 QY 901 GAGHRSAVYPSIADILHIGMMATAAAMSILOQFLSLTPRLLAEVEMEDDDTASLSKQ 960  
 Db 901 GAGHRSAVYPSIADILHIGMMATAAAMSILOQFLSLTPRLLAEVEMEDDDTASLSKQ 960  
 QY 961 SCITTEOTYFFENDSKSFSGVLDGNCSTRIFHEKLMNTNLFIIVESKGTGCTPCTRLI 1020  
 Db 961 SCITTEOTYFFENDSKSFSGVLDGNCSTRIFHEKLMNTNLFIIVESKGTGCTPCTRLI 1020  
 QY 1021 QABQTSIDGPPCDMVKOPRYRKGPVDCFDNNALEDTDCGGVS 1063  
 Db 1021 QABQTSIDGPPCDMVKOPRYRKGPVDCFDNNALEDTDCGGVS 1063

## RESULT 2

A44147

calcium channel protein alpha-2 chain precursor - rat

N:Alternate names: dihydropyridine-sensitive L-type

C:Species: Rattus norvegicus (Norway rat)

C:Date: 27-Jun-1994 #sequence\_revision 1

C:Accession: A44147

R:Kim, H.L.; Kim, H.; Lee, P.; King, R.G.; Chih, H.

Proc. Natl. Acad. Sci. U.S.A. 89, 3251-3255, 1992

A:Title: Rat brain expresses an alternatively spliced form of the dihydropyridine-sensit

A:Reference number: A44147; MUID:9228762; PMID:1314383

A:Accession: A44147

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-1091 &lt;KIM&gt;

A:Cross-references: GB:M66621; NID:g203954; PIDN:AAA41088.1; PID:g203955

C:Superfamily: calcium channel alpha-2 chain

C:Keywords: calcium; glycoprotein; ion channel; transmembrane protein

Query Match 96.8%; Score 5420; DB 2; Length 1091;

Best Local Similarity 96.2%; Pred. No. 3.5e-317; Matches 1024; Conservative 23; Mismatches 15; Indels 2; Gaps 2;

QY 1 MAACCLALTLTLTFOSLIGPSSQEPSPAVTIRKSWDKMOEDLVTLAKTASGVNOLVDI 60  
 Db 1 MAACCLALTLTLTFOSLIGPSSQEPSPAVTIRKSWDKMOEDLVTLAKTASGVNOLVDI 60  
 QY 61 YEKYODLYTEPPNAROLVETIAROTIEKLSNRSKALVRLAEVQAAHOMREDFASN 120  
 Db 61 YEKYODLYTEPPNAROLVETIAROTIEKLSNRSKALVRLAEVQAAHOMREDFASN 120  
 QY 121 EYVYNAKDLDDEKNDSEPGSORIKPVFIDANFROISYQAAVHPTIDYESTITL 180  
 Db 121 EYVYNAKDLDDEKNDSEPGSORIKPVFIDANFROISYQAAVHPTIDYESTITL 180  
 QY 181 NELNMTSALDEVKKNRREDPSILMOVFGSATGLARYAPSPWVNSRTPNKLIDLYDVR 240  
 Db 181 NELNMTSALDEVKKNRREDPSILMOVFGSATGLARYAPSPWVNSRTPNKLIDLYDVR 240  
 QY 241 RPYIIOGAASPKDMLILVDVSGVSGTLKLRISVSEMLETLSDDDFYNVASFNSMOD 300  
 Db 241 RPYIIOGAASPKDMLILVDVSGVSGTLKLRISVSEMLETLSDDDFYNVASFNSMOD 300  
 QY 301 VSCFOHLVQANRNNKVLKDAVNNITAKGIDTYKKGFSFAEQLLNNTVSRANCKIIML 359  
 Db 301 VSCFOHLVQANRNNKVLKDAVNNITAKGIDTYKKGFSFAEQLLNNTVSRANCKIIML 359  
 QY 361 FTDDGGERAOEIFAKYNNKDKVRVFTFSVGOHNDRGPIOMMACENKGYEIPISGAIR 420  
 Db 361 FTDDGGERAOEIFAKYNNKDKVRVFTFSVGOHNDRGPIOMMACENKGYEIPISGAIR 420  
 QY 421 INTQGYLVLGPRMVLADGKAKOVMTNVLDALEGLVITGTLPEVNTIGQFENKTNLK 480  
 Db 421 INTQGYLVLGPRMVLADGKAKOVMTNVLDALEGLVITGTLPEVNTIGQFENKTNLK 480  
 QY 481 NOLLIGVGVDSLEDIKRLTPRTFLCPNGYFAIDPNGYVLLHPNLOPKPKSOEPTVL 540  
 Db 481 NOLLIGVGVDSLEDIKRLTPRTFLCPNGYFAIDPNGYVLLHPNLOPKPKSOEPTVL 540  
 QY 541 DFLDALENDIKVEIRNNKMDIGSEGEKTFRLVKSODERYIDKGNRTYTWPVNGTDSL 600  
 Db 541 DFLDALENDIKVEIRNNKMDIGSEGEKTFRLVKSODERYIDKGNRTYTWPVNGTDSL 600  
 QY 601 ALVLPYTSFYIYKAKIEETITQARSKKGMKDSFTLKPDNFEEGTYFIAPRDYCNLDKI 660  
 Db 601 ALVLPYTSFYIYKAKIEETITQARSKKGMKDSFTLKPDNFEEGTYFIAPRDYCNLDKI 660  
 QY 660 ISDNTEFLNFEIDKRTPNPNSCNTDLINRVLLDAGFTNELVQNTWSKOKNIKGYKAR 720  
 Db 660 ISDNTEFLNFEIDKRTPNPNSCNTDLINRVLLDAGFTNELVQNTWSKOKNIKGYKAR 720  
 QY 720 FVVTDDGITRYPKEAGENNQENPEYEDSFYKRSILDNDNYVTPAPYFNKSGCAVESGI 780  
 Db 720 FVVTDDGITRYPKEAGENNQENPEYEDSFYKRSILDNDNYVTPAPYFNKSGCAVESGI 780  
 QY 780 MVSRAVEIYIOGKLKPAVVGIKIDVNSWIENFTKTSIRPCAGPVDCCKRNSDVMDCVI 840  
 Db 780 MVSRAVEIYIOGKLKPAVVGIKIDVNSWIENFTKTSIRPCAGPVDCCKRNSDVMDCVI 840  
 QY 840 LDGGEFLMANHNDYTNQIGRFGELIDPSCMLRHVNISYAFNKSYDYOSVCEPGAAPKQ 900  
 Db 840 LDGGEFLMANHNDYTNQIGRFGELIDPSCMLRHVNISYAFNKSYDYOSVCEPGAAPKQ 900  
 QY 900 GAGHRSAVYPSIADILHIGMMATAAAMSILOQFLSLTPRLLAEVEMEDDDTASLSKQ 959  
 Db 900 GAGHRSAVYPSIADILHIGMMATAAAMSILOQFLSLTPRLLAEVEMEDDDTASLSKQ 959  
 QY 959 QSCITTEOTYFFENDSKSFSGVLDGNCSTRIFHEKLMNTNLFIIVESKGTGCTPCTRLI 1019  
 Db 959 QSCITTEOTYFFENDSKSFSGVLDGNCSTRIFHEKLMNTNLFIIVESKGTGCTPCTRLI 1019  
 QY 1019 QABQTSIDGPPCDMVKOPRYRKGPVDCFDNNALEDTDCGGVS 1063  
 Db 1019 QABQTSIDGPPCDMVKOPRYRKGPVDCFDNNALEDTDCGGVS 1063

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 10, 2003, 14:13:54 ; Search time 20.2324 Seconds  
(without alignments)  
5050.861 Million cell updates/sec

Title: US-10-090-827-8

Perfect score: 5602  
Sequence: 1 MAAGCLALTLTLFQSLILG.....PDVCFDNNALDPTDGGVS 1063

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum First 100%  
Listing first 45 summaries

Database : PIR\_73:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5532	98.8	1091	2 JH0565	calcium channel al
2	5420	96.8	1091	2 A44147	calcium channel pr
3	5405.5	96.5	1106	1 CHRA2	calcium channel pr
4	1145.5	20.4	1091	2 T30256	calcium channel al
5	611	10.9	794	2 S44617	C50C3.11 protein
6	579.5	10.3	1148	2 T18770	probable calcium c
7	196.5	3.5	886	2 S54355	inter-alpha-trypsi
8	190.5	3.4	1450	2 C86880	hypothetical prote
9	188	3.4	885	2 S30350	inter-alpha-trypsi
10	170.5	3.0	1819	2 D97033	uncharacterized pr
11	168.5	3.0	575	2 D6498	hypothetical prote
12	166	3.0	889	2 JCS576	inter-alpha-trypsi
13	165	2.9	459	2 F64688	proteinase (EC 3.4
14	160.5	2.9	420	2 S76691	hypothetical prote
15	160.5	2.9	2364	2 I40884	cytochrome L - Clos
16	159	2.8	932	2 JCS953	inter-alpha-inhibi
17	158.5	2.8	918	2 E90542	lipoprotein [impor
18	155.5	2.8	946	1 IYH2	inter-alpha-trypsi
19	155	2.8	1315	2 T28679	fibrogen-binding
20	155	2.8	1984	2 A44396	P-type cation tran
21	154	2.7	688	2 D96930	methyl-accepting c
22	153.5	2.7	1426	2 A99580	hypothetical prote
23	153	2.7	946	2 JCS575	inter-alpha-trypsi
24	152.5	2.7	5005	2 F82884	hypothetical prote
25	152	2.7	1516	2 E71619	membrane associate
26	150.5	2.7	680	2 A97331	methyl-accepting c
27	149.5	2.7	654	2 A69656	inter-alpha-trypsi
28	149.5	2.7	921	2 JCA625	hypothetical prote
29	149.5	2.7	926	2 D86897	hypothetical prote

#### ALIGNMENTS

RESULT 1  
JH0565  
Calcium channel alpha-2b chain precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1992 #sequence, revision 30-Jun-1992 #text, change 20-Aug-1999  
C:Accession: JH0565  
R:Williams, M.E.; Feldman, D.H.; McCue, A.F.; Brenner, R.; Vellocelbi, G.; Ellis, S.B.  
Neuron 8, 71-84, 1992  
A:Title: Structure and functional expression of alpha1, alpha2, and beta subunits of  
A:Reference number: JH0564; MUID:92110010; PMID:1309651  
A:Accession: JH0565  
A:Molecule type: mRNA  
A:Residues: 1-1091 <MTL>  
A:Cross-references: GB:M6559; NID:q179761; PIDN:AAA51903.1; PID:q179762  
A:Experimental source: basal ganglia  
A:Note: Several conflicts are found between Genbank submission, authors' translation  
C:Comment: This protein is a subunit of the voltage dependent calcium channel.  
C:Superfamily: calcium channel alpha-2 chain  
C:Keywords: glycoprotein; phosphoprotein  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-1067/Product: calcium channel alpha-2b chain #status predicted <CAL>  
F:32,268,326,539,635,1087/Binding site: phosphate (Thr) (covalent) (by protein kinase  
F:91,142,250,625,817/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #  
F:92,136,184,324,348,468,475,585,594,663,682,769,812,876,883,973,986/Binding site: ca  
F:501/Binding site: phosphate (Thr) (covalent) #status predicted  
F:833/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status pre

Query Match 98.8% Score 5532; DB 2; Length 1091;  
Best Local Similarity 98.7%; Pred. No. 0;  
Matches 1049; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY	1	MAAGCLALTLTLFQSLILGSSQEPFSAVYIKSWDKMDELTALAKTASGVQVLDI	60
DB	1	MAAGCLALTLTLFQSLILGSSQEPFSAVYIKSWDKMDELTALAKTASGVQVLDI	60
QY	61	YEYQDLYVERPNNAQVLEIARDIEKLNSKALVLALEAKVQAAHQMRDPASN	120
DB	61	YEYQDLYVERPNNAQVLEIARDIEKLNSKALVLALEAKVQAAHQMRDPASN	120
QY	121	EYVYNAKDDLPDEKNDSEPGSQRIRKPFIDANFGROISYQAAVHPTDIYEGSTVL	180
DB	121	EYVYNAKDDLPDEKNDSEPGSQRIRKPFIDANFGROISYQAAVHPTDIYEGSTVL	180
QY	181	NEIWNLSALDEVEFKKREEDPSLLMOVFGSAGLARVYASFWVDSRPNKIDLYDVR	240
DB	181	NEIWNLSALDEVEFKKREEDPSLLMOVFGSAGLARVYASFWVDSRPNKIDLYDVR	240
QY	241	RPWTIGASPKMLILVYSGVSGITLKITVSSEMLFTLSDDPFNVAASPNNAOD	300
DB	241	RPWTIGASPKMLILVYSGVSGITLKITVSSEMLFTLSDDPFNVAASPNNAOD	300
QY	301	VSCFOHLVQANVANKKVLKDAVNNITAKGITDYKKGFSFAFELLNMYNVRANCKIIML	360

```

FT CHAIN 945 1091 (BY SIMILARITY)
FT TRANSMEM 446 469 L-TYPE CALCIUM CHANNEL DELTA SUBUNIT (BY
FT TRANSMEM 906 930 SIMILARITY)
FT TRANSMEM 1067 1086 POTENTIAL.
FT DOMAIN 253 430 POTENTIAL.
FT CARBOHYD 92 92 N-GLYCOSYLATION
FT CARBOHYD 136 136 N-GLYCOSYLATION
FT CARBOHYD 184 184 N-GLYCOSYLATION
FT CARBOHYD 324 324 N-GLYCOSYLATION
FT CARBOHYD 348 348 N-GLYCOSYLATION
FT CARBOHYD 475 475 N-GLYCOSYLATION
FT CARBOHYD 585 585 N-GLYCOSYLATION
FT CARBOHYD 594 594 N-GLYCOSYLATION
FT CARBOHYD 663 663 N-GLYCOSYLATION
FT CARBOHYD 769 769 N-GLYCOSYLATION
FT CARBOHYD 812 812 N-GLYCOSYLATION
FT CARBOHYD 876 876 N-GLYCOSYLATION
FT CARBOHYD 883 883 N-GLYCOSYLATION
FT CARBOHYD 973 973 N-GLYCOSYLATION
FT MOD.RES 986 986 N-GLYCOSYLATION
FT MOD.RES 501 501 N-GLYCOSYLATION
FT MOD.RES 833 833 N-GLYCOSYLATION
SQ SEQUENCE 1091 AA: 123183 MW: 26413229447837 CRC64;

```

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Query Match 98.9% Score 5288; DR 1; Length 1091;
Best Local Similarity 98.8%; Pred. No. 1.7e-307;
Matches 1006; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

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QY 1 MAAGCLLALTLTLFOSLIGSSOEPFSAVTIKSVWDMODDLVTLAKTASGVNOVDI 60
DB 1 MAAGCLLALTLTLFOSLIGSSOEPFSAVTIKSVWDMODDLVTLAKTASGVNOVDI 60
QY 61 YERYODLYVEENNAQVEIARDEIKLSNRSAALVRLAEKVAQAQWREDFAASN 120
DB 61 YERYODLYVEENNAQVEIARDEIKLSNRSAALVRLAEKVAQAQWREDFAASN 120
QY 121 EYVYVYNAKDDLPPEKNDSPGSGRIKPVIEDANFGROISVQAAVHPDIDYESTYL 180
DB 121 EYVYVYNAKDDLPPEKNDSPGSGRIKPVIEDANFGROISVQAAVHPDIDYESTYL 180
QY 181 NELNMTSALDEVFKKREEDPSLLMQVGSATGALRYYPASFWNDSTPNKIDYDVR 240
DB 181 NELNMTSALDEVFKKREEDPSLLMQVGSATGALRYYPASFWNDSTPNKIDYDVR 240
QY 241 RFWYIOGASPKDMLLVDSVSGSLTLKLRISVSEMLETSLDDDEVNAVSFNSNAD 300
DB 241 RFWYIOGASPKDMLLVDSVSGSLTLKLRISVSEMLETSLDDDEVNAVSFNSNAD 300
QY 301 VSCFOLVQANRNKKVYLKDAVNNITANGIDYKGFSPAFOLLNVVSRANCKITML 360
DB 301 VSCFOLVQANRNKKVYLKDAVNNITANGIDYKGFSPAFOLLNVVSRANCKITML 360
QY 361 FPDGGEERAQEIFANKDKKRVTFVSGVGHNDGRPIOMWACENKGYEISIGAIR 420
DB 361 FPDGGEERAQEIFANKDKKRVTFVSGVGHNDGRPIOMWACENKGYEISIGAIR 420
QY 421 INTQYLVIVLGRPMVLADGKAKOVQWTVVYLDALGLVITGLTLPVNTICQENKTNL 480
DB 421 INTQYLVIVLGRPMVLADGKAKOVQWTVVYLDALGLVITGLTLPVNTICQENKTNL 480
QY 481 NGLILGVAVVSLIEDIRLTPRFLCPNGYFAIDPAGYLLHPNLOPKPKSOEPTL 540
DB 481 NGLILGVAVVSLIEDIRLTPRFLCPNGYFAIDPAGYLLHPNLOPKPKSOEPTL 540
QY 541 DFLAELENDIKVEIRKMDIGESGEKTFRLVRSQDERYIDKGNRTYTWTPVNGTDSL 600
DB 541 DFLAELENDIKVEIRKMDIGESGEKTFRLVRSQDERYIDKGNRTYTWTPVNGTDSL 600
QY 601 ALVLPYTFYIKAKIETITQARSKGKMDSEFLKPDNEESGTYFIARVDCNDLKI 660
DB 601 ALVLPYTFYIKAKIETITQARSKGKMDSEFLKPDNEESGTYFIARVDCNDLKI 660

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```

QY 661 SDNTEFLNENEFIDRKPNNPSCNTDILNVLADAGFTNELYONVWSKONIKGYAR 720
DB 661 SDNTEFLNENEFIDRKPNNPSCNTDILNVLADAGFTNELYONVWSKONIKGYAR 720
QY 721 EYVYVYNAKDDLPPEKNDSPGSGRIKPVIEDANFGROISVQAAVHPDIDYESTYL 180
DB 721 EYVYVYNAKDDLPPEKNDSPGSGRIKPVIEDANFGROISVQAAVHPDIDYESTYL 180
QY 781 MYSKAVEIYIOGKLKPAVVGKIDVNSWIEFRTSTIRDCACPVDCCKNSVDMCVI 840
DB 781 MYSKAVEIYIOGKLKPAVVGKIDVNSWIEFRTSTIRDCACPVDCCKNSVDMCVI 840
QY 841 IDDGSEFLMANHDYTNQIGRFGEIDPSLRHLVNIISVAFNSYDQVSCBPAAPKQ 900
DB 841 IDDGSEFLMANHDYTNQIGRFGEIDPSLRHLVNIISVAFNSYDQVSCBPAAPKQ 900
QY 901 GAGHSASVPSIADLIHGMWATAAASIILOOFLISTEPRLAEVEMEDDFTASLSKQ 960
DB 901 GAGHSASVPSIADLIHGMWATAAASIILOOFLISTEPRLAEVEMEDDFTASLSKQ 960
QY 961 SCITQOTQYFFDNDKSKFSGVLDGCGNSRIFHYKIMNTNLIETVWSKGTCPDTRL 1018
DB 961 SCITQOTQYFFDNDKSKFSGVLDGCGNSRIFHYKIMNTNLIETVWSKGTCPDTRL 1018

```

```

RESULT 2
CIC2_RAT STANDARD; PRT: 1091 AA.
ID P54290:
AC 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 11-JUN-2002 (Rel. 41, Last annotation update)
DE Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta
DE subunits precursor.
GN CACNA2D1 OR CACNA2L2 OR CCHL2A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP MEDLINE=92228762; PubMed=1314383;
RA Kim H.L., Kim H., Lee P., King R.G., Chin H.;
RT "Rat brain expresses an alternatively spliced form of the
RT dihydropyridine-sensitive L-type calcium channel alpha 2 subunit.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:3251-3255(1992).
CC -1- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN
CC EXCITATION-CONTRACTION COUPLING.
CC -1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:
CC ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS
CC HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM
CC A PRECURSOR FORM (BY SIMILARITY).
CC -1- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.
CC -1- SIMILARITY: CONTAINS 1 WFA DOMAIN.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb.slb.ch).
CC -----
DR EMBL: M86621; AAA1088.1; -
DR InterPro: IPR004010; Cache.
DR InterPro: IPR002035; WFA_A.
DR Pfam: PF00092; WFA; 1.
DR Pfam: PF02743; Cache; 1.

```



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2003, 14:13:50 ; Search time 9.33945 Seconds

(without alignments)  
4520.920 Million cell updates/sec

Title: US-10-090-827-6

Perfect score: 5349  
Sequence: 1 MAAGCIALATLTLFQSLILG.....TNLIFIMESKGTCPDTRL 1018

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5288	98.9	1091	1	CIC2_HUMAN
2	5174	96.7	1091	1	CIC2_RAT
3	5156.5	96.4	1106	1	CIC2_RABIT
4	739.5	13.8	1205	1	Y1J9_CAEEL
5	611	11.4	734	1	UN36_CAEEL
6	196.5	3.7	886	1	ITR3_MOUSE
7	185	3.5	885	1	ITR3_HUMAN
8	183.5	3.4	887	1	ITR3_RAT
9	168.5	3.2	575	1	YF8K_ECOLI
10	162	3.1	886	1	ITR3_MESAU
11	162	3.0	1829	1	DPOL_THEST
12	160.5	3.0	420	1	Y103_SYNY3
13	155.5	2.9	946	1	ITR2_HUMAN
14	155	2.9	1956	1	ATX1_PLAFA
15	153	2.9	946	1	ITR2_MESAU
16	149.5	2.8	654	1	MCPC_BACSU
17	149.5	2.8	921	1	ITR4_PIG
18	147	2.7	1087	1	XYNX_CLOTM
19	144.5	2.7	929	1	CALC_NOTVI
20	144	2.7	930	1	ITR4_HUMAN
21	143.5	2.7	935	1	ITR2_PIG
22	142	2.7	964	1	DPOL_CHEPV
23	142	2.7	3063	1	CALC_HUMAN
24	141.5	2.6	946	1	ITR2_MOUSE
25	141	2.6	1290	1	BXCI_CLOBO
26	140.5	2.6	764	1	PAG_BACAN
27	140	2.6	1180	1	C4AA_BACCTI
28	138.5	2.6	382	1	Y1J0_CAEEL
29	137.5	2.6	862	1	MUTS_BORBU
30	137	2.6	3305	1	APLP_MANSE
31	136	2.5	697	1	YE9G_SCHPO
32	134	2.5	1251	1	RBP2_PLAIVB
33	133	2.5	1169	1	SMC_METUA

34	132	2.5	984	1	HYSA_STRAG	Q53591 streptococ
35	132	2.5	1875	1	MLP1_YEAST	Q02455 saccharomyc
36	131.5	2.5	1487	1	BLM_DROME	Q9V618 drosophila
37	131	2.4	1513	1	STUI_YEAST	P38198 saccharomyc
38	131	2.4	2710	1	TOXA_CRODI	P16154 clostridium
39	131	2.4	3119	1	CALC_MOUSE	Q60847 mus musculu
40	130.5	2.4	1323	1	ADRI_YEAST	P07748 saccharomyc
41	130	2.4	3712	1	IMA_DROME	Q00174 drosophila
42	129.5	2.4	1254	1	UBPC_YEAST	P39538 saccharomyc
43	128.5	2.4	547	1	SYM_BICAI	P57210 buchnera ap
44	128	2.4	1658	1	YM67_YEAST	Q03661 saccharomyc
45	127.5	2.4	1176	1	SLAP_BACSH	P38537 bacillus sp

## ALIGNMENTS

RESULT 1	ID	CIC2_HUMAN	STANDARD;	PRT;	1091 AA.
AC	P54289;				
DT	01-OCT-1996 (Rel. 34, Created)				
DT	01-OCT-1996 (Rel. 34, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta				
DE	subunits precursor.				
GN	CACNA2D1 OR CACNA12A OR CCHL2A.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
ON	NCBI_TaxID=9606;				
OX	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=9211010; PubMed=1309651;				
RA	Williams M.E., Feldman D.H., McGue A.F., Brenner R.,				
RA	Wellcreek G., Ellis S.B., Harpold M.M.;				
RT	Structure and functional expression of alpha 1, alpha 2, and beta				
RT	subunits of a novel human neuronal calcium channel subtype.";				
RL	Neuron 8:71-84(1992).				
CC	- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN				
CC	EXCITATION-CONTRACTION COUPLING.				
CC	- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:				
CC	ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS				
CC	HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).				
CC	- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	- TISSUE SPECIFICITY: CENTRAL NERVOUS SYSTEM, SKELETAL MUSCLE AND				
CC	AORTA TISSUES.				
CC	- PFM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM				
CC	A PRECURSOR FORM (BY SIMILARITY)				
CC	- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.				
CC	- SIMILARITY: CONTAINS 1 WVF DOMAIN.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>				
CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).				
CC	EMBL; M76559; AAA51903.1; -				
DR	Genew; HGNC:1399; CACNA2D1.				
DR	MIM; 114204; -				
DR	InterPro; IPR004010; Cache.				
DR	InterPro; IPR002035; WVF_A.				
DR	Pfam; PF00092; wva; 1.				
DR	Pfam; PF02743; Cache; 1.				
DR	SMART; SM00327; WVF; 1.				
DR	PROSITE; PS50334; WVF; 1.				
KW	Ionic channel, Transmembrane; Ion transport; Voltage-gated channel;				
KW	Calcium channel; Glycoprotein; Phosphorylation; Signal.				
FT	SIGNAL	1	24	POTENTIAL.	
FT	CHAIN	25	944	L-TYPE CALCIUM CHANNEL. ALPHA-2 SUBUNIT	



```

Db 310 SDPLPTITQ-VOTQVQPSDVOVQESITLTLAKYRQTOIETKIKGDRGCAATMLQTAAK 368
QY 591 TPVNGDYSIALVLPYSEFYIAKIEETITQARSKKGMKSETLKP 638
Db 369 TALOMGDKNGATILQNTA---TRLOSGEDLSGDRKKTMTVMKSTLIQ 413

RESULT 15
140884
cytoxin L - Clostridium sordeilli
C:Species: Clostridium sordeilli
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 15-Oct-1999
C:Accession: I40884
R:Green, G.A.; Schue, V.; Montell, H.
Gene 161, 57-61, 1995
A:Title: Cloning and characterization of the cytoxin L-encoding gene of Clostridium so
A:Reference number: I40884; MUID:95369733; PMID:7642137
A:Accession: I40884
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2364 <RBS>
A:Cross-References: EMBL:X82638; NID:g1000694; PIDN:CAA57959.1; PID:g1000695
C:Superfamily: cpl repeat homology
C:Keywords: cytoxin

Query Match 3.0%; Score 160.5; DB 2; Length 2364;
Best Local Similarity 18.0%; Pred. No. 0.64;
Matches 219; Conservative 142; Mismatches 346; Indels 513; Gaps 58;

QY 6 LALATLTLQSLIGPSQEPFPAATIKSWVDKMGEDLVTLAKTASGNOIVD----- 59
Db 1066 IMAVNTITASTAIV-----TSALGIASFSIL---LVPLAGISAGIPSLVNNELIIO 1114
QY 60 -----IYERYODLYVEPNNAQV-----EIAARDIEKLNSRSKALVRLAE 105
Db 1115 DKATKVIDYFKHISLAETGCAFLTDKTIPODDLVEID--FNNSITLGKEIMRA 1172
QY 106 KYQAAMHOMED---FASNEVY---YNA---KDDLPDK----- 135
Db 1173 EGSGHTLTDIDHFFSPSITRYKPMWLSIYDLNKKKIDFSKDLMLVLPNAPNRVGV 1232
QY 136 -----NDEPFGSQRIRP-----VFIDANFGR-QLSYOAAVHIPD 171
Db 1233 EMGWTPGFSLNDGKLLDRIRHDEGQFYRYFAFLDALITLKRYEETNTRIND 1292
QY 172 IYEGSTIVLNLMTSALDEVEFKKREDDPSLLQVFGSATGLARYYPASPVWNSRTPN 231
Db 1293 GMTRSFIV-----PVITTEQIRKN-----LSYSFGS--CGSYSLSPYNNM----- 1333
QY 232 KITDLVRRRRPYIGASAPKMDLLIVSGSVGLITKLRTSVSEMLETISDDDFVAV 291
Db 1334 -IDLNLVENDTV-----VIDDVYKNITIESEIQKELENT----- 1371
QY 292 ASFNSNAQDVSCFOHLYQANVRNKKVLKDAVNNITAK---GITDYKKGFSPAFEOQLNVN 348
Db 1372 -----LSKINIEDNKII---LNNHTINFYGDINESNRPISLFSILEDIN 1413
QY 349 -----VSRA-----NCKIIMLFTD-----GGEERAQEIFA-----KYN- 377
Db 1414 IITLIDLVSKSYKILLSCMCKLIENSSDIQKIDHIGFNGEHQKIPYSYIDNETKYNG 1473
QY 378 ---KDKKRVVETFSVGQNNHYDGFQWMAACEKGYEYELPSIGAIRINTQETLDVLRPM 434
Db 1474 FIDYSKKEGLTAEPFSNESIIRN--TYPDSNNLFYSSKDKLDIRINK-----GDVK 1525
QY 435 VLAGDKAKO-----VQMTNVYDALELGLVITGLPVPFNITGQNNENKTNL 479
Db 1526 LLIQNTFKDMKVSLSFTIEDNTIKNGVLYDE-----NGVAQILKFMNNAKSALNT 1578
QY 480 KQOLLIGWGVDSLEDIKRLTPRTLCPNGYFAIDPNGVYLLHPNLQPKNPKSQEPVT 539
Db 1579 SNSLNMFESINIK-----NIFYNNLDPNIEFILDTNF----- 1611

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QY 540 LDFLDALELNDIKVEIRNMKIDGSGEKTFRILYKSDERYIDKGNRTYTWTVPNGTDYS 599
Db 1612 -----IISGNSISQFE-LICDDKN----- 1631
QY 600 LALVLPYSEFYIAKIEETITQARSKKGMKSETLKPDNEEGSYFTIAPRDYCNL 659
Db 1632 ---IOP---YFINKEIKET-----SYTLVYGNRON---LIVEPSYHLDD-- 1666
QY 660 ISDNTEFLNENE---FIDR---KTPNNSCMTDLIN-----RYLDPAGF 699
Db 1667 -SGNISSTVINFQKYLXGIDRYNKKYIADNLYTDELINTPYKPNVICOPEVILLDANY 1725
QY 700 TNE-----LVQNVY-----SKQNRINGKARFVTDGITRVYPKRAGE 738
Db 1726 INEKINVININDLSIRYVMDNDSPLLILIANSEEDNOQVKIRFV-----NVEKSDTAA 1778
QY 739 -----NMQENE-----TEDSYKR-----SLDNDNYVFTIAPYENKSGPGA 775
Db 1779 DKLSPFSDKODSVSKIIITFSLAAYSDGFDEYFGLVSLDND-----YFYINSFGN 1831
QY 776 YESGIMVSKAVEIYIOGKL--LKP---AVYGI-KIDVNSWIENTKTSIRDPQAGPYCD 828
Db 1832 MVSGL-----IYINDSLYFKRPKNLITGFTTIDGNKYFPDPTKSG-----AAST-- 1877
QY 829 CKRNSDVNDVILDDGCFLLMANHDDYTNN-----QIG-----RPF---GEIDPSLMR 872
Db 1878 -----GEITIDGKDYFNKQILQYGVINTSDGLKYFAPAGTIDENLEG 1921
QY 873 HLNVN-----SVYAFNKSIDYDQVSCFPCAAKQAGHRSATVPSIADILHIGWATA 924
Db 1922 ESNVFIGLNLIDGKIYFEDNY-----RAA 1946
QY 925 AAWSILOQFLSLTFPRLLEAVEMEDDEFTASLSKQSCITEPOYFPDNDKSPSGVLD 984
Db 1947 VEMKLLD-----DEITYFPKTKGALKGLHQI 1973
QY 985 GNCRIHFVEKLMNTNLIET 1004
Db 1974 GDNRYFEDDNGIMOTGFYTI 1993

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Search completed: February 10, 2003, 14:21:45  
 Job time : 29.3759 secs

that the complexes play important role for pancreatic cancer.  
C:Superfamily: inter-alpha-trypsin inhibitor complex component II  
F:236-239,664-865/Disulfide bonds: #status predicted

Query Match 3.1%; Score 166; DB 2; Length 889;  
Best Local Similarity 23.2%; Pred. No. 0.064;  
Matches 66; Conservative 57; Mismatches 111; Indels 51; Gaps 11;

QY 202 SLMOYVGSATGLARYPASPMDNSRT-PNKID-----LYVRRR-PWYIGA-- 248  
DB 211 SALTSPSGKKGVSEKPS--LDQOQSCPTCTSLINDGFTIVYVNRSPGVYVNG 267  
QY 249 -----ASPKMDLLVDGSGVSGITLKLRTSVSEMLFTLSDDEPNVAFSPNS 296  
DB 268 YVHFHFAPOGLPVPRKIVVIDISGMGRKIQOTRVALTKLDDMKQDDYINFLFST 327  
QY 297 MAODVSCQHLVOANVRNKKVLDVANNITAKGIDYKGFSAFEGQLN-----YVNSRA 352  
DB 328 GV--TWKDSLVOATPANTLEARTFVRSISDQGMTNINDLGLGIMLTARQHTVPER 385  
QY 353 NCKMTLFTDQ-----GEERAQELFAKYNKDKRVYFTSVG-QHNYDRGPIQMACEK 407  
DB 386 STSIIML-TDGDANTGESPEKIQENVRKALIEGRPLYNLGFNNLNYFLETMALENH 444  
QY 408 GYVVEIPISGAIRINTQEVLDVGRPVVLADGKAKOVQWNTVYL 452  
DB 445 GVARRIEDSDANLQLOGFEYEVANPL-----TNVEVE 478

## RESULT 13

F64688  
Proteinase (EC 3.4.-.-) - Helicobacter pylori (strain 26695)  
C:Species: Helicobacter pylori  
C:Date: 09-Aug-1997 #sequence-revision 15-Aug-1997 #text-change 29-Sep-1999  
C:Accession: F64688  
R/Tomb: J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.; Nature 388, 539-547, 1997  
A:Authors: Wallin, E.; Hayes, W.S.; Bordovsky, M.; Karpek, P.D.; Smith, H.O.; Fraser, C.  
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.  
A:Reference number: A64520; MUID:97394467; PMID:9252185  
A:Accession: F64688  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-459 <TOM>  
A:Cross-references: GB:AE000636; GB:AE000511; NID:g2314517; PIDN:AAD08394.1; PID:g231452  
C:Genetics:  
A:Start codon: GTG  
C:Superfamily: carboxyl-terminal processing proteinase  
C:Keywords: hydrolase

Query Match 3.1%; Score 165; DB 2; Length 459;  
Best Local Similarity 22.2%; Pred. No. 0.026;  
Matches 138; Conservative 69; Mismatches 198; Indels 216; Gaps 30;

QY 6 LLAATLTLFQSLIGSSQEPFSAVTKSMVDMQEDVTLAKTASGV-----NOTV 58  
DB 3 LMTTKLFLGGLAVSLAVSLHGGVEYKPKVPKEDPELA--AKVFAFRSFWVS 60  
QY 59 DIYEKYODLTYVEPNNAKQVETAAARDIEKLSNRKALVRLALEAKVQAAHQWRDPA 118  
DB 61 EIEKKYVDKISIS-----EIMTKAIEGLISNLD-----AHS----- 91  
QY 119 SNEVYVYNAKDDLDPEKNDSEPSQRIRKPFIDANGRQISYQHAHVIPTIYEGSTI 178  
DB 92 ----AYLN-----EKKFRE-----FOATBEGFGLGITTVMKRGVLT 125  
QY 179 VLNEMLNTSAL-----DEVFKNRREDDPSLMOVFGSATGLARYYPASPWNDSKTPN 231  
DB 126 VIAPLESTPAYKAGVSGNIIKINNE--STLSMSIDAINIMRGKPKP----- 173  
QY 232 KIDLYVRRRWYIQCAAFKDML--LLVDVSGSVSGITLKLRTSVSEMLFTLSDDDV 289

DB 174 -IQITVVRKN-----EPKRVENIIRDI-----ILPSVYVKKIKET--PIYLV 214  
QY 290 NVASFRNSAODVSCQHLVOANVRNKKVLDVANNITAKGIDYKGFSAF----- 341  
DB 215 RVSGFDKNVTK-SVLEGL-KANPKAKGIVLDLRGN--PGGLINQAVGSLNFIKGVLYS 270  
QY 342 -----EOLNANVRAN-----CNKIIMLTDDGEERAQELFAKYNKDKRVYFTSVG 390  
DB 271 QKQKKKEENLEY--KANGRAPYTNLPLAVLVNGSGASASAVAGALDDHRAVI--TG 324  
QY 391 QHNYDRGPIQMACEKGYVEIPISGAIRINTQEVLDVGRPVVLADGKAKOVQWNTV 450  
DB 325 EKFPGKSGQMLPVNKO-----EAKKITTAARYLPSGR-----TIQAGIT 366  
QY 451 LDALGLVYITGTLFVFNITGONENKTLKNOILLGVGVDSLEDIKRLTPRTLLCPNG 510  
DB 367 PDI-----VYIPGKVP-----ENENKPSLKE-----ADLKH----- 392  
QY 511 YVFAIDPNGVYLH-----PNLQPNKPSQEPVTLDFDALELNDIKYIRKMKIDR-- 563  
DB 393 -----HLEQELKTIIDKTPNSKE-----ADKQKKEEKETTPKMINDDIQ 433  
QY 564 -----SGEKFPRLVKSQDER 579  
DB 434 LKTAIDSLKTSIIVDEKMEK 454

## RESULT 14

S76691  
hypothetical protein - Synechocystis sp. (strain PCC 6803)  
C:Species: Synechocystis sp.  
A:Variety: PCC 6803  
C:Date: 25-Apr-1997 #sequence-revision 25-Apr-1997 #text-change 08-Oct-1999  
C:Accession: S76691  
R/Kaneiko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O.; K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas  
DNA Res. 3, 109-136, 1996  
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis.  
A:Reference number: S74322; MUID:97061201; PMID:8905231  
A:Accession: S76691  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-420 <KAN>  
A:Cross-references: EXBL:D64004; GB:AB001339; NID:91001701; PIDN:BAI0635.1; PID:d101  
A>Note: the nucleotide sequence was submitted to the EXBL Data Library, June 1996

Query Match 3.0%; Score 160.5; DB 2; Length 420;  
Best Local Similarity 21.1%; Pred. No. 0.042;  
Matches 86; Conservative 86; Mismatches 181; Indels 55; Gaps 16;

QY 251 PKDMLIVDVSGSVSGITLKLRTSVSEMLFTLSDDEPNVAVNSNADVSCQHLVQA 310  
DB 41 PLNLCLVLDHSGSGMDGQPLETVKSAALGLIDRLIEDDRISVIAFDHRAKIV-----IENQ 95  
QY 311 NVRNKKVLDVANNITAKGIDYKGFSAFEGQLNLYNVNSPANCNKIIMLTDDGGEERAQ 370  
DB 96 QVRNGAALAKALERLAKBEGTALIDGLKLGIDQEAQKEDRS--HIFILTDGSENHGD 152  
QY 371 E-----IFAKYNKDKRVYFTSVGQHNDRGPIQMACEKNG--YVVEIPISGAIRINTQ 424  
DB 153 NDRCKLGTVASDYKLTLYTTLGFGDH--WNQDVLFAIASAGSLSIYNPS--EALHTPRQ 210  
QY 425 EYLDVLRWVLAGSKAKOVQWNTVYLDALLEG--LVITGTLFVFNITGONENKTLK 480  
DB 211 LF-----ORMSNVGLTNAHL-LLELAPDAHLAI--VKPVAQVSPETMDLT-VQ 254  
QY 481 NOLLIGVMGVDSLEDIKRLTPRTLLCPNGYFAIDPNGVYLHPNLOPKPKPSQE----- 536  
DB 255 NGALIEEVRALGDLMDQGERV-----LLNLVYLDQLPGQHYIGVQVIYDDPASPQNTLL 309  
QY 537 ----PVTLDFDALELNDIKYIRKMKIDGSEKET--FRLVWSQDERVYIDKGNRYTW 590



R;Bourguignon, J.  
 submitted to the EMBL data library, June 1992  
 A:Reference number: S34123  
 A:Accession: S34123  
 A:Molecule type: mRNA  
 A:Residues: 1-310, 'K', 312-343, 'R', 345-885 <BOU2>  
 A:Cross-references: EMBL:X67055; NID:9288562; PIDD:CAA47439.1; PID:9288563  
 R;Diarra-Mehpout, M.; Bourguignon, J.; Sessbouee, R.; Mattei, M.G.; Passage, E.; Salier, Eur. J. Biochem. 179, 147-154, 1989  
 A:Title: Human plasma inter-alpha-trypsin inhibitor is encoded by four genes on three chromosomes  
 A:Reference number: S02141; MUID:89137072; PMID:2465147  
 A:Accession: S02141  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 341-356, 'G', 358-845, 'H', 847-885 <DIA1>  
 A:Cross-references: EMBL:X14690; NID:935464; PIDD:CAA32821.1; PID:935465  
 R;Engblid, J.J.; Thøgersen, I.B.; Pizzo, S.V.; Salvesen, G.  
 J. Biol. Chem. 264, 15975-15981, 1989  
 A:Title: Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-alpha-1  
 A:Reference number: A92736; MUID:89380192; PMID:2476436  
 A:Accession: D34245  
 A:Molecule type: protein  
 A:Residues: 30-49 <ENG1>  
 R;Engblid, J.J.; Salvesen, G.; Hefta, S.A.; Thøgersen, I.B.; Rutherford, S.; Pizzo, S.V.  
 J. Biol. Chem. 266, 747-751, 1991  
 A:Title: Chondroitin 4-sulfate covalently cross-links the chains of the human blood prot  
 A:Reference number: A39079; MUID:91093267; PMID:1898736  
 A:Accession: A39079  
 A:Molecule type: protein  
 A:Residues: 631-647 <ENG2>  
 R;Diarra-Mehpout, M.; Bourguignon, J.; Sarafan, N.; Bost, F.; Sessbouee, R.; Muschio-Bon  
 Biochim. Biophys. Acta 1219, 551-554, 1994  
 A:Title: Tandem orientation of the inter-alpha-trypsin inhibitor heavy chain H1 and H3 g  
 A:Reference number: S50132; MUID:95002116; PMID:7522574  
 A:Accession: S50132  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-27 <DIA2>  
 A:Cross-references: EMBL:X75318  
 R;Misiulewicz, H.G.; Burgess, W.H.; Oppenheim, J.D.; Vilcek, J.  
 Biochemistry 33, 7423-7429, 1994  
 A:Title: TSG-6, an arthritis-associated hyaluronan binding protein, forms a stable comp  
 A:Reference number: A53642; MUID:94271799; PMID:7516184  
 A:Accession: B53642  
 A:Molecule type: protein  
 A:Residues: 30-34, 'X' <WIS>  
 R;Jessen, T.E.; Faarvang, K.L.; Ploug, M.  
 FEBS Lett. 230, 195-200, 1988  
 A:Title: Carbohydrate as covalent crosslink in human inter-alpha-trypsin inhibitor: a no  
 A:Reference number: S02431; MUID:88167187; PMID:2450785  
 A:Accession: A59167  
 A:Molecule type: protein  
 A:Residues: 30-32, 'GEKEQAVDT' <JES>  
 C:Comment: As pre-alpha-inhibitor, this protein is covalently cross-linked by chondroitin  
 C:Genetics: GDB:ITIH3  
 A:Gene: GDB:ITIH3  
 A:Cross-references: GDB:120109; OMIM:146650  
 A:Map position: 3p13-3p12  
 C:Superfamily: Inter-alpha-trypsin inhibitor complex component II  
 C:Keywords: chondroitin sulfate proteoglycan, glycoprotein, heterodimer, proteinase inh  
 F:1-19/Domin: signal sequence #status predicted <Sto>  
 F:20-29/Domin: signal sequence #status predicted <Sto>  
 F:30-647/Product: Inter-alpha-trypsin inhibitor heavy chain 3 #status experimental <MAT>  
 F:548-885/Domin: carboxyl-terminal propeptide #status predicted <CTP>  
 F:87-576/Binding site: carboxylate (Asp) (covalent) #status predicted  
 F:647/Modified site: chondroitin sulfate ester carboxyl end (Asp) (in mature form) #stat

Query Match 3.5%; Score 188; DB 2; Length 885;  
 Best Local Similarity 21.5%; Pred. No. 0.003;  
 Matches 138; Conservative 112; Mismatches 243; Indels 150; Gaps 36;

45 VTLAKTASGVNQLVDYERKODLYTEPNNAARQLVEIAADIEKLSSNRKALVRLALEA 104

Db 77 VELPKAFITNPLTIT-----DGVTY-PCNVKE-KEVAKQYKAVSOGKTAGL----- 123  
 Qy 105 EKYQAAHQRDEP-----ASNEVYTYAKADDLPEKNDSEPGSQRKPFITDANGR 157  
 Db 124 --VKASGRLEKFTVSVNVAAGSKYFELTYELLRRHKGXYMLKQV-----K 172  
 Qy 158 QLSYQAAHPIPDYEGSTIVLNLMTSALDEFKRRKREDEPGLMOCFSA-----T 212  
 Db 173 QL-VKHFEEV--DIFEPQGT-----SMD-----AEASTITDLGSLATKFS 214  
 Qy 213 GLARYYPASPMWNSRT-PNKID-----LYVRRRP-----WTI-----OG- 247  
 Db 215 GKGHVSFKPSIDQRCPTCTDNLNGDFTTYVNSRPGNVQIVANGVFHFAPQGL 274  
 Qy 248 AASPKDMLLVDSGVSGLTKLRTSYSEMELFSDDDPVNVAFSNADVSCF-QH 306  
 Db 275 PVVKNVAVVIDISGSMARKLEQTKELRLLEMOEDYINFLFSG--DVTWEH 331  
 Qy 307 LVQANVRNKKVLKDAVNNITAKGIDYKGFSAFEPOLLNVSR-----ANCKIIML 360  
 Db 332 LVQATPENTQEAQTYKSMEDKGMNINDGLRGLSML--NKAEHRIRPERSTIYM 388  
 Qy 361 FTDG-----GEERAQETFAKYN--DKYRVFTFSVGHNYDGPLOMACENKGYEIP 414  
 Db 389 LINDGANVESRPEKIQEVRNAIGKRPFLYNLGGF--NNLNVNPLENMALEHGFARIT 447  
 Qy 415 SIGAIRINQELDLVGRMYLAGSKAKOVCTNYDALE-----LGLVITGLP 465  
 Db 448 EDSADLQLGFEVYANPL-LTGVMEYEP--NAILLDTQNTQHFYDSEIIVAGRLV 504  
 Qy 466 VENITGONENKTNLK-----NOLILGVMGVDSLEDIRLPRFLCPNGYFAIDPN-- 518  
 Db 505 DEDM--NSFKADVGHGATNLL--TTEVDKMEKEMK-----ALQERDITFG--NYI 550  
 Qy 519 ----GVLHPMLQK--NPKSQEPVILDFDALENDIKVLRNKKMIDGSEKERT 571  
 Db 551 ERLMAVLTLEQLLEKRNKNAHGEKENTLARAALDSIKHFVPLTSMVTPKE----- 603  
 Qy 572 LVKSODERYI-DKGNRTYTWTPVN-GTDSLALVLPFSFYI 612  
 Db 604 --DNEDERALADKPGEDAEATVVSAMSLTISYQPPNPYYIV 644

RESULT 10  
 D97033  
 uncharacterized protein, probably surface-located [imported] - Clostridium acetobutyli  
 C:Species: Clostridium acetobutylicum  
 C:date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001  
 C:Accession: D97033  
 R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; zeng, Q.; Gibson, R.; L  
 J. Bacteriol. 183, 4823-4838, 2001  
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium  
 A:Reference number: A96900; MUID:21359325; PMID:21359325  
 A:Accession: D97033  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1819 <KUR>  
 A:Cross-references: GB:AE001437; PIDD:AAK79055.1; PID:915023996; GSPDB:GN00168  
 A:Experimental source: Clostridium acetobutylicum ATCC824  
 C:Genetics: CAC1081  
 A:Gene: CAC1081

Query Match 3.2%; Score 170.5; DB 2; Length 1819;  
 Best Local Similarity 18.8%; Pred. No. 0.11;  
 Matches 194; Conservative 153; Mismatches 334; Indels 351; Gaps 53;

24 QEPFSAVYIKSWVKMOEDL-VTLAKTASGVNQLVD-----IYKYQDLYTEPNNA 75  
 Db 133 EQGKNARSKG-ALUTDEIGTITANSTDSIKGIFDMGTGAVNSDYQFLITQVNSN 191  
 Qy 76 ROLVETIARDIEKLSSNRKALV-----RLALEKVOAAHQWRDFAASNEVYVNA 127

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Db 449 EDSNALQLOGFEYEVANPL-----TNYEVEYEPNA-----ILLDTNRSY 489
Qy 475 NKTNLKNOILLGWDVSLIEDIKRLTPRETLCPNGYYPALDPNGYVLHPNLOPKNKS 534
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 490 PHEYDSEIIVAGRLVDRMNDN-----FKADYKGGHGLN-----DLTF 527
Qy 535 QEYVTLDFDALDELDAIKKRNKMDGSEK--TFRLVKSQDERITDKGNRTYTP 592
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 528 TEEVDMEEDDAALK-----EÖGYIFGDYIERLMAVITLQGLKRNKAKDEKENIT 579
Qy 593 VNGTDSLAL--LVLPYSPFYIKAKLEITQARSKKCKMKDSEF-----LKPDPNEESG 645
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 580 AEMLDLSLKHHTVPLTSNMYTKRPEDNEDQTSIADNAGEAFAETTSFLTQOSSSP 639
Qy 646 YFFIAPRDYCNLDKISDNTEFLNFEIDRKTPNPSCNTDLINRYLLDAGFTNELVQ 705
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 640 YYYV-----DGDPHFIIQI-----PCKNDISCFNIDKPGVLRILIQ 676
Qy 706 NWSKOKNIKVKARFVYTDGSTRVYKREAGENNOENPETEDSFYKSLDNDNYVTA 765
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 677 D-----PVT--GIT-VTQGIID-----KRS--NASSRTGK 702
Qy 766 PFYKSGPAYESGILWYKAVEIYQKLLKPAVVGIRKIDVNSWIEFNTKTSIRDPGAP 825
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 703 YTFGKIGITNAMMDPRVEYTTKEILG-----TGAELSTFSWLDYTVQ-----TGL 750
Qy 826 VCDCKRNSDVMDCVILLDG--GFLMAN-----HDDYTNQIGRFEGEIDPSLRHLVN 876
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 751 SVYINKKKMNV--VSEGDISFVILLHWYKKRPHQDPLG-----FYVVDSHRMSAQTH 803
Qy 877 ISVYANFKSYDQSV--CEPGAP 898
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 804 GLDGQFPDFKVFEGIRPGSDP 826

RESULT 8
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C:Accession: C86880
R:Bolotin, A.; Wincker, P.; Manger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s.s.
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: C86880
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1450 <SNO>
A:Cross-references: GB:A8005176; PID:912725093; PIDN:AAK06141.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: yvcc

Query Match 3 6% Score 190.5; DB 2; Length 1450;
Best Local Similarity 19.4%; Pred. No. 0.0046;
Matches 203; Conservative 148; Mismatches 359; Indels 339; Gaps 51;

```

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Qy 224 VDN-----SRTPNKIDLY--DYRRRPYIGASAPKMDLIVDVGSSVGLTLK 270
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 288 VNNPVDALRRYAKETETPGIYDVLNRCN---VQNPDKPVDIVLVIDSGSMQAKET 344
Qy 271 LIRTSVSEMLETSSD---DEVNV--ASFNSNADVSCFQHLVQANRNKKVYLD-----A 321
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 345 AVROGSDLESTIONTAYADVNVGVIGYSSPGNVYVAGSGYITVPI--DKVSESEHVKS 402
Qy 322 VNNITTA---KGIPTYKKGFSFAFQGLNLYNWSRANKKIIIMLFDDGGEBAOEFAFYK 378
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 403 INQALAPQSGGTFTQLGRKGTML---EQDSSDNKKMIIMTLDG---VPFFSYKVN 435
Qy 379 DKYVR--VFETSVQHNDRG---PIQ---WMAECNKYYEYI---PSIGAIRINTOE 425
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 456 ASKYDNYVYGQSFASBREDPNTSKIOSPYVKDINGNSNIEIRDTWAATLGEAISKOE 515
Qy 426 YLDVLRPMVLAGD-----KAKQVMTNVIYDLELGLVITGTLPRVNIQNE 474
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 516 ISEIHTLGIQNGDSYLSQSEYKSRSLATTGLYODANSAN-----DITDYLK 565
Qy 475 NKTN-----LNKOLLGWDVSLIEDIK 498
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 566 NQAVNVLRFNTITNGILDLPLGAGQFEKDKTFITSVGEDSIDNLPFGKINEKLEISN 625
Qy 499 -----RLTPRETLCPNGYYPALDPNGYVLHPNLOPKNPSQ----- 535
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 626 LNIKKNOEVQIHYQVRINTETEDFKTNWYQM--NGETTLTPN--GSPDNKYNVGPVSA 681
Qy 536 --EPTLDFDLAELENDIKVYIRNKMIDG-----SSEKTFRLYKSDERYIDKGRTY 588
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 682 KSSGINLLEKQWLANSNPENVELIGRRSAQISSDWTKYTLKEDD----- 721
Qy 589 TWTPVNGTDVSLALVLPYS-----FYIYIKAKI-----EETIQARSKK 629
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 732 -WR-----SQLENLPYSILGEEFIYEIKDELVLNSELIDWTITGEDTITANIEKR 783
Qy 630 MKDSETLKPDNPFESGYFIAPRDYCN--DKISDNTEFL-----LNENE--FIDRKT 679
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 784 LQILKTSNHDNEPLSEVEFVLKNSQGEIDKAVYNEGELLFDKTRINYEVEYOLHEIKS 843
Qy 680 PNN-----PSCNTD-----LINVLDAAGTNTL--VQNWSKKN 714
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 844 PHSIEGCPWKIKTEFENGQPIIKYDGEQIALDEHYNFKMISLNTINDINVEF---RNS 899
Qy 715 KGVARFVYT---DGGITRVYPKKA--GENWQENP-----EYEDSFYK 753
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 900 VTIDKRAVDSEKLDGAVENLYQIESVDDELQKPLEITNNLLPGYALQESVSPGY 959
Qy 754 RSLDNDNYVFTA-----PYFNKSGPAYESGILWYKAV--EYIQGKL 795
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 960 R--DDEVHFFRVKFNKSGIIVAIGSEGDIDPFLDENESG--KNGLVLNDEMGDLHLTLFY 1015
Qy 796 KPAVYGIKIDVNSWIEFNTKTSIRDPGAG 824
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1016 NQAVPPIQLEVDKIDDDFT-----SPLAG 1039

RESULT 9
S30350
Inter-alpha-trypsin inhibitor heavy chain 3 precursor - human
N:Alternate names: H33; Inter-alpha-trypsin inhibitor chain H3; pre-alpha-inhibitor h
C:Species: Homo sapiens (man)
C:Date: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change 04-Feb-2000
C:Accession: S30350; S34123; S02141; D34245; A39079; S50133; B53642; A59167
R:Bourguignon, J.; Diarra-Mehrpuou, M.; Thiberville, L.; Bost, F.; Sebbouee, R.; Mart
Eur. J. Biochem. 212, 771-776, 1993
A:Title: Human pre-alpha-trypsin inhibitor precursor heavy chain cDNA and deduced ami
A:Reference number: S30350; MUID:93215656; PMID:7681778
A:Accession: S30350
A:Molecule type: mRNA
A:Residues: 1-885 <BOU1>
A:Cross-references: EMBL:X67055; NID:9288562

```

[illegible]

```

Db      187 NGVWSESLNKLVFVNDENRDESLIMQFGSAKGFRRQYPGIKWMPDE---NGVLAIFCRN 243
Qy      241 RRPVIOGAAPKMLLLIVDVGSGVGLTKLIRTSVSEMLETSDDDFVNVASENAOD 300
Db      244 RKMVIOAATSKDVLLIVDVGSMKGLRLTAKOTVSIILDTLDDDFNNITVNEELHY 303
Qy      301 VS-CFO-HLVOANRNKVKLDVANNITANGIDYDKKGFSAFQOLNVANSAN--CNK 336
Db      304 VEPCLNGLTVOADRTNKEHREHLDRKFAKIGMLDALNEANILSDFNHTGOSTGSCQ 363
Qy      357 IIMFTGGERRAOEIPAKYN-KDKKRVPTFSVGOHNDRPIOMWACENKGYEIPS 415
Db      364 AIMLITDGAADYDTLFAKYNMPDRKRIPTYLIGREAFADMLKMACCNKRFPIQIS 423
Qy      416 IGARINTOEYLDLGRPVPLADKAKOYQNTVYLD-----ALEGLVT--TGLT 464
Db      424 LADYQVEMVETLYLSPKVI--DOEHVYVTEAYIDSTLPOAKLADLQGLVLTMTVAM 481
Qy      465 PVENITGONENKTNLKNQILLGVGVDSLEDKRLTPRTLCPNGYFAIDPNGVLLH 524
Db      482 PVES-----KQNETRSKG-ILGVYGVDPVYKELTKTIPKTKIGHYARALTNNGILTH 536
Qy      525 PNIOP---KPKSQEP--VTLDFLAELENDLKEVIRNKKIDEGSEKTFRLVKSODER 579
Db      537 PELRLPYEECKRRKPNYSVDLSEVEMEDRDYV-LRNAMVNKRTGK--FSMEVK----K 589
Qy      580 YIDGNRT-----YTPVNGTGYSLAVLPT-YSFYITAK--LEETITQARSKKGM 630
Db      590 TVDKGRVLYMTNDYYTIDIKIPSLGVALSGHGKGYFRGNTVEBL----- 639
Qy      631 KQSETLKPNFEESGYTFIAPRDYCN-DLKISDNTEFLNFEIDRTPNPNPSCNTDL 689
Db      640 -----HDLHPDVSILADEWSYCNTDLHPEHRLHSQLEALIKYIKGEP-LIQCKEL 690
Qy      690 INNVILADGFTIELVONKMS-----KQNIKGVARFVYDGGITRYVP----- 733
Db      691 IQEVLFLDA-VSAPLEAVETSLANKSENSDKGEVAEFAFGTGTGSLRILFEGABQLTNO 749
Qy      734 --KEGEMNQENPETEYEDSFYKRSIDN--DNYVETAPY----FNKSGGAYSSGIMVSKA 785
Db      750 DELKAGDKENIFNADHPLWYRRAABQLAGSHVYSIPSTGTVNKS-----NVYTAISTS 803
Qy      786 VEIYIQQKLKRAVVGIKIDVNSMILENFTKTSIRDPGAGPVDCRNSDVMDCVLLDDG 845
Db      804 IQLDBERSPVVAAGIGCMKLEFFQKFEWTASRQCASLDGKCSISCDDETVNLCYLIDNG 863
Qy      846 FLTMANHDYTNQIGRFGEDIPSLMRHLVNSVYAFPKSDYQVCEPGAAPKQAGHR 905
Db      864 FLVLS-EDYT-QTGDFFGEVGAVMKLLTMGSFKRLTLVDYQAMCR--ANKSSDSA 917
Qy      906 SAIYVSIADILHIGMMATTAAMSILOFLILSTPRLLEAVEMEDDPTASLSK-----Q 960
Db      918 HGLDIPYKAFV-----SAAKIMIMELVFLVER-----NLCSMWHSMDITAAQKLTLE 967
Qy      961 SCITBQYQFFPDNDKSFSGVLDCNGCRIRHVEKLMNTNLIETIMVSKGTCPCDT 1016
Db      968 PCDTIYPAFVSEKRTKETTGNACDCSKSFVIOIIPSSNLFMYVDS--SCLCES 1021

```

## RESULT 5

S44617  
C50C3.11 protein - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 30-Jun-2001  
R:Favella, A.D.  
submitted to the EMBL Data Library, May 1993  
A:Description: Sequence of the C. elegans cosmid C50C3.  
A:Reference number: S44627  
A:Accession: S44617  
A:Status: preliminary  
A:Molecule type: DNA

A:Residues: 1-734 <FAV>  
A:Cross-references: EMBL:L14433; NID:g289649; PID:g289650  
C:Genetics:  
A:Introns: 24/2; 87/3; 175/1; 259/1; 290/3; 346/3; 460/3; 538/3

Query Match 11.4%; Score 611; DB 2; Length 734;  
Best Local Similarity 26.5%; Pred. No. 7.6e-29;

Matches 179; Conservative 127; Mismatches 261; Indels 108; Gaps 19;

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Qy      47 LAKTAGVQQLDIYEKQDLYTEPPNNAKQVLEIARIDIEKLSNRKAL--VELALEA 104
Db      36 MKETTSKISHETILLQNEKEIVEEOPDPRALKSKRIEDYLYKRSQFAKAKISLEA 95
Qy      105 EKVQAAHQRREDFASNEVYNAKDDLDEPK--NDSEPSORIKP-----VFIDANF-G 156
Db      96 RSRVNDSTVNDPQSKSFLIRFMSAKQNGDGTITYESNHLGKRLKVNETSFNULTQANFTT 155
Qy      157 RQISTQHAANHPTDLYRQSTVVLNLMWTSALDRFVKRNEEDPSLLMQVFGSATGLAR 216
Db      156 LPTSSVSSAVHITPFLYDRNEDLLRKIDW-SDIDAVYRTNREFTKDLAFLQCEAGYMR 214
Qy      217 YYPASPMV--DNGRTFNKIDLYDRRRPWTYIOGAAPKMLLLIVDVGSGVGLTKLIRTS 275
Db      215 YTPASPMWMDN--DEHLDLFDCCNTEWYINSATNSKRVLLIMDMGSMLGQREYVAKQT 272
Qy      276 VSEMLETISDDFPVNVASFNSNA--ODVSCFOHLVQANVKNKTVLDAVANNITAKGTTD 332
Db      273 TEALLETLSHNDYFNIMFKNFTFLDCCNGTNGLLQATMKNKALKRKMDTYOSEGRKE 332
Qy      333 YKKGFSFAPFQOLNIN-----VSRANCKITMLFTDGEERRAOETFAKYNKDKVRVFTF 387
Db      333 YEKALPIAFSVLLDINNCGDNNGACENVYIMLTDDAPNAYKKIFPMYNAADKKVRVFTF 392
Qy      388 SVGOHNDRGPDIOMWACENKGYEIPSIGAIRINTQEYL-----DVGPRVYLAGDKAQ 443
Db      393 LVGDEALIDFNEVRREKACNKRGYMHVAMADVDEKIHHTYIRMSRVGRYKSGOLS-- 450
Qy      444 VQMTNRYVLDALDELQ--VITGTLFPVFNITGQNEKNTN----- 478
Db      451 -WMTGVYRERLYLPPELFAEPVITNQSFVNMKMSRRKIRLQKSEARSRYFTVTSY 509
Qy      479 --LKNQILLGVGVDSLEDKRLTPRTLCPNGYFAIDPNGVLLIHPMLQKPNP----- 532
Db      510 PVIYNETPMGCAAVNITPLEVAQKSHPANIGSYFFMLDQNFVMTHPQLRPIDEFTKY 569
Qy      533 KSGEPVTLDFLD-----AELENDIKVEITNKKMIDG 563
Db      570 HKQYNNMDLLELVGQNONVRSSQSAVSDLVCEGAGNYACVDLRAKRAVKMILTDCD 629
Qy      564 SGEKTFRLVKSODER-----IDK--GNRTYTWTPVNGTGYSLAVLPTYSFYITAKI 616
Db      630 NSD-----VQQLDVLVATELDRVYPQNTYYAEICINHANFVILGAVAKGDDRYVVK 682
Qy      617 EERTQARSKKGMK 631
Db      683 -----QKKYDFGRVK 692

```

## RESULT 6

T18770  
Probable calcium channel protein - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 29-Oct-1999  
R:Sulston, J.  
submitted to the EMBL Data Library, June 1995  
A:Reference number: Z19019  
A:Accession: T18770  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1148 <WII>  
A:Cross-references: EMBL:Z49907; PIDN:CAA90091.1; GSPDB:GN00020; CESP:T24FL.6  
A:Experimental source: clone B0491

```

C>Date: 31-Mar-1992 #sequence-revision 31-Mar-1992 #text-change 22-Jun-1999
C:Accession: S10579; A39518; A33409
R:Ellis, S.B.; Williams, M.E.; Wasy, N.R.; Brenner, R.; Sharp, A.H.; Leung, A.T.; Campe
Science 241, 1661-1664, 1988
A>Title: Sequence and expression of mRNAs encoding the alpha(1) and alpha(2) subunits of
A:Reference number: S10579; MUID:88336904; PMID:2458626
A:Accession: S10579
A:Molecule type: mRNA
A:Residues: 1-1106 <ELL>
A:Cross-references: EMBL:M21948; NID:g164762; PIDD:AAA81562.1; PID:g164763
A>Note: 57-Asn, 106-Tyr, and deletion of 620-ser were also found
R:Jay, S.D.; Sharp, A.H.; Kohl, S.D.; Vedvick, T.S.; Harpell, M.M.; Campbell, K.P.
J. Biol. Chem. 266, 3287-3293, 1991
A>Title: Structural characterization of the dihydropyridine-sensitive calcium channel al
Biochemistry 28, 7820-7828, 1989
A>Title: Subunit composition of the purified dihydropyridine binding protein from skele
A:Reference number: A39518; MUID:91131638; PMID:1847144
A:Accession: A39518
A:Molecule type: protein
A:Residues: 961-973 <JAY>
A>Note: this sequence represents the amino end of a glycosylated peptide that appears af
e at the amino end and identical molecular weights (17k) following deglycosylation
R:Hamilton, K.L.; Hawkes, M.J.; Brush, K.; Cook, R.
Biochemistry 28, 7820-7828, 1989
A>Title: Subunit composition of the purified dihydropyridine binding protein from skele
A:Reference number: A33409; MUID:90122765; PMID:2558713
A:Accession: A33409
A>Status: preliminary
A:Molecule type: protein
A:Residues: 27-44, 'S', '46-47 <HAM>
C:Superfamily: calcium channel alpha-2 chain
C:Keywords: calcium; disulfide bond; glycoprotein; ion channel; membrane protein; phosph
F:1-26/Domains: signal sequence #status predicted <SIG>
F:1-27/106/Product: calcium channel alpha-2 chain #status predicted <Mat>
F:94,138,186,326,350,470,477,606,615,678,697,784,827,891,898,988,1001,1081/Binding site:
Query Match 96.4%; Score 5156.5; DB 1; Length 1106;
Best Local Similarity 95.3%; Pred. No. 3,3e-302;
Matches 991; Conservative 11; Mismatches 9; Indels 29; Gaps 4;
QY 1 MAAGCLALTLTFEFS--LLIGPSSQEPPEPSAVITKSWDKQEDLVTLAKTASGVNOLY 58
Db 1 MAAGPPLAWTLTLMOAWMLILIGPSSSEPEPSPAVITKSWDKQEDLVTLAKTASGVHOLY 60
QY 59 DIYEKYODLYTEPPNNAQOLVETIARDLIELKLSNSKALVRLAEKVOAHHQREDEFA 118
Db 61 DIYEKYODLYTEPPNNAQOLVETIARDLIELKLSNSKALVRLAEKVOAHHQREDEFA 120
QY 119 SNEVYYNAKKDLDEPEKNDSEPGSORIKRVFTIDANFGQISYQHAHHVPTDIYEGSTI 178
Db 121 SNEVYYNAKKDLDEPEKNDSEPGSORIKRVFTIDANFRROVSVOHAHHVPTDIYEGSTI 180
QY 179 VNEINMTNSALDEVRKKKNSEEDPSILMOVFGSATGLARYPPSPVWDSRRTPNKIDELYDV 238
Db 181 VNEINMTNSALDEVRKKKNSEEDPSILMOVFGSATGLARYPPSPVWDSRRTPNKIDELYDV 240
QY 239 RRRPWYIQAASPKDMLILVDVSGSVGLTLKILRTSVSEMLETSLDDEDFVNVASFNSNA 298
Db 241 RRRPWYIQAASPKDMLILVDVSGSVGLTLKILRTSVSEMLETSLDDEDFVNVASFNSNA 300
QY 299 QVVSFGQHLVQAVNRRKATLKDAVNNITAKGTTDYKKGSFPEQLNINVSRANCKNTI 358
Db 301 QVVSFGQHLVQAVNRRKATLKDAVNNITAKGTTDYKKGSFPEQLNINVSRANCKNTI 360
QY 359 MLFTGGEGEAAEIEFAKYKDKKRVRTFSSVQOHNDRPIOMACENKGYEYEIPSTGA 418
Db 361 MLFTGGEGEAAEIEFAKYKDKKRVRTFSSVQOHNDRPIOMACENKGYEYEIPSTGA 420
QY 419 IRLNTOEYLDVIGRPWYLAGDKAKOVQNTNYLDALLEGVLTITGLPVNITGONENKTN 478
Db 421 IRLNTOEYLDVIGRPWYLAGDKAKOVQNTNYLDALLEGVLTITGLPVNITGONENKTN 480
QY 479 LKNOLLIGWGVDSLEDIKRLTPRTLCPNGYFFIIDNGVYLLHPNLQPK----- 530
Db 481 LKNOLLIGWGVDSLEDIKRLTPRTLCPNGYFFIIDNGVYLLHPNLQPKIGVGITP 540

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QY	531	-----NPKSSEPVTLDFDAELDENIYKVEIRKMKLDGSGEFTPLVKSOER	579
Db	541	INLKRKRPVNPSPKSOEVTLDLDFDAELDENIKVEIRKMKLDGSGEFTPLVKSOER	600
QY	580	YIDKGNRIYTWTPVNGTDY-SIALVLPTSPFYVIAKAEETITQARSKGKMKDSETLKP	638
Db	601	YIDKGNRIYTWTPVNGTDYSIALVLPTSPFYVIAKAEETITQARY-----SETLKP	653
QY	639	DNFEESGTFIAPRDYCDLKTISDNNTFFLLNFENFIDRKTPNPNPSCDTDLINRVLIDAG	698
Db	654	DNFEESGTFIAPRDYCDLKPSDNNTFFLLNFENFIDRKTPNPNPSCDTDLINRVLIDAG	713
QY	699	FTNLEIVONYWSEKOKIKIKVKARFYVTDGIRRVYPKEGEMWMOENPETYEDSFYKRSIDN	758
Db	714	FTNLEIVONYWSEKOKIKIKVKARFYVTDGIRRVYPKEGEMWMOENPETYEDSFYKRSIDN	773
QY	759	DNVYETAIFYFNKSGPGAYESGIMVSKAVEIYIOGKLKPAVVGIRKIDVNSWIENFTKTSI	818
Db	774	DNVYETAIFYFNKSGPGAYESGIMVSKAVEIYIOGKLKPAVVGIRKIDVNSWIENFTKTSI	833
QY	819	RDPCAGPVCDCCKRNSDVNDVCIYLLDDGGFLLMANHDDYTNQIGRFGELIDPSLMRLVNIS	878
Db	834	RDPCAGPVCDCCKRNSDVNDVCIYLLDDGGFLLMANHDDYTNQIGRFGELIDPSLMRLVNIS	893
QY	879	VYAFAKSYDYOSVCEPGAPKOGAGHRAVPSIADIIHIGWATPAVAMSIIQOFLSLST	938
Db	894	VYAFAKSYDYOSVCEPGAPKOGAGHRAVPSIADIIHIGWATPAVAMSIIQOFLSLST	953
QY	939	FPRLIEAEMEDDDFTASLSKOSCITEBOTOFPFDDNDSFSFSGVLDGCGNSRIFHYEKLKN	998
Db	954	FPRLIEAEMEDDDFTASMSKOSCITEBOTOFPFDDNDSFSFSGVLDGCGNSRIFHYEKLKN	1013
QY	999	TNLIIFIMWSEKGTCPCDTRL 1018	
Db	1014	TNLIIFIMWSEKGTCPCDTRL 1033	
RESULT 4			
T30256			
calcium channel alpha-2-delta-C chain - mouse			
C:Species: Mus musculus (house mouse)			
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 20-Jun-2000			
C:Accession: T30256			
R:Klugbauer, N.; Lacinova, L.; Marais, E.; Hobom, M.; Hofmann, F.			
A:Title: Molecular diversity of the calcium channel alpha2delta subunit.			
A:Reference number: Z20794			
A:Accession: T30256			
A:Status: Preliminary; translated from GH/EMBL/DBU			
A:Molecule type: mRNA			
A:Residues: 1-1091 <KBL>			
A:Cross-references: R190949; PIDN:CAA09423.1			
A:Experimental source: brain			
C:Superfamily: calcium channel alpha-2 chain			
Query Match			
Best Local Similarity 28.9%; Pred. No. 9, 8e-59;			
Matches 311; Conservative 224; Mismatches 411; Indels 130; Gaps 39.			
QY	3	ACCLIAATITLQSLIGSSOSEPPPSAATIKSWDMKQEDLVYTIAKTASGVNQLDIYIE	62
Db	14	ASALIA-TALLTAALGDVVRSEQLPLSV-VKLMSAFGEIKSTIAKTSGSOLLQKKTK	71
QY	63	KYODLVTVEPNNAARQVEIARDEIKLISNRKALVRLALEKYQAHQWREDFASNEY	122
Db	72	EYEKVADIEIDIGLQVKKLAKIMEMFHKKSAAVRLVAEAEALHKEHPADL--QY	128
QY	123	VYYNAK--DLDPEKNDSEFSQSRIKPVFIDANFGROISYQAAVHIFTDIYESTIYL	180
Db	129	EYFNNAVLIHERKDGNFLEIGKEFI--LAPNDFNNLIPVNISLSYQVPTNYMKNDPAIV	186
QY	181	NELNWTSAIDVEFFKKRRREDPSLIMQVPSGATGLAVIYASPAVVDNSRTPNKKIDLVAVR	240



Db 301 VSCFOHLVQAVNRKVKLADANNITAGITDYKKGFSFAEQLLNTVNSRANKIIML 360  
 Qy 361 FTDGGEERAOEIFAKYNRKQKVRVFTFSVGOHNYDRGPIDMACENKGYEIPISGAIR 420  
 Db 361 FTDGGEERAOEIFAKYNRKQKVRVFTFSVGOHNERGPIDMACENKGYEIPISGAIR 420  
 Qy 421 INTQYLDVIGRPVYLAGDRAKQVOMTNYVLDALDELGLVITGTLPVNTITGQENKTNL 480  
 Db 421 INTQYLDVIGRPVYLAGDRAKQVOMTNYVLDALDELGLVITGTLPVNTITGQENKTNL 480  
 Qy 481 NOLILGVAGVDSLEDIRKLTFRFTLCPNGYFAIDPNGVYLLHPNLOPKNPKSOEPTVL 540  
 Db 481 NOLILGVAGVDSLEDIRKLTFRFTLCPNGYFAIDPNGVYLLHPNLOPKNPKSOEPTVL 540  
 Qy 541 DFLDAELNDIKVEIRKMKIDGESGKFTLVKSODERYIDKGNRTYTWTPVNGTDSYL 600  
 Db 541 DFLDAELNDIKVEIRKMKIDGESGKFTLVKSODERYIDKGNRTYTWTPVNGTDSYL 600  
 Qy 601 ALVLPYTSFYIKAKIEETITQARSKKGMKDSSETLKPDEESGYTFIAPRDYCDLKI 660  
 Db 601 ALVLPYTSFYIKAKIEETITQARSKKGMKDSSETLKPDEESGYTFIAPRDYCDLKI 660  
 Qy 661 SDNNTTEFLNNEFIDRKTPNNPSCNTDLINRYLIDAGFTNELVQYWKSKOKNIKGVKAR 720  
 Db 661 SDNNTTEFLNNEFIDRKTPNNPSCNTDLINRYLIDAGFTNELVQYWKSKOKNIKGVKAR 720  
 Qy 721 FVYVDGKITRYPKEAGNMOENPETEEDSFYKRSIDNDNYVFTAPYFNKSGPGAYESGI 780  
 Db 721 FVYVDGKITRYPKEAGNMOENPETEEDSFYKRSIDNDNYVFTAPYFNKSGPGAYESGI 780  
 Qy 781 MYSKAVEITYOGKILKRPVAVGKIDVNSWIENFTKTSIRDPGAPVCDCKRNSDMDVCY 840  
 Db 781 MYSKAVEITYOGKILKRPVAVGKIDVNSWIENFTKTSIRDPGAPVCDCKRNSDMDVCY 840  
 Qy 841 LDGGEFLMANHDDYNOIGRFGELIDPSLMLRLVNI SYAFNKSYDYOSVCEPGAARQ 900  
 Db 841 LDGGEFLMANHDDYNOIGRFGELIDPSLMLRLVNI SYAFNKSYDYOSVCEPGAARQ 900  
 Qy 901 GAGHRSAYVPSIADILHIGMWATAAAMSTLQOFLSLTFPRLLAEVEMEDDFTASLSKQ 960  
 Db 901 GAGHRSAYVPSIADILHIGMWATAAAMSTLQOFLSLTFPRLLAEVEMEDDFTASLSKQ 960  
 Qy 961 SCITBOTQYFFPNDKSFSGVLDGCGNCSRIFFHEKLMNTNLFIVWESKGTGCPDTRL 1018  
 Db 961 SCITBOTQYFFPNDKSFSGVLDGCGNCSRIFFHEKLMNTNLFIVWESKGTGCPDTRL 1018

## RESULT 2

A44147  
 N:Alternate names: calcium channel protein alpha-2 chain precursor - rat  
 N:Contains: calcium channel alpha-2 chain  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 20-Aug-1999  
 R:Kim, H.L.; Kim, H.; Lee, P.; King, R.G.; Chin, H.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 3251-3255, 1992  
 A:Title: Rat brain expresses an alternatively spliced form of the dihydropyridine-sensit  
 A:Reference number: A44147; MUID:92228762; PMID:1314383  
 A:Accession: A44147  
 A:Status: Preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-1091 <KIM>  
 A:Cross-references: GB:M86621; NID:9203954; PIDN:AAA41088.1; PID:9203955  
 C:Superfamily: calcium channel alpha-2 chain  
 C:Keywords: calcium; glycoprotein; ion channel; transmembrane protein

Query Match 96.7%; Score 5174; DB 2; Length 1091;  
 Best Local Similarity 96.3%; Pred. No. 2,8e-303;  
 Matches 981; Conservative 22; Mismatches 14; Indels 2; Gaps 2;  
 Qy 1 MAAGCLALTLTLFQSLIGPSSQEPSPASVTIKSWDKMQEDLVTLAKTASGVNLVNI 60

Db 1 MAAGCLALTLTLFQSLIGPSSQEPSPASVTIKSWDKMQEDLVTLAKTASGVNLVNI 60  
 Qy 61 YKKYODLYTVEPNNAQOLVETIARDIEKLSNRKALVRLALEKQVAAHQREDFPAS 120  
 Db 61 YKKYODLYTVEPNNAQOLVETIARDIEKLSNRKALVRLALEKQVAAHQREDFPAS 120  
 Qy 121 EYVYNAKDOLDPKENDSPGSOIRIKPVFIDANFGKQISYOHAAVHIPTDIESTIYL 180  
 Db 121 EYVYNAKDOLDPKENDSPGSOIRIKPVFIDANFGKQISYOHAAVHIPTDIESTIYL 180  
 Qy 181 NELMNTSALDEVEFKNRDEPSSILMOYGSATGARVPASPVNDKSRPNKIDLYDVR 240  
 Db 181 NELMNTSALDEVEFKNRDEPSSILMOYGSATGARVPASPVNDKSRPNKIDLYDVR 240  
 Qy 241 RPWYIOGASPKDMLLVDSGVSGITLKLITSVSEMLETISDDPFVNASFNSNAD 300  
 Db 241 RPWYIOGASPKDMLLVDSGVSGITLKLITSVSEMLETISDDPFVNASFNSNAD 300  
 Qy 301 VSCFOHLVQAVNRKVKLADANNITAGITDYKKGFSFAEQLLNTVNSRANKIIML 360  
 Db 301 VSCFOHLVQAVNRKVKLADANNITAGITDYKKGFSFAEQLLNTVNSRANKIIML 360  
 Qy 361 FTDGGEERAOEIFAKYNRKQKVRVFTFSVGOHNYDRGPIDMACENKGYEIPISGAIR 420  
 Db 361 FTDGGEERAOEIFAKYNRKQKVRVFTFSVGOHNYDRGPIDMACENKGYEIPISGAIR 420  
 Qy 421 INTQYLDVIGRPVYLAGDRAKQVOMTNYVLDALDELGLVITGTLPVNTITGQENKTNL 480  
 Db 421 INTQYLDVIGRPVYLAGDRAKQVOMTNYVLDALDELGLVITGTLPVNTITGQENKTNL 480  
 Qy 481 NOLILGVAGVDSLEDIRKLTFRFTLCPNGYFAIDPNGVYLLHPNLOPKNPKSOEPTVL 540  
 Db 481 NOLILGVAGVDSLEDIRKLTFRFTLCPNGYFAIDPNGVYLLHPNLOPKNPKSOEPTVL 540  
 Qy 541 DFLDAELNDIKVEIRKMKIDGESGKFTLVKSODERYIDKGNRTYTWTPVNGTDSYL 600  
 Db 541 DFLDAELNDIKVEIRKMKIDGESGKFTLVKSODERYIDKGNRTYTWTPVNGTDSYL 600  
 Qy 600 LALVLPYTSFYIKAKIEETITQARSKKGMKDSSETLKPDEESGYTFIAPRDYCDLKI 660  
 Db 600 LALVLPYTSFYIKAKIEETITQARSKKGMKDSSETLKPDEESGYTFIAPRDYCDLKI 660  
 Qy 660 ISDNNTTEFLNNEFIDRKTPNNPSCNTDLINRYLIDAGFTNELVQYWKSKOKNIKGVKAR 720  
 Db 660 ISDNNTTEFLNNEFIDRKTPNNPSCNTDLINRYLIDAGFTNELVQYWKSKOKNIKGVKAR 720  
 Qy 720 RFVYVDGKITRYPKEAGNMOENPETEEDSFYKRSIDNDNYVFTAPYFNKSGPGAYESG 780  
 Db 720 RFVYVDGKITRYPKEAGNMOENPETEEDSFYKRSIDNDNYVFTAPYFNKSGPGAYESG 780  
 Qy 780 MYSKAVEITYOGKILKRPVAVGKIDVNSWIENFTKTSIRDPGAPVCDCKRNSDMDVCY 840  
 Db 780 MYSKAVEITYOGKILKRPVAVGKIDVNSWIENFTKTSIRDPGAPVCDCKRNSDMDVCY 840  
 Qy 840 IIDDGFLMANHDDYNOIGRFGELIDPSLMLRLVNI SYAFNKSYDYOSVCEPGAARQ 900  
 Db 840 IIDDGFLMANHDDYNOIGRFGELIDPSLMLRLVNI SYAFNKSYDYOSVCEPGAARQ 900  
 Qy 900 GAGHRSAYVPSIADILHIGMWATAAAMSTLQOFLSLTFPRLLAEVEMEDDFTASLSK 959  
 Db 900 GAGHRSAYVPSIADILHIGMWATAAAMSTLQOFLSLTFPRLLAEVEMEDDFTASLSK 959  
 Qy 960 QSCITEOTQYFFPNDKSFSGVLDGCGNCSRIFFHEKLMNTNLFIVWESKGTGCPDTRL 1018  
 Db 960 QSCITEOTQYFFPNDKSFSGVLDGCGNCSRIFFHEKLMNTNLFIVWESKGTGCPDTRL 1018

## RESULT 3

CHRA2  
 N:Alternate names: dihydropyridine-binding protein - rabbit  
 C:Species: Oryctolagus cuniculus (domestic rabbit)

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 10, 2003, 14:13:54 ; Search time 19.3759 Seconds  
(without alignments)  
5050.861 Million cell updates/sec

Title: US-10-090-827-6

Percent score: 5349  
Sequence: 1 MAAGCLLALTLTLFQSLILG.....TNLIIFWESKGNPCDTRL 1018

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_73:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5288	98.9	1091	2 JH0565	calcium channel al
2	5174	96.7	1091	2 A44147	calcium channel pr
3	5156.5	96.4	1106	1 CHRA2	calcium channel al
4	1112	20.8	1091	2 T30256	calcium channel al
5	611	11.4	734	2 S44617	C50C3.11 protein -
6	570.5	10.7	1148	2 T18770	probable calcium c
7	196.5	3.7	886	2 S54355	inter-alpha-trypsi
8	190.5	3.6	1450	2 C86880	hypothetical prote
9	188	3.5	885	2 S30350	inter-alpha-trypsi
10	170.5	3.2	1819	2 D97033	uncharacterized pr
11	168.5	3.2	575	2 D64998	hypothetical prote
12	166	3.1	889	2 JC5576	inter-alpha-trypsi
13	165	3.1	459	2 F64688	proteinase (EC 3.4
14	160.5	3.0	420	2 S76691	hypothetical prote
15	160.5	3.0	2364	2 I40884	cytotoxin I - Clos
16	159	3.0	932	2 JC5953	inter-alpha-inhibi
17	158.5	3.0	918	2 E90542	lipoprotein (impor
18	155.5	2.9	946	1 IYH02	inter-alpha-trypsi
19	155	2.9	1315	2 T28679	fibronogen-binding
20	155	2.9	1984	2 A44396	p-type cation tran
21	154	2.9	688	2 D96930	methyl-accepting c
22	153.5	2.9	1426	2 A99580	hypothetical prote
23	153	2.9	946	2 JC5575	inter-alpha-trypsi
24	152.5	2.9	5005	2 F82884	hypothetical prote
25	152	2.8	1516	2 E71619	RAD2 endonuclease
26	150.5	2.8	680	2 A97331	membrane associate
27	149.5	2.8	654	2 A69656	methyl-accepting c
28	149.5	2.8	921	2 JC4625	inter-alpha-trypsi
29	149.5	2.8	926	2 D86897	hypothetical prote

## ALIGNMENTS

Query Match	Best Local Similarity	98.8%	Score 5288	DB 2	Length 1091	Pred. No. 3.9e-310	Mismatches 5	Indels 7	Gaps 0
Matches 1006	Conservative								
QY	1	MAAGCLLALTLTLFQSLILGSSQEPFSAVTIKSWDKMOEDIVTLAKTASGNOIYDI	60						
DB	1	MAAGCLLALTLTLFQSLILGSSQEPFSAVTIKSWDKMOEDIVTLAKTASGNOIYDI	60						
QY	61	YKTYDLYTVEPNNARQIVETIAARDIEKLNSRAIVRLALAEKVOAAHQWEDPASN	120						
DB	61	YKTYDLYTVEPNNARQIVETIAARDIEKLNSRAIVRLALAEKVOAAHQWEDPASN	120						
QY	61	YKTYDLYTVEPNNARQIVETIAARDIEKLNSRAIVRLALAEKVOAAHQWEDPASN	120						
DB	61	YKTYDLYTVEPNNARQIVETIAARDIEKLNSRAIVRLALAEKVOAAHQWEDPASN	120						
QY	121	EVVYNNAKDDLPPEKNDESPGSRIRKPFIDANFGROISYOHAAVHIPTDIYEGSTIVL	180						
DB	121	EVVYNNAKDDLPPEKNDESPGSRIRKPFIDANFGROISYOHAAVHIPTDIYEGSTIVL	180						
QY	121	EVVYNNAKDDLPPEKNDESPGSRIRKPFIDANFGROISYOHAAVHIPTDIYEGSTIVL	180						
DB	121	EVVYNNAKDDLPPEKNDESPGSRIRKPFIDANFGROISYOHAAVHIPTDIYEGSTIVL	180						
QY	181	NELNMTSALDEVEFKKRNREDEPSLIMQVFGSATGLARTYPASRWVNSRTPKIDLYDVR	240						
DB	181	NELNMTSALDEVEFKKRNREDEPSLIMQVFGSATGLARTYPASRWVNSRTPKIDLYDVR	240						
QY	181	NELNMTSALDEVEFKKRNREDEPSLIMQVFGSATGLARTYPASRWVNSRTPKIDLYDVR	240						
DB	181	NELNMTSALDEVEFKKRNREDEPSLIMQVFGSATGLARTYPASRWVNSRTPKIDLYDVR	240						
QY	241	RPWYTOGAASPRKMDLIVDVGSGVSGITLKLRTSVSEMLETLSDDDPVNNAFSPNSNOD	300						
DB	241	RPWYTOGAASPRKMDLIVDVGSGVSGITLKLRTSVSEMLETLSDDDPVNNAFSPNSNOD	300						
QY	301	VSCFQLHVQANVRNKKVILKADAVNNITAKGITDKGFSFAFQOLLNMYNSRANCKIITML	360						



Db 298 SDIVQVYGLNPEDIKNIGDKPNNGETIATAKH-----DTANLITTYFTD 344  
QY 333 YKGFSEAFEOQLNPNV-----SRANC-----NK 356  
Db 345 YVDRFN-SVQMGINYSIYMDADTIPVSKNDYEFNVTIGNTTKTANIQPPDYVNEKNS 403  
QY 357 IIMLFTD-----GGER-----AOEIFAKYKDK-----KRVYETP-----SVGOHNTDRG 397  
Db 404 IGSAPTEIVSHVGNKENPGYKOTIYVNPSENLSLNKAKVQAVHSSYPNNIGQINKDVT 463  
QY 398 PIQWACE-----NKGYEELPSGAIRINTOEYLDVLRPM--VLADKAKOV-----444  
Db 464 DIKIYQVKEGYLANKY-----DVNTKELTDVNTQYLOKITYGDNNNSAVIDFGNA 513  
QY 445 -----QMTN-----448  
Db 514 DSAVYVWNTKQYTNSESPLVOMATLSTGKNSVSTGNALGFTNNOSGAGOEYKIG 573  
QY 449 --VYIDALEIGVITGLPVENIT-GONENKTNLKNQILIGVGVDSLEDIKRLTPRET 505  
Db 574 NYWEDTNNKNGVQELGEKGVGNVTVFEDNNTNTK-----VGRAYKEDGSYLIPNL- 625  
QY 506 ICPNGY--FAIDPNGYVLLHPNLOPKNPK-----SOEPTLDFLAELENDIKVEITRN 557  
Db 626 --PNGDYREFGNLPKGYEVT-PSKOGNNEELDSNGLSSVITVNGKD-NLSADLGIYKPK 681  
QY 558 KNIDGESGKTRTLYKSDERYIDKGNRTYWTVPVNGDYSALVLPYSPFYIKAKIE 617  
Db 682 YNLCDYWEDTNNKNGIQDDEKGI--SGVTYTLKDENG-----DYL 720  
QY 618 ETTQARSKKGMKDSITLKPNEESGYTFLAPRDYCNDLKSIDNTEFLNNEFIDR 677  
Db 721 KYVTTDADCKYKFTD--LHNGNYK--VEFTTPEGYTPVTYVSGSDIE-----763  
QY 678 KTPNPNSCNTDLIN--RVLDAQFTN---ELVQNYW-----SKOKINIGV---717  
Db 764 -KDSNGLITTTGVYNGADNMTLDSGFYKTPKYNLGNVYWEDTNKDGKODSTEGISGVYVT 822  
QY 718 -----KARFVYTDGGITRV-----YPRAGENMOE-----742  
Db 823 LKNNEGEVLQTKTKDKGKYOTFTGLENGTYKVFETPSGYTPQVGSCTDEGIDSNGTST 882  
QY 743 -----NPETYEDSFYKRSLDNDNYVFTAPYFNKSGPAYE---SGIMVSKAVEITYQ 791  
Db 883 TGVIXKDKNDTIDSGFYKPTYNLGDYWEDT--NKNGVQDKDEKGISGVTVTLKDE---N 937  
QY 792 GKLLK 796  
Db 938 DKVLLK 942

Search completed: February 10, 2003, 14:48:51  
Job time : 13.5273 secs

ORGANISM: Staphylococcus aureus  
US-09-815-242-5898

Query Match 2.8%; Score 152; DB 10; Length 1349;  
Best Local Similarity 19.3%; Pred. No. 0.014; Mismatches 198; Conservative 124; Indels 366; Gaps 48;

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QY 16 SLIGPSSQEPFSAVTIKSWVDKMODLVTLAKTASGVNQ--LVDIYEKYODLYTVEP 72
DB 40 TLIFGLGNQAKAAESTNKE-----LNENATISADNQSDDKDMQOLNEDNEDTKND 90
QY 73 NNAQVLEIAARDIEKLISRSKALVRLAEAKVQAHOHWRDEPASNVEVYVYNAKDIDD 132
DB 91 NQK---EMVSSQENETTSNGNK-----LIEKESVOST--TGNKVEVSTAKSD-- 132
QY 133 PEKNDSEPGSQRIRKPYFIDANFGROIYQHAHVH1PTDIYEGSTIV----- 179
DB 133 ---EQASPKSTN-----EDLNTKQITISNOEA---LQPDLOENKSVVNVQPTNEENKKVD 180
QY 180 -----LN-----ELNMTSALDEVFKKRNREDPSILW-----QVFSATGLARYPA 220
DB 181 AKTESTTLNKSDAIKSNDETIVDNNSNSNNENNADILIPKSTAPKRLMTRIRIAVQPS 240
QY 221 SPWVDN-----SRTPNKIDLYVRRRPWTIGCAASPCKMLILVDVSGVSGLTFLKLIPT 274
DB 241 STEAKVNDLITNTLLTVVADAKNNKIVPADDYLSLKSOITVDDKVGSGDYFTIKY--- 297
QY 275 SVSEMLETISDDDFVNVASFN--SNAOVSCFOHLVQAVNRKKVYLKDAVNNITAKGITD 332
DB 298 SDIVQVYGLNPEIDIKNIGIKPNNGETIATYAKH-----DTANNLLTYTFTD 344
QY 333 YKGFSEFAPBOLINNV-----SRANC-----NK 356
DB 345 YVDREN-SYQMGINSIYDADTIPYSKNDVEFNVTIGTITTKITANIOPTYVNNENKS 403
QY 357 IIMLFND-----GGEER---AQELIFAKNNK---KRVYTF-----SVGOHNYDRG 397
DB 404 IGSAPTEYSHVGNENKPEYKOTIYVNPSENSLNAKIYQAHSSYPNNIGINKDVT 463
QY 398 PIOWMACE-----NKGYEIPISGAIRINTOEYDLYGRPK--VLASGRKAGY----- 444
DB 464 DRIKIVQVPRGYTLNKGY-----DVNTEKELDYTNQYLOKITTYGDNNSAVDPGNA 513
QY 445 -----QMTN----- 448
DB 514 DSAYVVMVTKFQYNTNSESPTLVQATLSSTGKSVSTGMALGFTNNOSGAGQEVYKIG 573
QY 449 --VYIDALELGLVITGILPYFNIT--GQENKTNLKNQOLILGVMGVDSLEDIKRLTPRPT 505
DB 574 NYVWEDTNKNGVQELGEGVGVNTVTFDNTNTK-----VGBAVYKEDGSYLIPML- 625
QY 506 LCPNGYV---FAIDPNGYVLLHPNLQPKNPK-----SOEPTYLDLFDLDELNDIKVELRN 557
DB 626 --PNCQDYRVERSENLPKGEVY--PSKQGNNEELDSNGLSVITVNGKD--NLSADIGIYKPK 681
QY 558 KHIIDSEGEKTRILYKSQDERYIDKGNRYTWTPVNGTJDYSLALVLPYTSFYIYKAKIE 617
DB 682 YNLCOYVWEDNKNKGIQDQDEKGI--SGVTVTLKDENG-----DVL 720
QY 618 ETIQARSKKGMKSETLKPDNFESEGYTFLAPDYCNOLKISDNTTEFLNNEFIDR 677
DB 721 KTVITDAGCKKFTD--LHNGNFK--VEFTTPGYPPTVTVTSQSDIE----- 763
QY 678 KTPNPNSCNTDLIN--RYLLDAGFTN--ELVQNYV-----SKQKNIKGY-- 717
DB 764 -KDSNGLTGTVINGADWMLTDSGFYKPKYNLGNVWEDNKNKQKODSTKGISGVYVIT 822
QY 718 -----KARFVYTDGICITRY-----YPKRAGENWQD----- 742
DB 823 LKNENGEVLQTTKTDKDKQYQFTGLENGTYKVEFEETPSGYPPTQVGSCTDEGIDNSGTST 882
QY 743 -----NPETYEDSFYKRSIDNDINNYVTAFYFNKSGCAEA-----SGIMSKAVEIYIQ 791

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DB 883 TGVYDKNDNDTIDSGFYKPYNLGDIWEDT--NKNQVQDDEKIGISGVYTLADE---N 937
QY 792 GKLLK 796
DB 938 DKVLLK 942

RESULT 15
US-09-815-242-13137
; Sequence 13137, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 13137
; LENGTH: 1349
; TYPE: PRF
; ORGANISM: Staphylococcus aureus
US-09-815-242-13137

Query Match 2.8%; Score 152; DB 10; Length 1349;
Best Local Similarity 19.3%; Pred. No. 0.014; Mismatches 198; Conservative 124; Indels 366; Gaps 48;

```

```

GENERAL INFORMATION:
APPLICANT: Feltelson, Jerald S.
Schnepf, H. Ernest
Narva, Kenneth E.
Stockhoff, Brian A.
Schmeltz, James
Loewer, David
Dullum, Charles Joseph
Muller-Cohn, Judy
Stamp, Lisa
Morrill, George
TITLE OF INVENTION: No. US2002010080A1el Pesticidal Toxins and Nucleotide
Sequences Which Encode These Toxins
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESS: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/850,351A
FILING DATE: 07-May-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/073,898
FILING DATE: 06-MAY-1998
APPLICATION NUMBER: US 08/960,780
FILING DATE: 30-OCT-1997
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-708CD1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 790 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Jay90
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-850-351A-8
Query Match 2.9%; Score 157.5; DB 10; length 790;
Best Local Similarity 19.7%; Pred. No. 0.0026;
Matches 138; Conservative 102; Mismatches 217; Indels 245; Gaps 35;
QY 231 NKIDLYRRRPWYIQGNASPKMLIIVDYSVSGITLKLIRTSVSEMLETISDD-DFV 289
DB 105 NKLDAIWTMLRYVL-----PKITSMISDVWKQNYALSLQI--EYLSKOLQETISDKDII 156
QY 290 NV-ASFSNADVS-----CQHLVQAVNRKKYVLKDA-----VNNIT-----A 327
DB 157 NVNVLINSTLEITPAVQRIKYVEKEELTFATETSKYKKGSPADIIIDELTELTELA 216
QY 328 KGIDYKGSFAFEQLIN--YNSRANCKITIMLFTDGEERAQETFAKYNKDKQVRF 385
DB 217 KSVT---KNVDYGFELNTHFDVWGN-----NLFRSALKTKTASELITKEN-----VKT 264
QY 386 TFSVGQ-HNDRGPIDWMAKCNKGYEYIETDISGAIINTQETIDVLTGRPVVLGDKAKOV 444

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DB 265 GSEGVNRYNF---LIVTALQAKAFLETTCKRKLGLADIDYTSIMNHL-----NKEKEE 317
QY 445 QMTNYYLDALEGLVITGTLPPVFNITGONENKTNKN-----QILL-----GWGVDVS 493
DB 318 FRYNT-----LPTLSNFTSPNRYAKVKGSDQEDAKIVKAPGHALIGFETS 363
QY 494 LEDI-----KRLTPRF-----TLCPNG-----YFP--AIDPGVYLL 523
DB 364 NDSITVLAKYFEAKLQONQVQDKSLSEVYIGMDKLLCPDQSEQIYYNNINIVFPREYIT 423
QY 524 HNNLPKNPKSOEPYTLDFLDALENDIKVEIRKMKIDGESGKTEFRLVKSQDERYDK 583
DB 424 KIDFTKMKMTLREYVTANFYDSSTG---EIDLNKKV--ESEKAYRILSNNDGVYVPL 478
QY 584 GARTYTW-PPVAGTGYSLALVLPYSPYIKAKIETITQARSKKMKKDSFTLKPDQFE 642
DB 479 GVISETFLTPINGFC-----LQAD--E 498
QY 643 ESGYTFIAPRDYCNLDKISDNTTEFLNFEFIDRKTNNPNSCNTDLNR-----VLADAG 698
DB 499 NSRLITLTCCKSYLRELLA-----TDSNKEFKLIVPPSG 533
QY 699 FTELNVQN-----YMSKQKN-----IKGVAREVYDGGITRYYPKEAGENW 740
DB 534 FLSNIYENGSIEDNLEPFAKNNKANNAYDHTGVNGFALYVHKDGISQF-----IGDKL 589
QY 741 QENPEY-----EDSEFYKRSIUNDVYVTFAPYFN----- 770
DB 590 KRRETEVIQTYTKKRPSTHLKDENTGYIHEDPTNNNLDYOTINKRFTTGIDLKGVIYLL 649
QY 771 ---SGPAGESIMVSKAVEIYIOGKLKPAVYGIKIDVNSW 809
DB 650 KQNGDEAMGDNFII---LEISPSKLLSPEL---INTMNM 684
RESULT 14
US-09-815-242-5898
Sequence 5898, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5898
LENGTH: 1349
TYPE: PRT

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QY 250 S-----PKDMLILVDGSGVSLTLKLTIRTSVSEMLFETLSDDDPVNVAFNSNAQDVC 303  
 Db 301 PDLNLPKRLNLEFVLDVSGSMGVMKQTFVEMAKTIIIDDLAEHDFSTIDNQIR--TW 358  
 QY 304 FOHLVQANRKKVYLKADVANNITAKGTDYKGF---SFAEQLLVNVSRANCKIIML 360  
 Db 359 RNDLEFQLOKHRIQIAKRYIERIOPSGGGINNEALLRAIFILNEANNHGLDPPNSVLITL 418  
 QY 361 FTDG-----GERRAOEIFAKYKDKKVRFTFSVQO--HNYDGPLOMACENK-----408  
 Db 419 VSDGPTGELKLSKIQKNVKNENIQDNISLFLSGMGFDVVDYDLKRLSNENHGIQRIY 478  
 QY 409 -----YYEIT--PSIGAIRIN--TOEYLDVL-----GRPMVLAG--DKAQ 443  
 Db 479 NQDTSSQLKRFYNGVSTPLKNOVFNPHTSVTDVTONNPHNFGSGSEIYVAGKFDPAK- 537  
 QY 444 VQWTVNYDLDELGLVITGLTPVNTGONENKTNLKNOLIGVAGVDSLEDI---KR 499  
 Db 538 -----LDOTE--SVITA-----TSANTQVLLETIAQMDLDQFLSKDK 574  
 QY 500 LTPRETLCPNGYPAIDPNGVYLHPNLOPKNPKSQEPVLDFLDALENDIYEIRNK 559  
 Db 575 ADPFTFR-KLMAYLTLN---QLAERSLAP-TAAAKRRTIRSLQMSLDHHTVPLTSLV 629  
 QY 560 IDGSGEKTRFTLVKSD 577  
 Db 630 IENEGDERMLADAPD 647

## RESULT 12

US-09-850-351A-6  
 ; Sequence 6, Application US/09850351A  
 ; Patent No. US20020100080A1

## GENERAL INFORMATION:

APPLICANT: Feltelson, Jerald S.  
 Schnepf, H. Ernest  
 Narva, Kenneth E.  
 Stockhoff, Brian A.  
 Schmelts, James  
 Loewer, David  
 Dullum, Charles Joseph  
 Muller-Cohn, Judy  
 Stamp, Lisa  
 TITLE OF INVENTION: No. US20020100080A1 Pesticidal Toxins and Nucleotide  
 Sequences Which Encode These Toxins  
 NUMBER OF SEQUENCES: 144  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
 STREET: 2421 N.W. 41st Street, Suite A-1  
 CITY: Gainesville  
 STATE: FL  
 COUNTRY: US  
 ZIP: 32606-6669  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/850,351A  
 FILING DATE: 07-May-2001  
 CLASSIFICATION: <unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 09/073,898  
 FILING DATE: 06-MAY-1998  
 APPLICATION NUMBER: US 08/960,780  
 FILING DATE: 30-OCT-1997  
 APPLICATION NUMBER: US 60/029,848  
 FILING DATE: 30-OCT-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sanders, Jay M.  
 REGISTRATION NUMBER: 39,355

REFERENCE/DOCKET NUMBER: MA-708CD1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 352-375-8100  
 TELEFAX: 352-372-5800  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 789 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 ORIGINAL SOURCE:  
 INDIVIDUAL ISOLATE: 81F  
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
 US-09-850-351A-6

Query Match 2.9%; Score 157.5; DB 10; Length 789;  
 Best Local Similarity 20.1%; Pred. No. 0.0026;  
 Matches 138; Conservative 103; Mismatches 231; Indels 215; Gaps 35;

QY 231 NKIDLYVRRRPYIGGASPKDMLILVDGSGVSLTLKLTIRTSVSEMLFETLSDD-DFV 289  
 Db 105 NKLDALNTMLRYTL-----PKITSLSDVMKQNTALSLQI--EYLSQLOEISDKIDI 156  
 QY 290 NV-ASFNNAQDVS-----CFQHLVQANVRNKKVLKDA-----VNNIT-----A 327  
 Db 157 NVNVLNLTLEITPAYQRIKYVNEKEFELTFATETSSKVKKDSPADIIDELTELTA 216  
 QY 328 KGITDYKKGFSFAFOLLN--YNVSRANCKIIMLFTGGGERRAOEIFAKYKDKVRF 385  
 Db 217 KSVT---KNDVGFERYLTFPDVWGN---NLFGRSAUKTASELTIKEN---VQTS 264  
 QY 386 TFSVQO--HNYDRGPLOMACENKGYEIPISGAIRINTOEYLDVIGRPMVLADKAKOV 444  
 Db 265 GSEVGNVNF---LTVLALAKAFLTLTCKRLGLADIDYTSIMENH---NKEKE 317  
 QY 445 QMTNYYDLALGLVITGLTPVNTGONENKTNLKN---OLIL-----GYMGVDS 493  
 Db 318 FRVNI-----LPTLSNFTSPNPAVAKVGSDEDAKMIVEAKPGHALVGEIS 363  
 QY 494 LEDI-----KRLTPRE-----TLCPNG---YF--AIDNGVYL 523  
 Db 364 NDSITVLKVEEKLKONQVUKDSLSEVYIGDMDKLCPDQSEQIYTTNNIVFPNEYVIT 423  
 QY 524 HPNLOPKNPKSQEPVLDFLDALENDIYEIRNKIMIDIEGSEKTFRTLVKSOEERYIDK 583  
 Db 424 KIDFTKKKRLRYEVTANFYDSSTG---EIDLNKKV--ESEAEYRTLSANDGYTMPL 478  
 QY 584 GNRITVW--TPVNG---TDYSLAVLPTPSFYIYKAKIETTTQARSKKGMDSSETLKP 638  
 Db 479 GVISEFTLTPINGGLADENSRLITLTCRSYLRKELLALDLSN-----KETKLIVP 530  
 QY 639 -----DNEESGYTFIAPRDYCNCLKISDNNTT--FLNNEFDIKRTPNPNPCNDLIN 691  
 Db 531 PSGFINKIVENG-----SIEDNLEFWKANNKNEYVDH-----563  
 QY 692 RVLDAQFTVELVONVSKOKNIKGRARFVTDGKIT---RYVPK-----734  
 Db 564 -----TGVGNGTKALYVHKDGGISGFIQKLRKPKTYIVYQYVKGK 604  
 QY 735 -----EAG-----ENMOENPEYEDSFYKRSISLDNDNYVFTAPYRNKSGPAGYESGIAY 782  
 Db 605 PSILAKENGTGYIHEDTNNLEDYQITTRKFTTGDKGVYLILKSQMGDEAMGDNFII 664  
 QY 783 SKAVEIYQGLKLPAPVAVGIKIDVNSW 809  
 Db 665 ---LEISPSSEKLSPEL---INTNMW 684

## RESULT 13

US-09-850-351A-8  
 ; Sequence 8, Application US/09850351A  
 ; Patent No. US20020100080A1

## ATTORNEY/AGENT INFORMATION:

NAME: Sanders, Jay M.  
 REGISTRATION NUMBER: 39,355  
 REFERENCE/DOCKET NUMBER: MA-708CD1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 352-375-8100  
 TELEFAX: 352-372-5800

## INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 790 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 ORIGINAL SOURCE:  
 INDIVIDUAL ISOLATE: 36a  
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
 US-09-850-351A-4

Query Match 3.0%; Score 160.5; DB 10; Length 790;  
 Best Local Similarity 19.7%; Pred. No. 0.0016;  
 Matches 138; Conservative 103; Mismatches 216; Indels 245; Gaps 35;

231 NKIDLVRRRPVYIOGAASPKMDLIVVSGVSGITLKLRTSYSEMLETLSDD-DFV 289  
 105 NKIDALNTMRYL-----PKITSLDVMKQNYALSIQI-EYLSKOLEISDKLDII 156  
 QY 290 NV-ASRNSNAQDVS-----CFQHLVQANVANKVLDK-----VNNT-----A 327  
 157 NVNVLNSTLTETTPAYQRIKYNKEFEELTFATEISAKVKDGPANILDELTELEA 216  
 QY 328 KGITDVKKGSFAFEQLLN-VNVSRAKCKIMLFTDGEERAOEIFAKYNNKDKVRYF 385  
 217 KSVT---KNDVGFETLTFHVMYGN-----NLEGRSLKTSASLITKEN-----VKTS 264  
 QY 386 TFSVGO-HNYDRGPIDMACENKGYEELPSIGAIRINQOYLIVLGRPVNLAGRAKOV 444  
 265 GSEGVNRYNF---LIVLTALQAKAFLLTLCRKLGLADIDYISINNEHL---NKEKEE 317  
 QY 445 QMNVYIDALELGLVITGLTPVNTGONKNTLNK-----OLIL-----GYMVDVS 493  
 318 FRVNI-----LPTLSNTPSNPVAKVGSDEDAKMIYEAHGAHLIGFEIS 363  
 QY 494 LEDI-----KRLTPRF-----TLCPNG---YVF-AIDPNGVYVL 523  
 364 NDSITVIAKYEAFLKQNYQYDKDSLSEVYIGMDKLLCPQSQEYITNNIVFPNEVYIT 423  
 QY 524 HPILOPKRKSQEBVTIDFLDALENDIKVEIRNNKMIIDSGSEKTRITLVKSODEKVIDK 583  
 424 KIDFTKKMKTLRYEVTFANFYDSSG---EIDLNKKVY-ESSBAEYKTTLSANDGVYML 478  
 QY 584 GNRFTW-FVNGDYSIALVLPYTSFYIYKAKIEETITQARSKKGMKSEFLKPDNFE 642  
 479 GVISEFTLTPINGG-----LQAD-E 498  
 QY 643 ESGYTFIAPRDYCNDLKISDNTEELLNFNEFIDRKTNNPNSCPWDLINR---VLIDAG 698  
 499 NSRLITITCKSYLRELLA-----TDLSNREFTKLIYPPSG 533  
 QY 699 PTNELVON-----YNSKQKN-----IKGVKARFVYTDGIIIVYKREGENW 740  
 534 FISIVNGSTIEEDNLEPMKANNKNAVVDHTGGVNGTKALYVHKDGISOF---ICDNL 589  
 QY 741 QENETV-----EDSFYKSLDNDNYVFATPYFNK-----770  
 590 KPKREVIYQTVKGRPSIHLDENTGSIYHEDTNNNLEDQOTINKRRTTGTDLKGVYLL 649  
 QY 771 ---SGPGAYBSGLINVSKAVELIYQKLLKPAVYGIKIDVNSW 809  
 650 KSONGDAMGDNFTI---LEISPEKILSPEL---INTNMW 684  
 Db

RESULT 11

## US-09-828-423-3

Sequence 3, Application US/09828423  
 Patent No. US20020099178A1

## GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

Guegler, Karl J.

Patterson, Chandra

TITLE OF INVENTION: GROWTH-ASSOCIATED TRYPSIN-TYPE  
 INHIBITOR HEAVY CHAIN PRECURSOR

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: Word Perfect 6.1/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/828,423

FILING DATE: 05-Apr-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/388,774

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Cerrione, Michael C

REGISTRATION NUMBER: 39,132

REFERENCE/DOCKET NUMBER: PF-0505 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 946 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GENEBANK

CLONE: 9133985

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-828-423-3

Query Match 3.0%; Score 160.5; DB 10; Length 946;

Best Local Similarity 19.8%; Pred. No. 0.0021;

Matches 134; Conservative 107; Mismatches 248; Indels 189; Gaps 31;

QY 33 IKSWDKQMEDLVTLAKTSGVNOVDIYERKQDLYVEPNNAQLV-----80  
 26 ISEFVD--YEDVEL--APGKQVLAENKRYQRL-----PGSEEMAEVYQVITLYSKV 77  
 QY 81 -----IAARDIEKLLNSRKALVRLALEAKVQAHAHQWREDFASN-----120  
 78 QSTIYSRAFTMIQSVYVNSPQPNVVDVQIPKGA-----FISNFSMTVDGKTFRSS 131  
 QY 121 -----EYVYVNAK-----DLDDEPKKNSE-----PGSORIRPVFIDANPGRQ 158  
 132 IREKTVGRALVQAARKGTAGLVSSALDMENFTENVVLPGARVOFELHYQEVKMKRL 191  
 QY 159 ISYOH-----AAVHIPTDIYEGSTIYLNELNMTSALD-----EYFKKNREB-----199  
 192 GSYEHRIYIQPGRIAKHLEVDVWVIEPQGLRFLHVPDIFEGHFDGVPVYSKQCOKAHRSF 251  
 QY 200 DPSLIMQVGSATGLIARYYPASPWNDSRTPKIDLYVDRRP-----WTIQGAA 249  
 252 KPIVAQO-----RICPSCR--ETAVDGEIVLVYDVKREKAGELEVFNGYVHFHFA 300  
 Db



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1  PRIOR APPLICATION NUMBER: US 09/608,408
2  PRIOR FILING DATE: 2000-06-30
3  PRIOR APPLICATION NUMBER: US 09/774,203
4  PRIOR FILING DATE: 2001-01-29
5  NUMBER OF SEQ ID NOS: 49117
6  SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
7  SEQ ID NO 36461
8  LENGTH: 35
9  TYPE: PRT
10 ORGANISM: Homo sapiens
11 FEATURE:
12 OTHER INFORMATION: MAP TO AC008283.2
13 OTHER INFORMATION: EXPRESSED IN HELL100, SIGNAL = 2.5
14 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.67
15 OTHER INFORMATION: EXPRESSED IN FETAL LAYER, SIGNAL = 0.67
16 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.6
17 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
18 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
19 OTHER INFORMATION: EST_HUMAN HIT: AW051755.1, EVALUE 3.00e-04
20 OTHER INFORMATION: SWISSPROT HIT: P54290, EVALUE 6.00e-15
21 US-09-864-761-36461

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Matches 3

1 GSQRKPVFIEDANFGROIYQHAAVHIPTDIYEG 35

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RESULT 10
US-09-850-351A-4
; Sequence 4, Application US/09850351A
; Patent No. US20020100080A1
GENERAL INFORMATION:
APPLICANT: Feltelson, Jerald S.
Schnepf, H. Ernest
Marva, Kenneth E.
Stockhoff, Brian A.
Schmeltz, James
Loewer, David
Dullum, Charles Joseph
Muller-Cohn, Judy
Stamp, Lisa
Morrill, George
TITLE OF INVENTION: No. US20020100080A1e1 Pesticidal Toxins and Nucleotides
Sequences Which Encode These Toxins
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSER: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/850,351A
FILING DATE: 07-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/073,898
FILING DATE: 06-MAY-1998
APPLICATION NUMBER: US 08/960,780
FILING DATE: 30-OCT-1997
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-OCT-1996

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RESULT 7  
US-09-86

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US-09-864-761-38318
: Sequence 38318, Application us/09864761
: Patent No. US20020048763A1
:
: GENERAL INFORMATION:
:   APPLICANT: Penn, Sharon G.
:   APPLICANT: Rank, David R.
:   APPLICANT: Hanzel, David K.
:   APPLICANT: Chen, Wensheng
:   TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
:   TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
:   FILE REFERENCE: Aecm1ca-X-1
:   CURRENT APPLICATION NUMBER: US/09/864,761
:   CURRENT FILING DATE: 2001-05-23
:   PRIOR APPLICATION NUMBER: US 60/180,312
:   PRIOR FILING DATE: 2000-02-04
:   PRIOR APPLICATION NUMBER: US 60/207,456
:   PRIOR FILING DATE: 2000-05-26
:   PRIOR APPLICATION NUMBER: US 09/632,366
:   PRIOR FILING DATE: 2000-08-03
:   PRIOR APPLICATION NUMBER: GB 24263.6
:   PRIOR FILING DATE: 2000-10-04
:   PRIOR APPLICATION NUMBER: US 60/236,359
:   PRIOR FILING DATE: 2000-09-27
:   PRIOR APPLICATION NUMBER: PCT/US01/00666
:   PRIOR FILING DATE: 2001-01-30
:   PRIOR APPLICATION NUMBER: PCT/US01/00667
:   PRIOR FILING DATE: 2001-01-30
:   PRIOR APPLICATION NUMBER: PCT/US01/00664
:   PRIOR FILING DATE: 2001-01-30
:   PRIOR APPLICATION NUMBER: PCT/US01/00669
:   PRIOR FILING DATE: 2001-01-30
:   PRIOR APPLICATION NUMBER: PCT/US01/00665
:   PRIOR FILING DATE: 2001-01-30
:   PRIOR APPLICATION NUMBER: PCT/US01/00668
:   PRIOR FILING DATE: 2001-01-30
:   PRIOR APPLICATION NUMBER: PCT/US01/00663
:   PRIOR FILING DATE: 2001-01-30
:   PRIOR APPLICATION NUMBER: PCT/US01/00662
:   PRIOR FILING DATE: 2001-01-30
:   PRIOR APPLICATION NUMBER: PCT/US01/00661
:   PRIOR FILING DATE: 2001-01-30
:   PRIOR APPLICATION NUMBER: PCT/US01/00670
:   PRIOR FILING DATE: 2001-01-30
:   PRIOR APPLICATION NUMBER: US 60/234,687
:   PRIOR FILING DATE: 2000-09-21
:   PRIOR APPLICATION NUMBER: US 09/608,408
:   PRIOR FILING DATE: 2000-06-30
:   PRIOR APPLICATION NUMBER: US 09/774,203
:   PRIOR FILING DATE: 2001-01-29
:   NUMBER OF SEQ ID NOS: 49117
:   SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
:   SEQ ID NO 38318
:   LENGTH: 35
:   TYPE: PRT
:   ORGANISM: Homo sapiens
:   FEATURE:
:   OTHER INFORMATION: MAP TO AC008283.2
:   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.84
:   OTHER INFORMATION: EST_HUMAN HIT: AW051755.1, EVALU0 1.00e-14
:   OTHER INFORMATION: SWISSPROT HIT: P54289, EVALU0 2.00e-15
US-09-864-761-38318

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Query Match	3.6%	Score 190	DB 10	Length 35
Best Local Similarity	100.0%	Pred. No. 1.3e-07		
Matches	35	Conservative	0	Mismatches 0
				Indels 0
				Gaps 0
QY	185	WTSAIDVEYFKKRRDDPSLLIMQVFGSATGIATARYP	219	
Db	1	WTSAIDVEYFKKRRDDPSLLIMQVFGSATGIATARYP	35	

RESULT  
US-09-82

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Sequence 5 Application US/09828423
Patent No. US20020099178A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
Guegler, Karl J.
Patterson, Chandra
TITLE OF INVENTION: GROWTH-ASSOCIATED TRYPsin-TYPE
INHIBITOR HEAVY CHAIN PRECURSOR
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Word Perfect 6.1/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/828,423
FILING DATE: 05-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/388,774
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0505 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 885 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENEBANK
CLONE: g1288563
SEQUENCE DESCRIPTION: SEQ ID NO: 5 :
US-09-828-423-5

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	Query Match	3.5%	Score 185;	DB 10;	Length 885;
	Best Local Similarity	21.3%	Pred. No. 3.3e-05;		
	Matches 137;	Conservative 113;	Mismatches 245;	Indels 150;	Gaps 36;
QY	45	YLAATAGSVNDLVDIYEKQYODLTVEBPNNARQOLVEIARDIEKLLSNRSKALVRLALEA	104		
DB	77	VELPRTAFITNTLTIT-----DGVITY-PGNVKE-KEVAKQYKEVASQGGKFTGL-----	123		
QY	105	EKVQAQAHQREDF-----ASNEVYYINAKDDLPDEKNDSPGSGORIKPVITIDANQGR	157		
DB	124	-VKASGRKLEKFTVSVNVAAAGSKYTFELTYELLKRNHKKYEMYLKVOP-----K	172		
QY	158	QISYQAAHVHPITDIYEGSTIVLELNMNTSALDVEYFKKNREDPSSLMOVPGSA-----T	212		
DB	173	QL-VKHFEEIV-DLFEPOGT-----SMLD-----AEASFTINDLGSALTAKRS	214		
QY	213	GLARYYPASPVWYDNSRT-PNKID-----LYDVRRRP-----WYI-----QG	247		
DB	215	GKKGVHVSFRLSDQGRSCPTCTDLSLNGDFTITDYVNNRSPGNYQIVNGYFVHPFAPQGL	274		
QY	248	AAAPPDMLTLVDVSSVSGCLTKLIRTSYSEMLEFTLSDDDFNVNVAFSNADQVSCF-QH	306		

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; Sequence 44281, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT FILING DATE: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 44281
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006145.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.86
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.91
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.93
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.81
; OTHER INFORMATION: SWISSPROT HIT: P54289, EVALU4 4.00e-25
; OTHER INFORMATION: EST_HUMAN HIT: H86016.1, EVALU4 1.00e-02
US-09-864-761-44281

Query Match 5.1%; Score 272; DB 10; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.1e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 6
US-09-864-761-38267
; Sequence 38267, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT FILING DATE: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 38267
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC008283.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.86
; OTHER INFORMATION: EST_HUMAN HIT: AL134437.1, EVALU4 3.00e-24
; OTHER INFORMATION: SWISSPROT HIT: P54289, EVALU4 4.00e-25
US-09-864-761-38267

Query Match 5.1%; Score 272; DB 10; Length 53;
Best Local Similarity 100.0%; Pred. No. 3.2e-13;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 241 RPYTIGGAASPKMDLLVDSVSGSLTLKILRTSVSEMLFTLSDDDPYNVASFNSMAD 300
Qy 301 VSCFOHLVOANRNKVKLDAVNNITAKITDYKKGSEFAEQLNLYNSRANCKIIML 360
Db 301 VSCFOHLVOANRNKVKLDAVNNITAKITDYKKGSEFAEQLNLYNSRANCKIIML 360
Qy 361 FPDGGERAOEIFAKYNNKRVKVFESVGOHNYDRGPLOMNAKCRKGYTTPSTGAIR 420
Db 361 FPDGGERAOEIFAKYNNKRVKVFESVGOHNYDRGPLOMNAKCRKGYTTPSTGAIR 420
Qy 421 INTQEVLDVGRPMVLADGKAKOVONTYLDALFELGTYTGLTPVFNITGONENKTNLK 480
Db 421 INTQEVLDVGRPMVLADGKAKOVONTYLDALFELGTYTGLTPVFNITGONENKTNLK 480
Qy 481 NQILIGVMGVDSLEDIKLTPREFLCPNGYFAIDPNGYVLLHNPLOPKRKSQEPYTL 540
Db 481 NQILIGVMGVDSLEDIKLTPREFLCPNGYFAIDPNGYVLLHNPLOPKRKSQEPYTL 540
Qy 541 DFLDAELNDIYVEIRNKKIDGSEKPEPRTLYKSODEXYIDKGRRTYTWTPVNGTDSL 600
Db 541 DFLDAELNDIYVEIRNKKIDGSEKPEPRTLYKSODEXYIDKGRRTYTWTPVNGTDSL 600
Qy 601 ALVLPYSFYIKAKIETITTOARSKKGMKDETLKPDNESEGYTFIAPDYCNDLKI 660
Db 601 ALVLPYSFYIKAKIETITTOARSKKGMKDETLKPDNESEGYTFIAPDYCNDLKI 660
Qy 661 SDNNTPELLNENEFIDRKTNNPNSCNTDLINRYLLDAGFTNELVONYSKONIKGVAR 720
Db 661 SDNNTPELLNENEFIDRKTNNPNSCNTDLINRYLLDAGFTNELVONYSKONIKGVAR 720
Qy 721 FVYTDGTRVYPRKAGEWMOENPEYEDSPYKRSIDNDNYVFTAPYNNKSGPAGYEGSI 780
Db 721 FVYTDGTRVYPRKAGEWMOENPEYEDSPYKRSIDNDNYVFTAPYNNKSGPAGYEGSI 780
Qy 781 MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIEFTKTSIRDPACAGVCCCKRSDVMDCVI 840
Db 781 MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIEFTKTSIRDPACAGVCCCKRSDVMDCVI 840
Qy 841 LDDGFEILMANHDDYTNQIGRFFGELIDPSLMHLVNIISYAFNKSYDYOSVCEPGAARQ 900
Db 841 LDDGFEILMANHDDYTNQIGRFFGELIDPSLMHLVNIISYAFNKSYDYOSVCEPGAARQ 900
Qy 901 GAGHRSAYVPSIADILHIGMMATAAASLLOOFLSLTFPRLLEAVEMEDDFTASLSKO 960
Db 901 GAGHRSAYVPSIADILHIGMMATAAASLLOOFLSLTFPRLLEAVEMEDDFTASLSKO 960
Qy 961 SCITEQOTYFFDNDKSFSGVLDGCGNSRIFHVEKIMNTNLIIFINVESKGTCPDTRL 1018
Db 961 SCITEQOTYFFDNDKSFSGVLDGCGNSRIFHVEKIMNTNLIIFINVESKGTCPDTRL 1018

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## RESULT 2

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US-09-875-423-5
; Sequence 5, Application US/09875423
; Patent No. US20020081657A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: 21784, A NOVEL HUMAN CALCIUM CHANNEL
; FILE REFERENCE: 10448-059001
; CURRENT APPLICATION NUMBER: US/09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,257
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1091
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-875-423-5

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Query Match 20.8%; Score 1112; DB 10; Length 1091;
Best Local Similarity 28.9%; Pred. No. 2,4e-71;
Matches 311; Conservatfive 224; Mismatches 411; Indels 130; Gaps 39;

Qy 3 AGCIIATLTLTFOSSLIGPSSOEPFPSPAATIKSWVDKQEDVLTATAGSVNOVDIYE 62
Db 14 ASALIA-TALLIYALGVYRSEQOIPUSV-VKIMASAFGGKIKIAKYSQOLLOKKYK 71
Qy 63 KYODLYVEPNNAQIYEAARDIEKLNSRKALVRLALEAEVQAQAHOMREDFASNEV 122
Db 72 EYKQVAIEEIDGLQVYKLLAKIMEEMFHKSEAVRLVEAEAAHLKHEDFADL---QY 128
Qy 123 VTYNAK--DDIDPEKNDSEPSQRIKPFVETIDANFGQISYQAAVHPIPDYEGSTIVL 180
Db 129 EYFNAVLINERDKQGNFLELKEFI--LAPDHNHNPVNISLSDVOVPTNMYNKKDAIY 186
Qy 181 NELMWTSAIDVFPKKNREDPSLLMOYFGSATGLARYPASPWVDSNRTNKLIDLYVR 240
Db 187 NGVYSESLNVFVNDNRPSLIMQYFGSAKGFROYPGIKWEPDE--NGVIAFDGRN 243
Qy 241 RPYTIGGAASPKMDLLVDSVSGSLTLKILRTSVSEMLFTLSDDDPYNVASFNSMAD 300
Db 244 RMYTIOAATSPKDVLLVDSVSGSKGLRLTIKQTVSIIIDTIGDDDFNITTYNEELHY 303
Qy 301 VS-CFO-HLVQANRNKVKLDAVNNITANGIDYKKGSEFAEQLNLYNSRAN--CNK 356
Db 304 VEPCLNGTLVQADRTNKEHREHLDKLFANGIGMDIALINEAFNIIISDFNHTGOGSICQ 363
Qy 357 IIMFTDGEERAOEIFAKYNNKRVKVFESVGOHNYDRGPLOMNAKCRKGYTTPSTGAIR 415
Db 364 AIMLITDGAUDTYTITRAKIMPDKRVKVFESVGOHNYDRGPLOMNAKCRKGYTTPSTGAIR 423
Qy 416 IGAIIRINTQEVLDVGRPMVLADGKAKOVONTYLD-----ALEGLYI--TGLT 464
Db 424 LADVOENMEYLAHLSRPKY--DQEHVYWTAEYIDSTLIPQAKLADDOGLVLTATYAM 481
Qy 465 PVFNITGONENKTNLKQILIGWGVVSLIEDIKLTPREFLCPNGYFAIDPNGYVLLH 524
Db 482 PVFS---KQNETRSKG--ILGVGVTDVPVKEELTKIPKYLGIHGAFAFIITNNGYILTH 536
Qy 525 PNLDP---KNPQSEB--VTLDFLAELNDIYVEIRNKKIDGSEKPEPRTLYKSODEX 579
Db 537 PELRPLVEEGKKRRKPYSSVDLSEVEMEDRDV-LRNAMVNNKTKG--FSMEVK---K 589
Qy 580 YIDKGNFT---YTWTPVNGTDSLALVLT--YSEFYIKAR--IEETITTOARSKKGM 630
Db 590 TVDKGRFVLVMTNDYYTIDIKGTFPFLSGVALSRHGKGYFRGNVTIEGL----- 639
Qy 631 KDSITLKPDPNESEGYTFIAPDYCN-DLKISDNNTPELLNENEFIDRKTNNPNSCNTDL 689
Db 640 -----HDEHPDVSIADEWSTCNTDLRHEHRHLSQLEAIRLYLKGRKP-LLOCDKEL 690
Qy 690 INRYLLDAGFTNELVONYS-----KQNIKGVKARFVYTDGTRVYR----- 733
Db 691 IOEVLFPDA-VYSAPITEVYTWSLALNSSENSDKGEVAEALGTRIGLSRINLEFGAEOLTNQ 749
Qy 734 --KEAGENMOENPEYEDSEYKRSIDN--DNVYFTAPY---FNKSGPAGESGIMVSKA 785
Db 750 DFLKAGDKRENIFNADHPLMYRRAAEQIAGSFYISIPFSGYTKS-----NVTYASIS 803
Qy 786 VEIYIOGKLLKPAVVGIKIDVNSWIEFTKTSIRDPACAGVCCCKRSDVMDCVIIDGG 845
Db 804 IQLDERKSPVAVAGIOMLEFFORFRTWASROCASLDGKCSISDDDEFVNCYLLIDNNG 863
Qy 846 FLTMANHDDYTNQIGRFFGELIDPSLMHLVNIISYAFNKSYDYOSVCEPGAARQAGHR 905
Db 864 FILVS--EDYT-QTGDPEGEVAGAVNKKLITMGSFRITLYIQACR---ANKSSDSA 917
Qy 906 SAYVPSIADILHIGMMATAAASLLOOFLSLTFPRLLEAVEMEDDFTASLSK-----Q 960
Db 918 HGLIDPYKAFU-----SAKKWTMTLVLFLVEF-----NLCSWMSHSDMAKAKOKLTQLE 967
Qy 961 SCITEQOTYFFDNDKSFSGVLDGCGNSRIFHVEKIMNTNLIIFINVESKGTCPDTRL 1016

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 10, 2003, 14:22:34 ; Search time 7.52732 Seconds  
(without alignments)  
2998.192 Million cell updates/sec

Title: US-10-090-827-6  
Perfect score: 5349  
Sequence: 1 MAGCLLALTLTFLFOSLLIG.....TNLIFIMVSKGNCPCDRL 1018

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 129505 seqs, 22169297 residues

Total number of hits satisfying chosen parameters: 129505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubppaa/US08\_NEW\_PUB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubppaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubppaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubppaa/US07\_NEW\_PUB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubppaa/PCTUS\_PUBCOMB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubppaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubppaa/US09\_NEW\_PUB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubppaa/US10\_NEW\_PUB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubppaa/US10\_PUBCOMB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5288	98.9	1091	10	US-09-875-423-4
2	1112	20.8	1091	10	US-09-875-423-5
3	1111	20.8	1091	10	US-09-875-423-2
4	319.5	6.0	223	12	US-10-005-168-2
5	272	5.1	51	10	US-09-864-761-44281
6	272	5.1	51	10	US-09-864-761-38267
7	190	3.6	35	10	US-09-864-761-38318
8	185	3.4	35	10	US-09-864-761-38318
9	182	3.4	35	10	US-09-864-761-36461
10	160.5	3.0	946	10	US-09-850-351A-4
11	160.5	3.0	946	10	US-09-850-351A-4
12	157.5	2.9	788	10	US-09-850-351A-6
13	157.5	2.9	790	10	US-09-850-351A-6
14	152	2.8	1349	10	US-09-815-242-5898
15	152	2.8	1349	10	US-09-815-242-5898
16	146.5	2.7	1781	9	US-09-995-749A-2
17	140	2.6	3169	9	US-10-114-170-257
18	133.5	2.5	764	9	US-10-105-695-4
19	133.5	2.5	764	9	US-10-105-694-4

20	133.5	2.5	764	10	US-09-747-521-4	Sequence 4, Appl1
21	133.5	2.5	764	12	US-10-106-014-4	Sequence 4, Appl1
22	131.5	2.5	2125	10	US-09-919-172-29	Sequence 29, Appl1
23	130.5	2.4	1323	10	US-09-801-368-34	Sequence 34, Appl1
24	130	2.4	3712	9	US-10-108-605-103	Sequence 103, Appl
25	127.5	2.4	956	9	US-10-121-032-63	Sequence 9, Appl1
26	126	2.4	876	10	US-09-815-242-12623	Sequence 12623, A
27	124	2.3	2285	10	US-09-932-183A-2	Sequence 2, Appl1
28	118.5	2.2	1183	9	US-09-870-759-45	Sequence 45, Appl1
29	118	2.2	103	9	US-10-050-786-9	Sequence 9, Appl1
30	118	2.2	5795	10	US-09-815-242-12610	Sequence 12610, A
31	117	2.2	3594	9	US-10-150-821-4	Sequence 4, Appl1
32	117	2.2	3594	10	US-09-911-842-4	Sequence 4, Appl1
33	116	2.2	911	10	US-09-828-423-4	Sequence 4, Appl1
34	114	2.1	549	9	US-09-712-363-190	Sequence 190, App
35	114	2.1	698	9	US-09-801-220-4	Sequence 4, Appl1
36	113.5	2.1	1430	10	US-09-740-274-6	Sequence 6, Appl1
37	113.5	2.1	3571	9	US-10-150-821-2	Sequence 2, Appl1
38	113.5	2.1	3571	10	US-09-911-842-2	Sequence 2, Appl1
39	113	2.1	1066	9	US-09-423-126-3	Sequence 3, Appl1
40	113	2.1	1066	10	US-09-280-197-5	Sequence 5, Appl1
41	112	2.1	2835	10	US-09-885-535-4	Sequence 4, Appl1
42	111.5	2.1	836	9	US-09-858-525A-10	Sequence 10, Appl1
43	111.5	2.1	871	9	US-09-850-351A-2	Sequence 32, Appl1
44	111.5	2.1	881	10	US-09-850-351A-32	Sequence 32, Appl1
45	111	2.1	811	9	US-10-011-588-29	Sequence 29, Appl1

## ALIGNMENTS

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RESULT 1
US-09-875-423-4
; Sequence 4, Application US/09875423
; Patent No. US20020081657A1
; GENERAL INFORMATION:
; APPLICANT: Curtiss, RORY A.J.
; TITLE OF INVENTION: 21784, A NOVEL HUMAN CALCIUM CHANNEL
; FILE OF INVENTION: FAMILY MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-059001
; CURRENT APPLICATION NUMBER: US/09/875,423
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1091
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-875-423-4

Query Match      98.9%; Score 5288; DB 10; Length 1091;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1006; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY      1  MAAGCLLALTLTFLFOSLLIGSSOEFPSPAVITIKSVNDKMOEDLYTIAKTASGVOLYDI 60
      1  MAAGCLLALTLTFLFOSLLIGSSOEFPSPAVITIKSVNDKMOEDLYTIAKTASGVOLYDI 60
DB      1  MAAGCLLALTLTFLFOSLLIGSSOEFPSPAVITIKSVNDKMOEDLYTIAKTASGVOLYDI 60
QY      61  YEKYODLYVEPNNAQOLVIAARDIEKLISNSKALVRIALPAEKVOAHOHREDPASN 120
      61  YEKYODLYVEPNNAQOLVIAARDIEKLISNSKALVRIALPAEKVOAHOHREDPASN 120
DB      61  YEKYODLYVEPNNAQOLVIAARDIEKLISNSKALVRIALPAEKVOAHOHREDPASN 120
QY      121  EYVYVNAKXDLDEPKNDSEPSORIKPVTLDANFROISYDHAHVHPTDIEGSTIYL 180
      121  EYVYVNAKXDLDEPKNDSEPSORIKPVTLDANFROISYDHAHVHPTDIEGSTIYL 180
DB      121  EYVYVNAKXDLDEPKNDSEPSORIKPVTLDANFROISYDHAHVHPTDIEGSTIYL 180
QY      181  NELNMTSALDEYVKRRREDPSILMOVFGSATGLAAYYRASPVDNSRTPNKIDLYDVR 240
      181  NELNMTSALDEYVKRRREDPSILMOVFGSATGLAAYYRASPVDNSRTPNKIDLYDVR 240
DB      181  NELNMTSALDEYVKRRREDPSILMOVFGSATGLAAYYRASPVDNSRTPNKIDLYDVR 240
QY      241  RPYVIOGAASPKDMLILVDVSGVSGTLTKLIRTSVSEMLFTLSDDDFVNVAFSNMAOD 300
      241  RPYVIOGAASPKDMLILVDVSGVSGTLTKLIRTSVSEMLFTLSDDDFVNVAFSNMAOD 300

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Query Match	96.1%;	Score 5229.5;	DB 1;	Length 1106;
Best Local Similarity	94.8%;	Pred. No. 0;		
Matches 1003;	Conservative 14;	Mismatches 12;	Indels 29;	Gaps
QY 1	MAAGCLLALTTLTFQS - LLIGPSSEEPSPASVTIKSWDKMOEDLVTLAKTAGSYNOLV	58		
Db 1	MAAGPRLAMTTLTLMQAMILLIGPSSEEPSPASVTIKSWDKMOEDLVTLAKTAGSYNOLV	60		
QY 59	DIYEKYODLVYEPNNAQOLVFIARDIFKLLSNSKALVSLALPAEKVQAHHOMREDPA	118		
Db 61	DIYEKYODLVYEPNNAQOLVFIARDIEKLLSNSKALVRLALPAEKVQAHHOMREDPA	120		
QY 119	SNEVYVYNAKDDLDEPEKNDSEPGSORIKPVFTIEDANFGHQSIOYHAHVHPIDIYEGSTI	178		
Db 121	SNEVYVYNAKDDLDEPEKNDSEPGSORIKPVFTIDPANFRQVQSYQAAHVHPIDIYEGSTI	180		
QY 179	VLNEINMTSALDVEFKKNEEDPSLLMOVFSSATGLARYYPASPVWNSRTPNKKIDLXDY	238		
Db 181	VLNEINMTSALDLDVEFKKNEEDPSLLMOVFSSATGLARYYPASPVWNSRTPNKKIDLXDY	240		
QY 239	RRRPYITOGAASPKMILLIVYSGSVGLTKLILRTSVSEMLFTJLSDDDFVAVASNSMA	298		
Db 241	RRRPYITOGAASPKMILLIVYSGSVGLTKLILRTSVSEMLFTJLSDDDFVAVASNSMA	300		
QY 299	QDVSCFOHLVQAVANNNKRVLPKAVANNITAKGTIDVKKGSPAFEOQLNANVRANCKLTI	358		
Db 301	QDVSCFOHLVQAVANNNKRVLPKAVANNITAKGTITDVKKGSPAFEOQLNANVRANCKLTI	360		
QY 359	MLFTDGGEEAEOETFNKYNKDKRVAFREPSVQHNTERGPIOMMACENKGYIYEIPSTIGA	418		

Search completed: February 10, 2003, 14:23:30  
Job time : 15.4906 secs



APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
NUMBER OF INVENTIONS: METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/223,305C  
FILING DATE: April 4, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 52516 (P519739)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1079 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-223-305C-55

Query Match 98.2%; Score 5347; DB 2; Length 1079;  
Best Local Similarity 98.7%; Pred. No. 0;  
Matches 1023; Conservative 0; Mismatches 1; Indels 12; Gaps 2;

QY 1 MAAGCLALTLTLFOSLLIGPSSEPPPSAVTIKSWVDKMOEDLVTLAKTASGVNQLVDI 60  
DB 1 MAAGCLALTLTLFOSLLIGPSSEPPPSAVTIKSWVDKMOEDLVTLAKTASGVNQLVDI 60  
QY 61 YEKYODLYVEENNAKOLVETIARIDIEKLISNRKALVSLAEAKKQAAQAWQWREDFASN 120  
DB 61 YEKYODLYVEENNAKOLVETIARIDIEKLISNRKALVSLAEAKKQAAQAWQWREDFASN 120  
QY 121 EVVYVNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROIYQHAHVHPTDIYEGSTIVL 180

DB 121 EVVYVNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROIYQHAHVHPTDIYEGSTIVL 180  
QY 181 NELNMTSALDEVPKKNREDEPSLIMOVGSAATGLARYPPASPWVDNRTNKLIDLYVR 240  
DB 181 NELNMTSALDEVPKKNREDEPSLIMOVGSAATGLARYPPASPWVDNRTNKLIDLYVR 240  
QY 241 RPPWYOGAASPKMDLIVDVSGSVGLTKLIRTSVSEMLETTISDDDFVVAASNSNAOD 300  
DB 241 RPPWYOGAASPKMDLIVDVSGSVGLTKLIRTSVSEMLETTISDDDFVVAASNSNAOD 300  
QY 301 VSCFOHLVQAVNRKKVYLKDAVNNITAKGITDYKGFSAFEQLLNTVSRANCKITML 360  
DB 301 VSCFOHLVQAVNRKKVYLKDAVNNITAKGITDYKGFSAFEQLLNTVSRANCKITML 360  
QY 361 FTDGGEERAQELFNKYNKDKVRFVRSVGOHNERGPIDQMACENKGYEELPSIGAIR 420  
DB 361 FTDGGEERAQELFNKYNKDKVRFVRSVGOHNERGPIDQMACENKGYEELPSIGAIR 420  
QY 421 INTQEYLDVIGRPVYLAGDKAKOVQWNTVYLDALGLVITGTLVPENITGOFEENKTNL 480  
DB 421 INTQEYLDVIGRPVYLAGDKAKOVQWNTVYLDALGLVITGTLVPENITGOFEENKTNL 480  
QY 481 NOLLIGVGVVSVLEDIKRLTPRTLPNGYFAIDNGVYLLHPNLOPKNSQEPVTL 540  
DB 481 NOLLIGVGVVSVLEDIKRLTPRTLPNGYFAIDNGVYLLHPNLOPKNSQEPVTL 540  
QY 541 DFLDAELENDIKVEIRNKMIDGSEKTFRTLVASODERYIDGNRTYMTPVNGTYSL 600  
DB 541 DFLDAELENDIKVEIRNKMIDGSEKTFRTLVASODERYIDGNRTYMTPVNGTYSL 600  
QY 596 ALVLPYTSFYIKAKLEETITQARY-----SETLAPDNPEESGYFIAPROYCNDLKI 648  
DB 596 ALVLPYTSFYIKAKLEETITQARY-----SETLAPDNPEESGYFIAPROYCNDLKI 648  
QY 601 ALVLPYTSFYIKAKLEETITQARY-----SETLAPDNPEESGYFIAPROYCNDLKI 660  
DB 601 ALVLPYTSFYIKAKLEETITQARY-----SETLAPDNPEESGYFIAPROYCNDLKI 660  
QY 661 SDNTEFLNNNEFIDKTPNNPSCNADLIRVLLDAGFNELVQYNTWSQKNIKVKAR 720  
DB 661 SDNTEFLNNNEFIDKTPNNPSCNADLIRVLLDAGFNELVQYNTWSQKNIKVKAR 720  
QY 649 SDNTEFLNNNEFIDKTPNNPSCNADLIRVLLDAGFNELVQYNTWSQKNIKVKAR 708  
DB 649 SDNTEFLNNNEFIDKTPNNPSCNADLIRVLLDAGFNELVQYNTWSQKNIKVKAR 708  
QY 721 FVVTIDGCTIRYVPEAGENNQENPEYEDSFYKSLDNDVYFTAPFNKSGGAYESGI 780  
DB 721 FVVTIDGCTIRYVPEAGENNQENPEYEDSFYKSLDNDVYFTAPFNKSGGAYESGI 780  
QY 709 FVVTIDGCTIRYVPEAGENNQENPEYEDSFYKSLDNDVYFTAPFNKSGGAYESGI 768  
DB 709 FVVTIDGCTIRYVPEAGENNQENPEYEDSFYKSLDNDVYFTAPFNKSGGAYESGI 768  
QY 781 MYSKAVEIYIOGKLLKPAVVGIRIDVNSWLENFTKISIRDPGAPVDCCKRNSDVMCVI 840  
DB 781 MYSKAVEIYIOGKLLKPAVVGIRIDVNSWLENFTKISIRDPGAPVDCCKRNSDVMCVI 840  
QY 769 MYSKAVEIYIOGKLLKPAVVGIRIDVNSWLENFTKISIRDPGAPVDCCKRNSDVMCVI 828  
DB 769 MYSKAVEIYIOGKLLKPAVVGIRIDVNSWLENFTKISIRDPGAPVDCCKRNSDVMCVI 828  
QY 841 LDDGFLIMAHNDYTNQIGRFEIDPSLMRHVYNSVYAFKNSYXOVSVCERGAAPKQ 900  
DB 841 LDDGFLIMAHNDYTNQIGRFEIDPSLMRHVYNSVYAFKNSYXOVSVCERGAAPKQ 900  
QY 829 LDDGFLIMAHNDYTNQIGRFEIDPSLMRHVYNSVYAFKNSYXOVSVCERGAAPKQ 888  
DB 829 LDDGFLIMAHNDYTNQIGRFEIDPSLMRHVYNSVYAFKNSYXOVSVCERGAAPKQ 888  
QY 901 GAGHRSAYVPSVADILIQMWATAAWSIIQOFLSLITFPRLLEAVEMEDDDTASLSKQ 960  
DB 901 GAGHRSAYVPSVADILIQMWATAAWSIIQOFLSLITFPRLLEAVEMEDDDTASLSKQ 960  
QY 889 GAGHRSAYVPSVADILIQMWATAAWSIIQOFLSLITFPRLLEAVEMEDDDTASLSKQ 948  
DB 889 GAGHRSAYVPSVADILIQMWATAAWSIIQOFLSLITFPRLLEAVEMEDDDTASLSKQ 948  
QY 961 SCITEQYQYFFDNDKSFSGVLDGNCSTRIFHGKELMNTMLIFIMESKCTCPDTRLI 1020  
DB 961 SCITEQYQYFFDNDKSFSGVLDGNCSTRIFHGKELMNTMLIFIMESKCTCPDTRLI 1020  
QY 949 SCITEQYQYFFDNDKSFSGVLDGNCSTRIFHGKELMNTMLIFIMESKCTCPDTRLI 1008  
DB 949 SCITEQYQYFFDNDKSFSGVLDGNCSTRIFHGKELMNTMLIFIMESKCTCPDTRLI 1008  
QY 1021 QABOTSDGPNPCDMVK 1036  
DB 1009 QABOTSDGPNPCDMVK 1024

RESULT 15  
US-08-435-675B-5  
Sequence 5, Application US/08435675B  
Patent No. 5710250  
GENERAL INFORMATION:  
APPLICANT: Ellis, Steven Bradley  
APPLICANT: Williams, Mark E.  
APPLICANT: Harpold, Michael Miller  
APPLICANT: Schwartz, Arnold

APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,543A  
FILING DATE: May 31, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/223,305  
FILING DATE: April 4, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-52517  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1079 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: Internal

Qy	121	EVYVYNAKDLDJEKNDSEGSORIKPVIEIDJANGRGROISYOHAAVHIPTDIEGSTYVL	180
Dp	121	EVYVYNAKKDLDJEKNDSEGSORIKPVIEIDJANGRGROISYOHAAVHIPTDIEGSTYVL	180
Qy	181	NELNMTSALDEVEKKNREEDPSLLMQVFSAGLARYYPASPMWNSRTPKIDLYDVR	240
Dp	181	NELNMTSALDEVEKKNREEDPSLLMQVFSAGLARYYPASPMWNSRTPKIDLYDVR	240
Qy	241	RPWYIOGAASPCKMDLLIYVSGVSGSLTILKIRTSYSEKLETLSDDDPVNAASFNSAOD	300
Dp	241	RPWYIOGAASPCKMDLLIYVSGVSGSLTILKIRTSYSEKLETLSDDDPVNAASFNSAOD	300
Qy	301	VSCGOHLYOVANVANKKVLDAVNNITAKITDYKKGGSFAEPOLLNTVASANCKIIML	360
Dp	301	VSCGOHLYOVANVANKKVLDAVNNITAKITDYKKGGSFAEPOLLNTVASANCKIIML	360
Qy	361	FTDGEERAQEIENKKNKKVYFVFSGOHNHYERGPIOMACENKGYEIEPSIGAIR	420
Dp	361	FTDGEERAQEIENKKNKKVYFVFSGOHNHYERGPIOMACENKGYEIEPSIGAIR	420
Qy	421	INTOEYLDVIGRPWVLADGAKAKOVMTNVYLDALBGLVITGTLPVFNITGOFENKTNLK	480
Dp	421	INTOEYLDVIGRPWVLADGAKAKOVMTNVYLDALBGLVITGTLPVFNITGOFENKTNLK	480
Qy	481	NOLILGAGVDSLEEDIKRLTTPRETLCPMGYFPAIDPNKYVLLHNNLOPKNPKSGEPYTL	540
Dp	481	NOLILGAGVDSLEEDIKRLTTPRETLCPMGYFPAIDPNKYVLLHNNLOPKNPKSGEPYTL	540
Qy	541	DFDLAELENDIKAEINKNKMDGSEGEKTRTYLKSODEERYIDKGNRTYTWTVPVNGTDSL	600
Dp	536	DFDLAELENDIKAEINKNKMDGSEGEKTRTYLKSODEERYIDKGNRTYTWTVPVNGTDSL	595
Qy	601	ALVLPYSPYYIKAKLEBTITQARSKKGMKUSEYLPKPNPEESGYTFLAPRDYCNLDKI	660
Dp	596	ALVLPYSPYYIKAKLEBTITQARY-----SETLPKPNPEESGYTFLAPRDYCNLDKI	648
Qy	661	SDNNTEFLNPFIDIRKTPNNNSCADLLINRYLIDAGTNTLNYONMSKOKNIRKGYAR	720
Dp	649	SDNNTEFLNPFIDIRKTPNNNSCADLLINRYLIDAGTNTLNYONMSKOKNIRKGYAR	708
Qy	721	FVYVTDGITRVYREKAGEENMOENPENVEDSFYKRSIDNOMNYFTAPRYNKSQPGAYESGI	780
Dp	709	FVYVTDGITRVYREKAGEENMOENPENVEDSFYKRSIDNOMNYFTAPRYNKSQPGAYESGI	768
Qy	781	MYSKAVEIITYOGKULKPAYVGIKIDVNSIENFTKTSIRDPCAGFYCCKKRNSVMDCVI	840
Dp	769	MYSKAVEIITYOGKULKPAYVGIKIDVNSIENFTKTSIRDPCAGFYCCKKRNSVMDCVI	828
Qy	841	LDDGCFLLMNHDDYNOIGRFGFELDPSLIMHIVNISTYANKSYDVOSCEPGAAPKQ	900
Dp	829	LDDGCFLLMNHDDYNOIGRFGFELDPSLIMHIVNISTYANKSYDVOSCEPGAAPKQ	888
Qy	901	GAGHRSAYVPSVADILIOIGWMTAAAMSILQOFLSLTFPRLLAEVEMEDDFTASLSKQ	960
Dp	889	GAGHRSAYVPSVADILIOIGWMTAAAMSILQOFLSLTFPRLLAEVEMEDDFTASLSKQ	948
Qy	961	SCITEGTQYFFNDKDSFSFSGVLDGCGCSRI FHEBKIMNTNLIF IWEVSKGTCPCDTRILI	1020
Dp	949	SCITEGTQYFFNDKDSFSFSGVLDGCGCSRI FHEBKIMNTNLIF IWEVSKGTCPCDTRILI	1008
Qy	1021	QABQTSQPCNDCMYK 1036	
Dp	1009	QABQTSQPCNDCMYK 1024	

RESULT14  
US-08-223-305C-55  
; Sequence 55, Application US/08223305C  
; Patent No. 5851824  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven

APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Hallier & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/223.305C  
FILING DATE: April 4, 1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
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PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 52516 (P519739)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1103 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-223-305C-53

Query Match 98.6%; Score 5367; DB 2; Length 1103;  
Best Local Similarity 97.4%; Pred. No. 0;  
Matches 1028; Conservative 0; Mismatches 1; Indels 26; Gaps 2;

QY 1 MAAGCLLALTLTLFOSLLIGPSSEPPPSAVTIKSMVDMQMDLVTLAKTASGVNQLVDI 60  
DB 1 MAAGCLLALTLTLFOSLLIGPSSEPPPSAVTIKSMVDMQMDLVTLAKTASGVNQLVDI 60  
QY 61 YEKYODLYVEENNAQOLVEIARQIEKLKSKRSKALVSLAEAKVQAARQWEDFASN 120  
DB 61 YEKYODLYVEENNAQOLVEIARQIEKLKSKRSKALVSLAEAKVQAARQWEDFASN 120

QY 121 EYVYNNANODDDPEKNDSEPSQRIKPYFIDANPGROIYQHAAYHPPDIYEGSTIVL 180  
DB 121 EYVYNNANODDDPEKNDSEPSQRIKPYFIDANPGROIYQHAAYHPPDIYEGSTIVL 180  
QY 181 NELNMTSALDEYFKKRNREDSLSLMQVGSATGLARYPAPAWDNSRTPKIDLYVRR 240  
DB 181 NELNMTSALDEYFKKRNREDSLSLMQVGSATGLARYPAPAWDNSRTPKIDLYVRR 240  
QY 241 RPYWYOGAASPRMDLILVDVSGSVGLTKLIRTSVSEMLETSLDDDFVNVASFNNAOD 300  
DB 241 RPYWYOGAASPRMDLILVDVSGSVGLTKLIRTSVSEMLETSLDDDFVNVASFNNAOD 300  
QY 301 VSCFQHLVQANVRKKVYLKADAVNNITAKGIDYKGGSFAPQOLLNVSRANCKIIML 360  
DB 301 VSCFQHLVQANVRKKVYLKADAVNNITAKGIDYKGGSFAPQOLLNVSRANCKIIML 360  
QY 361 FTDGEERAQELFNKYNKDKVYRFVSGOHNTERGDIOMACENNGYIEIPISAIR 420  
DB 361 FTDGEERAQELFNKYNKDKVYRFVSGOHNTERGDIOMACENNGYIEIPISAIR 420  
QY 421 INFOEYLDVIGRPMVLADGAKAOVMTNVYLDALGLVITGTLVPVNTIGQFENKTNL 480  
DB 421 INFOEYLDVIGRPMVLADGAKAOVMTNVYLDALGLVITGTLVPVNTIGQFENKTNL 480  
QY 481 NQLLIGVGVVSVLEDIRLTPRTLCNGYYPALDPNGVYLHPNLOPK----- 530  
DB 481 NQLLIGVGVVSVLEDIRLTPRTLCNGYYPALDPNGVYLHPNLOPK----- 530  
QY 531 -----NPKSOEPTVLDLELENDIKVEIRNMKIDSESEKFTPLVKSODRYI 581  
DB 531 -----NPKSOEPTVLDLELENDIKVEIRNMKIDSESEKFTPLVKSODRYI 581  
QY 581 LKRRPNQNKRSQEPYTLDDLDALENDIKVEIRNMKIDSESEKFTPLVKSODRYI 600  
DB 581 LKRRPNQNKRSQEPYTLDDLDALENDIKVEIRNMKIDSESEKFTPLVKSODRYI 600  
QY 601 DGNRTYTWTPVNGTDYSLSALVLPYSEFYIKAKLEETITQAR-----SETLKRDNF 653  
DB 601 DGNRTYTWTPVNGTDYSLSALVLPYSEFYIKAKLEETITQAR-----SETLKRDNF 653  
QY 653 EESGTFIAPRDYCNLDKISDNTEFLNFEIDRKTIPNPNSCNADLIRVLLDAGFTN 713  
DB 653 EESGTFIAPRDYCNLDKISDNTEFLNFEIDRKTIPNPNSCNADLIRVLLDAGFTN 713  
QY 713 ELVQNYWSKQKINIKVKAFFVTDGITRYPKRAGENMOENPTYDSFYKSLDNDY 761  
DB 713 ELVQNYWSKQKINIKVKAFFVTDGITRYPKRAGENMOENPTYDSFYKSLDNDY 761  
QY 761 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLKPAVVGIKIDVNSMIENFTKSI 821  
DB 761 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLKPAVVGIKIDVNSMIENFTKSI 821  
QY 821 CAGPYCOCCKRNSDVMDCYIILDDGFLLMANHDYTNQIGRFGRTDPSLMRHLVNSVYA 881  
DB 821 CAGPYCOCCKRNSDVMDCYIILDDGFLLMANHDYTNQIGRFGRTDPSLMRHLVNSVYA 881  
QY 881 FNSKSYDYSVCEPGAAPKQAGHRSAYVSAVDILQIGWATAAWSIILQOFLSLTFPR 941  
DB 881 FNSKSYDYSVCEPGAAPKQAGHRSAYVSAVDILQIGWATAAWSIILQOFLSLTFPR 941  
QY 941 LLEAVEMEDDFTASLSKQSCITEQTOYFEDNDSKSFSGVLDGNCRSRIFHGEKLMNTL 1001  
DB 941 LLEAVEMEDDFTASLSKQSCITEQTOYFEDNDSKSFSGVLDGNCRSRIFHGEKLMNTL 1001  
QY 1002 IFIWEKSGTCPCDTRLILQAEQTSIDGPNPCDMVK 1036  
DB 1014 IFIWEKSGTCPCDTRLILQAEQTSIDGPNPCDMVK 1048

RESULT 13  
US-08-455-543A-55  
Sequence 55 Application US/08455543A  
Patent No. 5792846  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark

APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
METHODS  
NUMBER OF SEQUENCES: 57  
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COUNTRY: USA  
ZIP: 92101-2926  
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MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,543A  
FILING DATE: May 31, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/223,305  
FILING DATE: April 4, 1994  
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APPLICATION NUMBER: 07/868,354  
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APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-52517  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0062  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1103 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-455-543A-53

Query Match 98.6%; Score 5367; DB 1; Length 1103;  
Best Local Similarity 97.4%; Pred. No. 0;  
Matches 1028; Conservative 0; Mismatches 1; Indels 26; Gaps 2;

QY 1 MAAGCLLALTLFOSLLIGPSSEPPSAVITIKSWNDKMOEDVLTAAAGVNOVDI 60  
DB 1 MAAGCLLALTLFOSLLIGPSSEPPSAVITIKSWNDKMOEDVLTAAAGVNOVDI 60  
QY 61 YEKYODLYVEPNNAQVLEIARDEKLLSNRSKALVSLAEAEVQAAHQWREDFASN 120

DB 61 YEKYODLYVEPNNAQVLEIARDEKLLSNRSKALVSLAEAEVQAAHQWREDFASN 120  
QY 121 EYVYYNADKDDLDPERNDSEPPGQRIRKPYFIEDANGROISYQAAVHLPTIYEGSTIVL 180  
DB 121 EYVYYNADKDDLDPERNDSEPPGQRIRKPYFIEDANGROISYQAAVHLPTIYEGSTIVL 180  
QY 181 NELNMTSALDEYFKKKRREDESLMQVGSATGLARYPAPWYDNRSTPKIDLYDVR 240  
DB 181 NELNMTSALDEYFKKKRREDESLMQVGSATGLARYPAPWYDNRSTPKIDLYDVR 240  
QY 241 RPWYIQGAASPCKDMLLDVSGSVGLTLKLIRTSVSEMLETLDSDDEVNVAFSNSNAOD 300  
DB 241 RPWYIQGAASPCKDMLLDVSGSVGLTLKLIRTSVSEMLETLDSDDEVNVAFSNSNAOD 300  
QY 301 VSCFOHVOANRNKKVLDKAVNNITAGIDYKKGSFAPFOLLNVAANCKNTIML 360  
DB 301 VSCFOHVOANRNKKVLDKAVNNITAGIDYKKGSFAPFOLLNVAANCKNTIML 360  
QY 361 FTDGGEERAQELFNKNKDKRVFRFSGOHNERGPIQMMACENKGYEIPISGAIR 420  
DB 361 FTDGGEERAQELFNKNKDKRVFRFSGOHNERGPIQMMACENKGYEIPISGAIR 420  
QY 421 INTQYLDVLRPNVLAGDKAKQVQWNTNVLDALGLVITGTLPEVNTIGOFENKTNLK 480  
DB 421 INTQYLDVLRPNVLAGDKAKQVQWNTNVLDALGLVITGTLPEVNTIGOFENKTNLK 480  
QY 481 NOLITGVWGVYSLIEDIRLTPRTICPNGYFPALDPNGYLLHPNLOPKIGVIGIPTIN 540  
DB 481 NOLITGVWGVYSLIEDIRLTPRTICPNGYFPALDPNGYLLHPNLOPKIGVIGIPTIN 540  
QY 531 -----NPKQEPVTLDFDLAELENDIVEIIRNKMIDESEKFTRTLYKSQDERYI 581  
DB 531 -----NPKQEPVTLDFDLAELENDIVEIIRNKMIDESEKFTRTLYKSQDERYI 581  
QY 581 LKRRPNQINPKSQEPVTLDFDLAELENDIVEIIRNKMIDESEKFTRTLYKSQDERYI 600  
DB 581 LKRRPNQINPKSQEPVTLDFDLAELENDIVEIIRNKMIDESEKFTRTLYKSQDERYI 600  
QY 601 DKGNTTYTWPNGTDYSLAVLPTYSFYTKAKLEETITQARSKKGMKSEPLKDPNF 641  
DB 601 DKGNTTYTWPNGTDYSLAVLPTYSFYTKAKLEETITQARSKKGMKSEPLKDPNF 641  
QY 642 EESGTYFTAPRDYCNLDKISDNTEFLNFEFIDRKPNNPSCNADLINVLDAQPTN 701  
DB 642 EESGTYFTAPRDYCNLDKISDNTEFLNFEFIDRKPNNPSCNADLINVLDAQPTN 701  
QY 701 ELVQNTYMSKQNKIKGVKARFVYTDGKITRVYPKEAGENWQENPETYEDSEFKRSILDNDY 761  
DB 701 ELVQNTYMSKQNKIKGVKARFVYTDGKITRVYPKEAGENWQENPETYEDSEFKRSILDNDY 761  
QY 714 ELVQNTYMSKQNKIKGVKARFVYTDGKITRVYPKEAGENWQENPETYEDSEFKRSILDNDY 773  
DB 714 ELVQNTYMSKQNKIKGVKARFVYTDGKITRVYPKEAGENWQENPETYEDSEFKRSILDNDY 773  
QY 762 VFTAPYFNKSGPGAVESQIMSKAVEITYQCKLKPAVVGKIKIDVNSKIENFTKTSIRDP 821  
DB 762 VFTAPYFNKSGPGAVESQIMSKAVEITYQCKLKPAVVGKIKIDVNSKIENFTKTSIRDP 821  
QY 774 VFTAPYFNKSGPGAVESQIMSKAVEITYQCKLKPAVVGKIKIDVNSKIENFTKTSIRDP 833  
DB 774 VFTAPYFNKSGPGAVESQIMSKAVEITYQCKLKPAVVGKIKIDVNSKIENFTKTSIRDP 833  
QY 822 CAGPYCDCKRNSDVMDCYITLDGGLFLMANHDDYTNOIGRFFGELDSLMHVLNISVYA 881  
DB 822 CAGPYCDCKRNSDVMDCYITLDGGLFLMANHDDYTNOIGRFFGELDSLMHVLNISVYA 881  
QY 834 CAGPYCDCKRNSDVMDCYITLDGGLFLMANHDDYTNOIGRFFGELDSLMHVLNISVYA 893  
DB 834 CAGPYCDCKRNSDVMDCYITLDGGLFLMANHDDYTNOIGRFFGELDSLMHVLNISVYA 893  
QY 882 FNKSYDYQVCEPGAAPKQAGHRSAYVSVADILQIGWMTAAMWSILOQFLSLTFPR 941  
DB 882 FNKSYDYQVCEPGAAPKQAGHRSAYVSVADILQIGWMTAAMWSILOQFLSLTFPR 941  
QY 894 FNKSYDYQVCEPGAAPKQAGHRSAYVSVADILQIGWMTAAMWSILOQFLSLTFPR 953  
DB 894 FNKSYDYQVCEPGAAPKQAGHRSAYVSVADILQIGWMTAAMWSILOQFLSLTFPR 953  
QY 942 LLEAVEMEDDPTASLSKQSCITTEQTYFFPNDKSKTSVGLDGCNGRIHGEKIAMTNL 1001  
DB 942 LLEAVEMEDDPTASLSKQSCITTEQTYFFPNDKSKTSVGLDGCNGRIHGEKIAMTNL 1001  
QY 954 LLEAVEMEDDPTASLSKQSCITTEQTYFFPNDKSKTSVGLDGCNGRIHGEKIAMTNL 1013  
DB 954 LLEAVEMEDDPTASLSKQSCITTEQTYFFPNDKSKTSVGLDGCNGRIHGEKIAMTNL 1013  
QY 1002 IFIWEKSGTCPCDPTRLILQAEQTSDDGNPCDMVK 1036  
DB 1002 IFIWEKSGTCPCDPTRLILQAEQTSDDGNPCDMVK 1036  
QY 1014 IFIWEKSGTCPCDPTRLILQAEQTSDDGNPCDMVK 1048  
DB 1014 IFIWEKSGTCPCDPTRLILQAEQTSDDGNPCDMVK 1048

RESULT 12  
US-08-223-305C-53  
Sequence 53, Application US/08223305C  
Patent No. 5851824  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael

```

1 APPLICANT: Harpold, Michael
2 APPLICANT: Ellis, Steven
3 APPLICANT: Williams, Mark
4 APPLICANT: Feldman, Daniel
5 APPLICANT: Mccue, Ann
6 APPLICANT: Brenner, Robert
7 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
8 TITLE OF INVENTION: METHODS
9 NUMBER OF SEQUENCES: 57
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: Brown, Martin, Haller & McClain
12 STREET: 1660 Union Street
13 CITY: San Diego
14 STATE: California
15 COUNTRY: USA
16 ZIP: 92101-2926
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Diskette
19 COMPUTER: IBM Compatible
20 OPERATING SYSTEM: DOS
21 SOFTWARE: FASTSEQ Version 1.5
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/08/223,305C
24 FILING DATE: April 4, 1994
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: 07/868,354
27 FILING DATE: April 10, 1992
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: US 07/745,206
30 FILING DATE: 15-AUG-1991
31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER: US 07/620,250
33 FILING DATE: 30-NOV-1990
34 PRIOR APPLICATION DATA:
35 APPLICATION NUMBER: US 07/482,384
36 FILING DATE: 20-FEB-1990
37 PRIOR APPLICATION DATA:
38 APPLICATION NUMBER: US 07/603,751
39 FILING DATE: 04-APR-1989
40 PRIOR APPLICATION DATA:
41 APPLICATION NUMBER: WO PCT/US89/01408
42 FILING DATE: 04-APR-1989
43 PRIOR APPLICATION DATA:
44 APPLICATION NUMBER: 33,779
45 FILING DATE: 04-APR-1988
46 ATTORNEY/AGENT INFORMATION:
47 NAME: Seidman, Stephanie L.
48 REGISTRATION NUMBER: 33,779
49 REFERENCE/DOCKET NUMBER: 52516 (P519739)
50 TELECOMMUNICATION INFORMATION:
51 TELEPHONE: (619)238-0999
52 TELEFAX: (619)238-0062
53 INFORMATION FOR SEQ ID NO: 56:
54 SEQUENCE CHARACTERISTICS:
55 LENGTH: 1084 amino acids
56 TYPE: amino acid
57 STRANDEDNESS: single
58 TOPOLOGY: linear
59 MOLECULE TYPE: protein
60 FRAGMENT TYPE: Internal
61 US-08-223-305C-56
62
63 Query Match 99.0%; Score 5386.5; DB 2; Length 1084;
64 Best Local Similarity 99.2%; Pred. No. 0;
65 Matches 1028; Conservative 0; Mismatches 1; Indels 7; Gaps 1;
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67 QY 1 MAAGCLALLTLFLFOSLLIGPSSEEPFSAVITKSWVDKMDQEDVTLAKTAGSVNQLVDI 60
68 1 MAAGCLALLTLTLFLFOSLLIGPSSEEPFSAVITKSWVDKMDQEDVTLAKTAGSVNQLVDI 60
69
70 DB 61 YEKYDDLTVPNNRNAROLVETIARPIEKLISNRKALVSLAEAKVQAHHQWRDFASN 120
71 YEKYDDLTVPNNRNAROLVETIARPIEKLISNRKALVSLAEAKVQAHHQWRDFASN 120

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QY	121	EWYVYNAKDDEDDPEKNDSEGSQOIKRVFLEDNFQGIStYQAAHlPTDlYBESSTYL	180
Db	121	EVYVYNAKDDEDDPEKNDSEGSQOIKRVFLEDNFQGIStYQAAHlPTDlYBESSTYL	180
QY	181	NELNMTSALDEVFFKNNEEDPESLlMQVFGSAtLARYPASpVNDVSrTPNkIDlDYVR	240
Db	181	NELNMTSALDEVFFKNNEEDPESLlMQVFGSAtLARYPASpVNDVSrTPNkIDlDYVR	240
QY	241	RPWYlQCAASrKDMlLlVDYSGVSGLTLKlRrSVSEMLETlSDDEpVNVASpFNSMAD	300
Db	241	RPWYlQCAASrKDMlLlVDYSGVSGLTLKlRrSVSEMLETlSDDEpVNVASpFNSMAD	300
QY	301	VSCROHlVOAVNRKKVYLKQAVNNITAKGTlDYKrkPFSrFEDlLlNYNSrRANCKlIML	360
Db	301	VSCROHlVOAVNRKKVYLKQAVNNITAKGTlDYKrkPFSrFEDlLlNYNSrRANCKlIML	360
QY	361	FTDGEERNAOEIfENKYNKDKRVrFRFSVQOHYERGPiQUMACENKGGYIElPSlGAR	420
Db	361	FTDGEERNAOEIfENKYNKDKRVrFRFSVQOHYERGPiQUMACENKGGYIElPSlGAR	420
QY	421	INTQEtLDVGRPVYLAGDKAKOVQNTNYLDALEGLVlTGTLpVFNlTGOFPENKTYNK	480
Db	421	INTQEtLDVGRPVYLAGDKAKOVQNTNYLDALEGLVlTGTLpVFNlTGOFPENKTYNK	480
QY	481	NOLlIGVGVNDVSLEdIKRlPrPrtLCpNkYrAIDpNGVlLHPLOKRNKSOEPYL	540
Db	481	NOLlIGVGVNDVSLEdIKRlPrPrtLCpNkYrAIDpNGVlLHPLOKRNKSOEPYL	540
QY	541	DELDALENDIKVEIRNKMDlDGESEKTEFTLlKVSODERIDKGNrTYWTPVNGTDYSL	600
Db	541	DELDALENDIKVEIRNKMDlDGESEKTEFTLlKVSODERIDKGNrTYWTPVNGTDYSL	600
QY	601	ALVlPYTSFYlTAKKEETlTQARSKKGKKMSDETLKPNFEBSGYrEiAPrDYOCDLKI	660
Db	601	ALVlPYTSFYlTAKKEETlTQARSKKGKKMSDETLKPNFEBSGYrEiAPrDYOCDLKI	660
QY	661	SDNNTEFLNNEFIIDKRTPNPNSCNAIDLINrVLDAGFTNELYONMYSKOKINlGVKAR	720
Db	661	SDNNTEFLNNEFIIDKRTPNPNSCNAIDLINrVLDAGFTNELYONMYSKOKINlGVKAR	720
QY	721	FVVTDDGITTrrYrPREAGENQENPETYEDSFYKRSIDNDONVYfTArPFNKSGPGAYESGI	780
Db	721	FVVTDDGITTrrYrPREAGENQENPETYEDSFYKRSIDNDONVYfTArPFNKSGPGAYESGI	780
QY	781	MYSRAVElTYlOGKlLKAAYVGIKlDYNStWENTKTSlNDPCAGPYCDCKRNSDVMdCVI	840
Db	781	MYSRAVElTYlOGKlLKAAYVGIKlDYNStWENTKTSlNDPCAGPYCDCKRNSDVMdCVI	840
QY	841	LDGCGFLlMANHDDYTQOIGrFGEIDPISLrMLVNIsvYrANKSsDVOsvCEPAAARQ	900
Db	841	LDGCGFLlMANHDDYTQOIGrFGEIDPISLrMLVNIsvYrANKSsDVOsvCEPAAARQ	900
QY	901	GAGHRASrYVESVADlIlQIGMMATrAAAMSlIQGLSLrTPRlLLEAVEMEDDFTASLSKQ	960
Db	901	GAGHRASrYVESVADlIlQIGMMATrAAAMSlIQGLSLrTPRlLLEAVEMEDDFTASLSKQ	960
QY	961	SClTEOrQYrFFDNDKSrFSsVLDGCMCSrIFHEKlMNTNlLlFIMVESGTCPCDTrLLI	1020
Db	961	SClTEOrQYrFFDNDKSrFSsVLDGCMCSrIFHEKlMNTNlLlFIMVESGTCPCDTrLLI	1020
QY	1021	QAEQTSDGPNPCDMVK	1036
Db	1021	QAEQTSDGPNPCDMVK	1036
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Db	1014	QARQTSOGPNPCDMVK	1029
RESULT 11			
US-08-455-543A-53			
: Sequence 53, Application us/0845543A			
: Patent No. 5792846			
: GENERAL INFORMATION:			
: APPLICANT: Harpold, Michael			
: APPLICANT: Ellis, Steven			

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? APPLICANT: Ellis, Steven
? APPLICANT: Williams, Mark
? APPLICANT: Feldman, Daniel
? APPLICANT: McCue, Ann
? APPLICANT: Brenner, Robert
? TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
? TITLE OF INVENTION: METHODS
? NUMBER OF SEQUENCES: 57
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Brown, Martin, Haller & McClain
? STREET: 1660 Union Street
? CITY: San Diego
? STATE: California
? COUNTRY: USA
? ZIP: 92101-2926
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ Version 1.5
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/455,543A
? FILING DATE: May 31, 1995
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/223,305
? FILING DATE: April 4, 1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 07/868,354
? FILING DATE: April 10, 1992
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/745,206
? FILING DATE: 15-AUG-1991
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/620,250
? FILING DATE: 30-NOV-1990
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/482,384
? FILING DATE: 20-FEB-1990
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/603,751
? FILING DATE: 04-APR-1989
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: WO PCT/US89/01408
? FILING DATE: 04-APR-1989
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/176,899
? FILING DATE: 04-APR-1988
? ATTORNEY/AGENT INFORMATION:
? NAME: Seidman, Stephanie L.
? REGISTRATION NUMBER: 33,779
? REFERENCE/DOCKET NUMBER: 6362-52517
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (619)238-0999
? TELEFAX: (619)238-0062
? INFORMATION FOR SEQ ID NO: 56:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1084 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? FRAGMENT TYPE: internal
?
? US-08-455-543A-56

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Query Match          99.0%; Score 5386.5; DB 1; Length 1084;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1028; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

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QY 1 MAAGCLATLTTLTFOSLIIPSSSEPPSAVTIKSWDKMOEDLVTLAKTASGVNOLVDI 60
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DB 1 MAAGCLATLTTLTFOSLIIPSSSEPPSAVTIKSWDKMOEDLVTLAKTASGVNOLVDI 60
QY 61 YEKYODLYVEPNNAQLEIARDIEKLISRSKALVSLALEAEKVQAHHQWREDFASN 120

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DB 61 YEKYODLYVEPNNAQLEIARDIEKLISRSKALVSLALEAEKVQAHHQWREDFASN 120
QY 121 EYVYINAKDLDPEKNDSEPSQRIKPVFIEDANFGROI SYOAAVHIPTDIYEGSTIVL 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 121 EYVYINAKDLDPEKNDSEPSQRIKPVFIEDANFGROI SYOAAVHIPTDIYEGSTIVL 180
QY 181 NELNMTSALDEYFKKREEDPSLIMOVGSATGLRKYYPASPMVNSSTPKNIDLYDVR 240
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 181 NELNMTSALDEYFKKREEDPSLIMOVGSATGLRKYYPASPMVNSSTPKNIDLYDVR 240
QY 241 RPYIIGASPKDMLILVDVSGSVGLTKLIRTSVSEMLETILSDDDVNVNASEFNSAQD 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 241 RPYIIGASPKDMLILVDVSGSVGLTKLIRTSVSEMLETILSDDDVNVNASEFNSAQD 300
QY 301 VSCFOHLVQANVRNKKVLDKAVNNITAGITDYKKGFSAFEOQLINYNVSRANCKIIML 360
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 301 VSCFOHLVQANVRNKKVLDKAVNNITAGITDYKKGFSAFEOQLINYNVSRANCKIIML 360
QY 361 FTDGGERAOELFNKYNKDKKRVFRFSYGOHNYERGPLOMACENKGYEIPISGAIR 420
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DB 361 FTDGGERAOELFNKYNKDKKRVFRFSYGOHNYERGPLOMACENKGYEIPISGAIR 420
QY 421 INTQETLDVLAGRPVYLAGDKAKOVQNTNYLDALGLVITGLTPVENITGOFENKTNLK 480
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DB 421 INTQETLDVLAGRPVYLAGDKAKOVQNTNYLDALGLVITGLTPVENITGOFENKTNLK 480
QY 481 NOLLIGVMGVDSLEDIKRLTRPFLCPNGYFAIDPNGYVLHPNLOPKNPKSGOEPTL 540
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DB 481 NOLLIGVMGVDSLEDIKRLTRPFLCPNGYFAIDPNGYVLHPNLOPKNPKSGOEPTL 540
QY 541 DELDAELENDIVEIRNKKIDSEGEKTRTVKSDERYIDKGRRTYTPVNGTDSL 600
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 541 DELDAELENDIVEIRNKKIDSEGEKTRTVKSDERYIDKGRRTYTPVNGTDSL 600
QY 601 ALVLPYTFYIIRAKLEETITQARSKKMKDSETLKPDNEESGYTPIAPDYCNLDKI 660
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DB 601 ALVLPYTFYIIRAKLEETITQARSKKMKDSETLKPDNEESGYTPIAPDYCNLDKI 660
QY 661 SDNTEFLINFEFIDRTPNPNPSCNADLINVLLDAGFTNELVQNTYKSKNITGVYAR 720
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DB 661 SDNTEFLINFEFIDRTPNPNPSCNADLINVLLDAGFTNELVQNTYKSKNITGVYAR 720
QY 721 FVYTDGGLTRVYPKRAGEWQENPETEYDSFYKSLDNDNYFTFPAFYNKSGPAGESGI 780
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 721 FVYTDGGLTRVYPKRAGEWQENPETEYDSFYKSLDNDNYFTFPAFYNKSGPAGESGI 780
QY 781 MYSKAVEIYIOGKLLKPAVAVGIKIDVNSWIENFTKTSIRDPAGPVCDCCKRNSDVCVI 840
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DB 781 MYSKAVEIYIOGKLLKPAVAVGIKIDVNSWIENFTKTSIRDPAGPVCDCCKRNSDVCVI 840
QY 841 LDDGGLFLMANHDDVTNOGRPFGEIDPSLMHLVNIISVAFNKSVDYQSCGEGAARKQ 900
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DB 841 LDDGGLFLMANHDDVTNOGRPFGEIDPSLMHLVNIISVAFNKSVDYQSCGEGAARKQ 900
QY 901 GAGHSAYVSVADILQIGWATAAAMSILQOFLSTLFFPRLLVEVEDDDFTASLSKO 960
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 901 GAGHSAYVSVADILQIGWATAAAMSILQOFLSTLFFPRLLVEVEDDDFTASLSKO 960
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DB 961 SCITEOTOYFFDNDKSFSGVLDCGNCRIHFGEKLMNTNLIIFINVESKGTGCPDTRLII 1020
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DB 1021 QAEQTSIDGPNPCDVMK 1036

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RESULT 10
US-08-223-305C-56
; Sequence 56, Application US/08223305C
; Patent No. 5851824
; GENERAL INFORMATION:

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GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/223,305C
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 52516 (P519739)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 1086 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-223-305C-54

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Query Match      99.3%; Score 5403.5; DB 2: Length 1086;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1031; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

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QY 1 MAACCLATLTTLTFLPSSEPPSAVTIKSWDKMOEDLVTLAKTASGVNOLVDI 60
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Db 1 MAACCLATLTTLTFLPSSEPPSAVTIKSWDKMOEDLVTLAKTASGVNOLVDI 60
QY 61 YEKIODLYTEPNNAKRLVEIARIDIEKLSNRSKALVSLAEKVOAHOHREDFASN 120
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Db 61 YEKIODLYTEPNNAKRLVEIARIDIEKLSNRSKALVSLAEKVOAHOHREDFASN 120
QY 121 EVVYNNAKDDLPEDKNDSEPSGQRIRKPFIEDAFNGHOISYQAAVHLPDIYEGSTIVL 180
    |||||||
Db 121 EVVYNNAKDDLPEDKNDSEPSGQRIRKPFIEDAFNGHOISYQAAVHLPDIYEGSTIVL 180
QY 181 NELMWTSLADEVEFKKNEDEPSLLMOVFGSATGLARYYPASPVWNSRTNKKIDLYVRR 240
    |||||||
Db 181 NELMWTSLADEVEFKKNEDEPSLLMOVFGSATGLARYYPASPVWNSRTNKKIDLYVRR 240
QY 241 RPWYIOGASPKDMLLVDSVGSGLTKLIRTSVSEMETLSDDDFVNVSFNSNAOD 300
    |||||||
Db 241 RPWYIOGASPKDMLLVDSVGSGLTKLIRTSVSEMETLSDDDFVNVSFNSNAOD 300
QY 301 VSCFOHLVQAVNRKRYLKDVAVNNITAKGTDYKKGSPFEBOLNANVRACNKTIML 360
    |||||||
Db 301 VSCFOHLVQAVNRKRYLKDVAVNNITAKGTDYKKGSPFEBOLNANVRACNKTIML 360
QY 361 FTDCGEERAQEIFNKYKDKVRFVRSVGOHNERGPIDMACENKGYEELPSIGAIR 420
    |||||||
Db 361 FTDCGEERAQEIFNKYKDKVRFVRSVGOHNERGPIDMACENKGYEELPSIGAIR 420
QY 421 INFOEYLDVIGRPWYLAGDKAKOVNTNVLDALEGLVTTGTLPPVNTIGOFENKTNLK 480
    |||||||
Db 421 INFOEYLDVIGRPWYLAGDKAKOVNTNVLDALEGLVTTGTLPPVNTIGOFENKTNLK 480
QY 481 NQLLIGVGVDSLEDIKRLTPRTLCPNGYFAIDPNGVLLHPNLOPNRPSQBPVL 540
    |||||||
Db 481 NQLLIGVGVDSLEDIKRLTPRTLCPNGYFAIDPNGVLLHPNLOPNRPSQBPVL 540
QY 541 DFLDAELENDIKVEIRKMTIDGESGKTFRTLVKSODERYIDKGNRTYWTVPNGTDSL 600
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Db 541 DFLDAELENDIKVEIRKMTIDGESGKTFRTLVKSODERYIDKGNRTYWTVPNGTDSL 600
QY 536 DFLDAELENDIKVEIRKMTIDGESGKTFRTLVKSODERYIDKGNRTYWTVPNGTDSL 595
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Db 536 DFLDAELENDIKVEIRKMTIDGESGKTFRTLVKSODERYIDKGNRTYWTVPNGTDSL 595
QY 601 ALVLPYTSFYIIRAKLEETITQARSKKGMKDEBTLKPNFEESGTTFTAPRYCDLKI 660
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Db 601 ALVLPYTSFYIIRAKLEETITQARSKKGMKDEBTLKPNFEESGTTFTAPRYCDLKI 660
QY 596 ALVLPYTSFYIIRAKLEETITQARSKKGMKDEBTLKPNFEESGTTFTAPRYCDLKI 655
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Db 596 ALVLPYTSFYIIRAKLEETITQARSKKGMKDEBTLKPNFEESGTTFTAPRYCDLKI 655
QY 661 SDNNTFELNFEIDRKTTPNNSCNADLINRYLDAGFTNELVQYWKSKOKNIKGVAR 720
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Db 661 SDNNTFELNFEIDRKTTPNNSCNADLINRYLDAGFTNELVQYWKSKOKNIKGVAR 720
QY 656 SDNNTFELNFEIDRKTTPNNSCNADLINRYLDAGFTNELVQYWKSKOKNIKGVAR 715
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Db 721 FVYTDGKITVYRKAGENKQENPEYEDSEFYKRSIDNDNYVTAFYFNKSGGAYESGI 780
QY 716 FVYTDGKITVYRKAGENKQENPEYEDSEFYKRSIDNDNYVTAFYFNKSGGAYESGI 775
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Db 716 FVYTDGKITVYRKAGENKQENPEYEDSEFYKRSIDNDNYVTAFYFNKSGGAYESGI 775
QY 781 MYSKAVEIYIOGKLLPAVVGIRKIDVNSWTEENTKTSIRDPGAPVCDCKRNSDWDVCYI 840
    |||||||
Db 781 MYSKAVEIYIOGKLLPAVVGIRKIDVNSWTEENTKTSIRDPGAPVCDCKRNSDWDVCYI 840
QY 776 MYSKAVEIYIOGKLLPAVVGIRKIDVNSWTEENTKTSIRDPGAPVCDCKRNSDWDVCYI 835
    |||||||
Db 776 MYSKAVEIYIOGKLLPAVVGIRKIDVNSWTEENTKTSIRDPGAPVCDCKRNSDWDVCYI 835
QY 841 LDDGCFLLMANHDDYTNOIGRFGELIDPSLMRLVNI SYAFAFKSYDYOVCPEGAAPQ 900
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Db 841 LDDGCFLLMANHDDYTNOIGRFGELIDPSLMRLVNI SYAFAFKSYDYOVCPEGAAPQ 900
QY 836 LDDGCFLLMANHDDYTNOIGRFGELIDPSLMRLVNI SYAFAFKSYDYOVCPEGAAPQ 895
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Db 836 LDDGCFLLMANHDDYTNOIGRFGELIDPSLMRLVNI SYAFAFKSYDYOVCPEGAAPQ 895
QY 901 GAGHRSAVYPSVADIIQIGMATLAAMSILQOFLSLTEPRLLAEVEMEDDFTASLSKO 960
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Db 896 GAGHRSAVYPSVADIIQIGMATLAAMSILQOFLSLTEPRLLAEVEMEDDFTASLSKO 955
QY 961 SCITTEOTYFFNDKSPFSGVLDGCMSCRIIFGEKLMNTNLIIFINVESGTCPCDTRLII 1020
    |||||||
Db 961 SCITTEOTYFFNDKSPFSGVLDGCMSCRIIFGEKLMNTNLIIFINVESGTCPCDTRLII 1020
QY 956 SCITTEOTYFFNDKSPFSGVLDGCMSCRIIFGEKLMNTNLIIFINVESGTCPCDTRLII 1015
    |||||||
Db 956 SCITTEOTYFFNDKSPFSGVLDGCMSCRIIFGEKLMNTNLIIFINVESGTCPCDTRLII 1015
QY 1021 QABQTSIDGPNPCDMVK 1036
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Db 1016 QABQTSIDGPNPCDMVK 1031
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RESULT 9
US-08-455-543A-56
; Sequence 56, Application US/0845543A
; Patent No. 5792846
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael

```

APPLICANT: Harpold, Michael  
 APPLICANT: Ellis, Steven  
 APPLICANT: Williams, Mark  
 APPLICANT: Feldman, Daniel  
 APPLICANT: McCue, Ann  
 APPLICANT: Brenner, Robert  
 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
 NUMBER OF SEQUENCES: 57  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Brown, Martin, Haller & McClain  
 STREET: 1660 Union Street  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92101-2926  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/455,543A  
 FILING DATE: May 31, 1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/223,305  
 FILING DATE: April 4, 1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/868,354  
 FILING DATE: April 10, 1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/745,206  
 FILING DATE: 15-AUG-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/620,250  
 FILING DATE: 30-NOV-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/482,384  
 FILING DATE: 20-FEB-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/603,751  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/US89/01408  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/176,899  
 FILING DATE: 04-APR-1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie L.  
 REGISTRATION NUMBER: 73,779  
 REFERENCE/DOCKET NUMBER: 6362-52517  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619)238-0999  
 TELEFAX: (619)238-0062  
 INFORMATION FOR SEQ ID NO: 54:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1086 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-455-543A-54

Query Match 99.3%; Score 5403.5; DB 1; Length 1086;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 1031; Conservative 0; Mismatches 0; Indels 5; Gaps 1;  
 QY 1 MAAGCLATLTITLFGSLLIGSPSEPPPSAVTIKSWDKMOEDLVTLATASGVNOLVDI 60  
 DB 1 MAAGCLATLTITLFGSLLIGSPSEPPPSAVTIKSWDKMOEDLVTLATASGVNOLVDI 60

QY 61 YEKYODLYTVEPNNAQOLVELIARDIEKLNSRKALVSLALEAKVQAAHQWREDFASN 120  
 DB 61 YEKYODLYTVEPNNAQOLVELIARDIEKLNSRKALVSLALEAKVQAAHQWREDFASN 120  
 QY 121 EYVYTNKADLDLPEKNDSEPSQRIKPYFIEDANFGQISTQHAAYIIPDIYEGSTIVL 180  
 DB 121 EYVYTNKADLDLPEKNDSEPSQRIKPYFIEDANFGQISTQHAAYIIPDIYEGSTIVL 180  
 QY 181 NELNMTSALDEVEFKKNEDEPSILMOYFGSATGLARYPASPWNDNRTNKKIDLYVRR 240  
 DB 181 NELNMTSALDEVEFKKNEDEPSILMOYFGSATGLARYPASPWNDNRTNKKIDLYVRR 240  
 QY 241 RPWYIQAASPKDMLLVDSGVSGLTLKLI RTSVSEMLETISDDDFVNVASFNSNAOD 300  
 DB 241 RPWYIQAASPKDMLLVDSGVSGLTLKLI RTSVSEMLETISDDDFVNVASFNSNAOD 300  
 QY 301 VSCFOHLVQANVRKKYKADAVNNITAKGTIDYKKGSSFAEQLANNVSRANCKITML 360  
 DB 301 VSCFOHLVQANVRKKYKADAVNNITAKGTIDYKKGSSFAEQLANNVSRANCKITML 360  
 QY 361 FTDGEERAQEIFNKKYKRVFRFSVGOHNERGPIDQMACENKGYEIEPSIGAIR 420  
 DB 361 FTDGEERAQEIFNKKYKRVFRFSVGOHNERGPIDQMACENKGYEIEPSIGAIR 420  
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 DB 421 INFOEYLDVIGRPVYLADGKAKQVQWTVNYLDALGLVITGTLPVENITGOEENKTNLK 480  
 QY 481 NQILIGVGVSVLEDIRLTPRTFLCPNGYFPAIDPBGVYLLHPNQPKQEPVTL 540  
 DB 481 NQILIGVGVSVLEDIRLTPRTFLCPNGYFPAIDPBGVYLLHPNQPKQEPVTL 540  
 QY 541 DFLDALENDIKVEIRNKMIDGSEGEKTRTLVASODERYIDKGNRTYTTPVNGTDSL 600  
 DB 541 DFLDALENDIKVEIRNKMIDGSEGEKTRTLVASODERYIDKGNRTYTTPVNGTDSL 600  
 QY 596 ALVLPYTFYIYIKAKLEETITQARSKGKMDSETLKPDNEESGYTFIAPROYCNDLKI 655  
 DB 596 ALVLPYTFYIYIKAKLEETITQARSKGKMDSETLKPDNEESGYTFIAPROYCNDLKI 655  
 QY 661 SDNTEFLNFEFLDRKTPNNPSCNDLIRVLLDGFTELQVONWSKOKNIKGVYKAR 720  
 DB 661 SDNTEFLNFEFLDRKTPNNPSCNDLIRVLLDGFTELQVONWSKOKNIKGVYKAR 720  
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 DB 721 FVYTDGGITRYYPKEAGENMOENPEYEDSFYKRSLLDNDNYVFTAPYFNKSGPAYESGI 780  
 QY 761 MYSKAVEIYIOGKLKLPAAVVGIKIDVNSWINEFTKTSIRDPACAPVDCCKRNSVMDCVI 840  
 DB 761 MYSKAVEIYIOGKLKLPAAVVGIKIDVNSWINEFTKTSIRDPACAPVDCCKRNSVMDCVI 840  
 QY 841 IDDGGEFLMANHNDYTNOIGRFFGIDPSLRHLVYNISVYAFNKSSTYDQSCCEGAAPKQ 900  
 DB 841 IDDGGEFLMANHNDYTNOIGRFFGIDPSLRHLVYNISVYAFNKSSTYDQSCCEGAAPKQ 900  
 QY 896 GAGHRSAYVPSVADILQIGMWATAAASIILOFLLSTLFPRLBAVEDEDDFTASISKQ 955  
 DB 896 GAGHRSAYVPSVADILQIGMWATAAASIILOFLLSTLFPRLBAVEDEDDFTASISKQ 955  
 QY 961 SCITRQTOYFFPDNDKSRFSGVLDGNCGRIFRGEKLMNTNLIIFIMVESKGCPCDDTLILI 1020  
 DB 961 SCITRQTOYFFPDNDKSRFSGVLDGNCGRIFRGEKLMNTNLIIFIMVESKGCPCDDTLILI 1020  
 QY 1021 CAEOTSDGPNPCDMMK 1036  
 DB 1021 CAEOTSDGPNPCDMMK 1036

RESULT 8  
 US-08-223-305C-54  
 ; Sequence 54, Application US/08223305C  
 ; Patent No. 3651824



Db 781 MSKAVEIYIOGKLLKPAVVGIRKIDVNSWIENFTKTSIRDPGAGVPCDCKRNSDVMDCVI 840  
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QY 901 GAGHRSAYVPSVADIIQIGWATAAAMSTLQOFLSLTFPRLLAEVEMDDDFSTASLSKQ 960  
Db 901 GAGHRSAYVPSVADIIQIGWATAAAMSTLQOFLSLTFPRLLAEVEMDDDFSTASLSKQ 960  
QY 961 SCITTEOTYFFENDSKSFSGVLDGNCNSRIFFGEKLMNTLFIWESKGTCPDTRLLI 1020  
Db 961 SCITTEOTYFFENDSKSFSGVLDGNCNSRIFFGEKLMNTLFIWESKGTCPDTRLLI 1020  
QY 1021 QAEOTSDGPNPCDMVK 1036  
Db 1021 QAEOTSDGPNPCDMVK 1036

RESULT 6  
US-09-452-007-4  
; Sequence 4, Application US/09452007  
; Patent No. 6140485  
; GENERAL INFORMATION:  
; APPLICANT: Franco, Rodrigo  
; APPLICANT: Sun Chen, Ai Ru  
; APPLICANT: Sney, David J.  
; TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Millitia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173-4799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/452,007  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/713,118  
; FILING DATE: 16-SEP-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mata, Elizabeth W.  
; REGISTRATION NUMBER: 38,236  
; REFERENCE/DOCKET NUMBER: ACC96-01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-861-6240  
; TELEFAX: 617-861-9540  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1091 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-452-007-4

Query Match 99.98; Score 5439; DB 4; Length 1091;  
Best Local Similarity 99.98; Pred. No. 0;  
Matches 1035; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAGCLALATLTLFOSLLIGPSSSEPPSAVTIKSWYDKMOEDIVTLAKTASGVNOIVDI 60  
Db 1 MAAGCLALATLTLFOSLLIGPSSSEPPSAVTIKSWYDKMOEDIVTLAKTASGVNOIVDI 60  
QY 61 YEKYODLYTVEPNNAKOLVETIARDIEKLLSNRSKALVSLALEAEKVOAQAHWREDFASN 120

Db 61 YEKYODLYTVEPNNAKOLVETIARDIEKLLSNRSKALVSLALEAEKVOAQAHWREDFASN 120  
QY 121 EVVYNNAKDDLDLPPKNSPEPQRIKRPVLTEDAFNGQISYQHAAYHPIPDIEGISTYL 180  
Db 121 EVVYNNAKDDLDLPPKNSPEPQRIKRPVLTEDAFNGQISYQHAAYHPIPDIEGISTYL 180  
QY 181 NELMWTSAIDVEFKKNEDEPSSLMOVFGSATGLARYPPASPWVDSRTPNKIDLYDVR 240  
Db 181 NELMWTSAIDVEFKKNEDEPSSLMOVFGSATGLARYPPASPWVDSRTPNKIDLYDVR 240  
QY 241 RPYITOGAASPKDMLILVDYSGSYGTLKILRISVSEMLFTSDDDFVAVASFNSAOD 300  
Db 241 RPYITOGAASPKDMLILVDYSGSYGTLKILRISVSEMLFTSDDDFVAVASFNSAOD 300  
QY 301 VSCFOHLVQANVRNKKVILKDVNNITAKGILTDYKKGSFAPBOLUNYNSRACNKTIML 360  
Db 301 VSCFOHLVQANVRNKKVILKDVNNITAKGILTDYKKGSFAPBOLUNYNSRACNKTIML 360  
QY 361 FTDGEERAQIEFNKYNKDKRVFRFSVGOHNERGPIDMACENKGYEELPSIGAIR 420  
Db 361 FTDGEERAQIEFNKYNKDKRVFRFSVGOHNERGPIDMACENKGYEELPSIGAIR 420  
QY 421 INTQEVLDVIGRPVYLAGDKAKOVQWNTNYLDALLEGVLTGTLPPVNTITGOFENKTNLK 480  
Db 421 INTQEVLDVIGRPVYLAGDKAKOVQWNTNYLDALLEGVLTGTLPPVNTITGOFENKTNLK 480  
QY 481 NQILIGVAGDVSLIEDIKRLTPRTLCPNGYFAIDPNGVYLHPNLOPNRPSQSPVTL 540  
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QY 541 DFLDAELENDIKVEIRNKMIDGESGEKTFRTLVKSODERYIDKGNRTYWTYPNGIDYSL 600  
Db 541 DFLDAELENDIKVEIRNKMIDGESGEKTFRTLVKSODERYIDKGNRTYWTYPNGIDYSL 600  
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Db 661 SDNNTTEFLNFEIDRKTPNPNPCNADLTNRVLDAGFTNGLVQYWKSKOKNIKGVAR 720  
QY 721 FVYTDGCTVYVYKREGENKQENPEYEDSFYKRSIDNDNYVTAFYFNKSGGAYESGI 780  
Db 721 FVYTDGCTVYVYKREGENKQENPEYEDSFYKRSIDNDNYVTAFYFNKSGGAYESGI 780  
QY 781 MSKAVEIYIOGKLLKPAVVGIRKIDVNSWIENFTKTSIRDPGAGVPCDCKRNSDVMDCVI 840  
Db 781 MSKAVEIYIOGKLLKPAVVGIRKIDVNSWIENFTKTSIRDPGAGVPCDCKRNSDVMDCVI 840  
QY 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRLVNIISYAFKNSDYOSVCEPGAARQ 900  
Db 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRLVNIISYAFKNSDYOSVCEPGAARQ 900  
QY 901 GAGHRSAYVPSVADIIQIGWATAAAMSTLQOFLSLTFPRLLAEVEMDDDFSTASLSKQ 960  
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QY 961 SCITTEOTYFFENDSKSFSGVLDGNCNSRIFFGEKLMNTLFIWESKGTCPDTRLLI 1020  
Db 961 SCITTEOTYFFENDSKSFSGVLDGNCNSRIFFGEKLMNTLFIWESKGTCPDTRLLI 1020  
QY 1021 QAEOTSDGPNPCDMVK 1036  
Db 1021 QAEOTSDGPNPCDMVK 1036

RESULT 7  
US-08-455-543A-54  
; Sequence 54, Application US/08455543A  
; Patent No. 5792846  
; GENERAL INFORMATION:



Db 61 YEKYODLYTVEPNNARQVLEIAARDIEKLISNSKALVSLALEAEVQAAHOREFASN 120  
QY 121 EYVYNAKDDLDPEKNDSEPSQRIKPVFIEDANFGROISYQAAVHIPTDIYEGSTIYL 180  
Db 121 EYVYNAKDDLDPEKNDSEPSQRIKPVFIEDANFGROISYQAAVHIPTDIYEGSTIYL 180  
QY 181 NELNMTSALDEVEFKKREDEPSLLMOVFGSATGLARYYPASPVWDSRTPNKIDLYVRR 240  
Db 181 NELNMTSALDEVEFKKREDEPSLLMOVFGSATGLARYYPASPVWDSRTPNKIDLYVRR 240  
QY 241 RPYWIOGASPKDMLILDVSGSVGLTLKLIPTSVSEMLETSDDDPFVAVASFNNAOD 300  
Db 241 RPYWIOGASPKDMLILDVSGSVGLTLKLIPTSVSEMLETSDDDPFVAVASFNNAOD 300  
QY 301 VSCFOHLYOANVRNKKVYLKDAVNNITAKGITYDKKGSFAEQLLNVNSRANCKITIML 360  
Db 301 VSCFOHLYOANVRNKKVYLKDAVNNITAKGITYDKKGSFAEQLLNVNSRANCKITIML 360  
QY 361 FTDGGEERAQEIFNKYNKDKKVVFRFVSQGHNERGPIDMACENKGYEYIETPSIGAIR 420  
Db 361 FTDGGEERAQEIFNKYNKDKKVVFRFVSQGHNERGPIDMACENKGYEYIETPSIGAIR 420  
QY 421 INTQEVLDVGRPMVLADGKAKQVMTNYLDALLEGVITGTPLPVFNITGOFENKTNLK 480  
Db 421 INTQEVLDVGRPMVLADGKAKQVMTNYLDALLEGVITGTPLPVFNITGOFENKTNLK 480  
QY 481 NOILITGVGVDSLEDIKRLTPFTLCPPNGYFAIDPNCVLLHPNLOPKNPKSQEPVTL 540  
Db 481 NOILITGVGVDSLEDIKRLTPFTLCPPNGYFAIDPNCVLLHPNLOPKNPKSQEPVTL 540  
QY 541 DFLDAELENDIKVEIKNNKMDGSGEKFTPLTKSODEBYIDKNGTNTWTPVNGDYSL 600  
Db 541 DFLDAELENDIKVEIKNNKMDGSGEKFTPLTKSODEBYIDKNGTNTWTPVNGDYSL 600  
QY 601 ALVLPYSEFYIKAKLEETITQARSKKGMKDETLKPNFESGYTFLAPRDYCDLKI 660  
Db 601 ALVLPYSEFYIKAKLEETITQARSKKGMKDETLKPNFESGYTFLAPRDYCDLKI 660  
QY 661 SDNTEFLNENFIDRKTPNNPNSCADLINRYLDAGTNNELVONTYSKOKNIKGVAR 720  
Db 661 SDNTEFLNENFIDRKTPNNPNSCADLINRYLDAGTNNELVONTYSKOKNIKGVAR 720  
QY 721 FVYTDGSTRVRYKPEAGEMOENPETEYEDSFYKRSLDNNYFTAYFNKSGPAAEESI 780  
Db 721 FVYTDGSTRVRYKPEAGEMOENPETEYEDSFYKRSLDNNYFTAYFNKSGPAAEESI 780  
QY 781 MYSKAVEIYIOGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPGACPVCDCKRNSDVMDCYI 840  
Db 781 MYSKAVEIYIOGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPGACPVCDCKRNSDVMDCYI 840  
QY 841 LDDGGFLMANHDDYTNQIGREFGEIDBSLMRLVNI SYAANKSTYDQSVCEPGAAPKO 900  
Db 841 LDDGGFLMANHDDYTNQIGREFGEIDBSLMRLVNI SYAANKSTYDQSVCEPGAAPKO 900  
QY 901 GAGHRSAYVPSVADIIQIOMMATAAAMSTIIOQLSLTFRPRLLEAVEMDDFTASLSKQ 960  
Db 901 GAGHRSAYVPSVADIIQIOMMATAAAMSTIIOQLSLTFRPRLLEAVEMDDFTASLSKQ 960  
QY 961 SCITTEQYFEPNDKSFSGVLDGCGNSRI FHEGKLMNTNLIF INVESKGTGPCDTRLI 1020  
Db 961 SCITTEQYFEPNDKSFSGVLDGCGNSRI FHEGKLMNTNLIF INVESKGTGPCDTRLI 1020  
QY 1021 OAEQTSIDGPNPCDMYK 1036  
Db 1021 OAEQTSIDGPNPCDMYK 1036

RESULT 4  
US-08-311-363-25  
; Sequence 25, Application US/08311363  
; Patent No. 5876958  
; GENERAL INFORMATION:

APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McQue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: Human Calcium Channel Compositions and  
TITLE OF INVENTION: Methods  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/311,363  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-51506  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1091 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-311-363-25  
Query Match 100.0%; Score 5443; DB 2; Length 1091;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAAGCLLALTTILFOSLLIGPSSEEPFSPATITKSWDKMOEDLVTLAKTASGVNOLYDI 60  
Db 1 MAAGCLLALTTILFOSLLIGPSSEEPFSPATITKSWDKMOEDLVTLAKTASGVNOLYDI 60  
QY 61 YEKYODLYTVEPNNARQVLEIAARDIEKLISNSKALVSLALEAEVQAAHOREFASN 120  
Db 61 YEKYODLYTVEPNNARQVLEIAARDIEKLISNSKALVSLALEAEVQAAHOREFASN 120  
QY 121 EYVYNAKDDLDPEKNDSEPSQRIKPVFIEDANFGROISYQAAVHIPTDIYEGSTIYL 180  
Db 121 EYVYNAKDDLDPEKNDSEPSQRIKPVFIEDANFGROISYQAAVHIPTDIYEGSTIYL 180  
QY 181 NELNMTSALDEVEFKKREDEPSLLMOVFGSATGLARYYPASPVWDSRTPNKIDLYVRR 240  
Db 181 NELNMTSALDEVEFKKREDEPSLLMOVFGSATGLARYYPASPVWDSRTPNKIDLYVRR 240  
QY 241 RPYWIOGASPKDMLILDVSGSVGLTLKLIPTSVSEMLETSDDDPFVAVASFNNAOD 300  
Db 241 RPYWIOGASPKDMLILDVSGSVGLTLKLIPTSVSEMLETSDDDPFVAVASFNNAOD 300  
QY 301 VSCFOHLYOANVRNKKVYLKDAVNNITAKGITYDKKGSFAEQLLNVNSRANCKITIML 360  
Db 301 VSCFOHLYOANVRNKKVYLKDAVNNITAKGITYDKKGSFAEQLLNVNSRANCKITIML 360  
QY 361 FTDGGEERAQEIFNKYNKDKKVVFRFVSQGHNERGPIDMACENKGYEYIETPSIGAIR 420  
Db 361 FTDGGEERAQEIFNKYNKDKKVVFRFVSQGHNERGPIDMACENKGYEYIETPSIGAIR 420

QY 61 YEKYODLYTEVPNNAROLVEIARDIEKLSNSKALVSLAEAEVVOAHQWREDFASN 120  
| | | | |  
Db 61 YEKYODLYTEVPNNAROLVEIARDIEKLSNSKALVSLAEAEVVOAHQWREDFASN 120  
QY 121 EYVYNNAKDLDPEKNDSEFSGORIKPVFIEDANFGROISYOHAAVHIPDIYEGSTIYL 180  
| | | | |  
Db 121 EYVYNNAKDLDPEKNDSEFSGORIKPVFIEDANFGROISYOHAAVHIPDIYEGSTIYL 180  
QY 181 NEINMTSALDEVEFKKNEEDPSILMOVFGSATGLARYPASPVWDSRTPNKIDLDVDR 240  
| | | | |  
Db 181 NEINMTSALDEVEFKKNEEDPSILMOVFGSATGLARYPASPVWDSRTPNKIDLDVDR 240  
QY 241 RPYVIGGAASPKMMLIVYSSVSGITLKLITSVSEMETISDDDFVNVASFNSNAD 300  
| | | | |  
Db 241 RPYVIGGAASPKMMLIVYSSVSGITLKLITSVSEMETISDDDFVNVASFNSNAD 300  
QY 301 VSCFOHLVQANVRNKKVYLKDAVNNITAKGTTDKKGFSAFEOLLVNVNSRACNKTIML 360  
| | | | |  
Db 301 VSCFOHLVQANVRNKKVYLKDAVNNITAKGTTDKKGFSAFEOLLVNVNSRACNKTIML 360  
QY 361 FTDGERAEQEIFNKNYKDKKRVFRPSVGOHNYERGPLOMMACENKGYEYIETPSIGAIR 420  
| | | | |  
Db 361 FTDGERAEQEIFNKNYKDKKRVFRPSVGOHNYERGPLOMMACENKGYEYIETPSIGAIR 420  
QY 421 INTQETLDVIGRPMVLAGDKAKOVONTNYLALGLVITGTLVPFNITGCEPKNTNLK 480  
| | | | |  
Db 421 INTQETLDVIGRPMVLAGDKAKOVONTNYLALGLVITGTLVPFNITGCEPKNTNLK 480  
QY 481 NOLILGVMGVDSLEDIKRLTPRETLCPPNGYPAIDPNCVLLHPMLQKRNPSOEPVTL 540  
| | | | |  
Db 481 NOLILGVMGVDSLEDIKRLTPRETLCPPNGYPAIDPNCVLLHPMLQKRNPSOEPVTL 540  
QY 541 DFLDAELNDIKVEIKRNKMDIGESGERTTLVKSODEERYIDKGNFTWTPVNGTDSYL 600  
| | | | |  
Db 541 DFLDAELNDIKVEIKRNKMDIGESGERTTLVKSODEERYIDKGNFTWTPVNGTDSYL 600  
QY 601 ALVLPYTSFYIYAKLEETITQARSKKGMKDESETIKPDNEESGTTFTAPRDYCDLKI 660  
| | | | |  
Db 601 ALVLPYTSFYIYAKLEETITQARSKKGMKDESETIKPDNEESGTTFTAPRDYCDLKI 660  
QY 661 SDNTEFEILNFNEFIDRKTPNNNSCANADLIRYLDAGFTNELVONYWYSKOKNIKGVKAR 720  
| | | | |  
Db 661 SDNTEFEILNFNEFIDRKTPNNNSCANADLIRYLDAGFTNELVONYWYSKOKNIKGVKAR 720  
QY 721 FVVTDCGTRVYRPEKAGEWMOENPETYEDSFYKRSIDNDNVYFTAFYFNKSGPAGAYESGI 780  
| | | | |  
Db 721 FVVTDCGTRVYRPEKAGEWMOENPETYEDSFYKRSIDNDNVYFTAFYFNKSGPAGAYESGI 780  
QY 781 MYSKAVEIYIOGKLLKPAVVGIRKIDVNSWIEFNTKTSINDPCAGPVCDCRNSDVWDCYI 840  
| | | | |  
Db 781 MYSKAVEIYIOGKLLKPAVVGIRKIDVNSWIEFNTKTSINDPCAGPVCDCRNSDVWDCYI 840  
QY 841 LDDGGFLMANHDDYTNQIGREFEIDPISLRHLVVISYAFANKSDVQSVCEPGAAPQ 900  
| | | | |  
Db 841 LDDGGFLMANHDDYTNQIGREFEIDPISLRHLVVISYAFANKSDVQSVCEPGAAPQ 900  
QY 901 GAGHRSAYVPSVADILQIGMATAAWSILQOFLSLTPRRLLEAVEMEDDFTASLSKO 960  
| | | | |  
Db 901 GAGHRSAYVPSVADILQIGMATAAWSILQOFLSLTPRRLLEAVEMEDDFTASLSKO 960  
QY 961 SCTTEGTOYFFPNDKSFSGVILDCGNCSTIFHEGKLMNTNLIIFINVESGTCPCDTRLII 1020  
| | | | |  
Db 961 SCTTEGTOYFFPNDKSFSGVILDCGNCSTIFHEGKLMNTNLIIFINVESGTCPCDTRLII 1020  
QY 1021 QAEQTSIDGPNPCDMYK 1036  
| | | | |  
Db 1021 QAEQTSIDGPNPCDMYK 1036

RESULT 3  
US-08-223-305C-52  
; Sequence 52, Application US/08223305C

Patent No. 5851824  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/223,305C  
FILING DATE: April 4, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 52516 (P519739)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1091 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: Internal  
US-08-223-305C-52

Query Match 100.0%; Score 5443; DB 2; Length 1091;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLIALTLTLFQSLIGSPSEPPSAVTIKSWDKMQEDLVTLAKTASGVNOLVDI 60  
| | | | |  
Db 1 MAAGCLIALTLTLFQSLIGSPSEPPSAVTIKSWDKMQEDLVTLAKTASGVNOLVDI 60  
QY 61 YEKYODLYTEVPNNAROLVEIARDIEKLSNSKALVSLAEAEVVOAHQWREDFASN 120

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QY 61 YEKYODLYTVEBNNAKOLVEIAARDIEKLSNRKALVSLALEAKVOAHOQWREDFASN 120
Db 61 YEKYODLYTVEBNNAKOLVEIAARDIEKLSNRKALVSLALEAKVOAHOQWREDFASN 120
QY 121 EYVYVYNAKDDLDPEKNDESPGSRKIPVFIEDANFGROISYOHAAVHIPTDIYESTIVL 180
Db 121 EYVYVYNAKDDLDPEKNDESPGSRKIPVFIEDANFGROISYOHAAVHIPTDIYESTIVL 180
QY 181 NELNMTSALDEVYKKNREEDPSLMQVFGSATGLARYYPASPMWDSRTPKIDLYDVR 240
Db 181 NELNMTSALDEVYKKNREEDPSLMQVFGSATGLARYYPASPMWDSRTPKIDLYDVR 240
QY 241 RFWYIOGAASPKDMLLVDSVSGSLTKLRISVSSEMLETSLDDDDVNAVASFNSNAD 300
Db 241 RFWYIOGAASPKDMLLVDSVSGSLTKLRISVSSEMLETSLDDDDVNAVASFNSNAD 300
QY 301 VSCFOHVOANRNKKVYLDVANNITAGITDYKKGFSFAEQLLNVVSRANCKITML 360
Db 301 VSCFOHVOANRNKKVYLDVANNITAGITDYKKGFSFAEQLLNVVSRANCKITML 360
QY 361 FTDGEEBAAQEIFNKYNKDKAVRFESVGOHNERGPIQWMAKCNKGYEIPSIGAIR 420
Db 361 FTDGEEBAAQEIFNKYNKDKAVRFESVGOHNERGPIQWMAKCNKGYEIPSIGAIR 420
QY 421 INTQEVLYIGRPMVLAGDKAKOVQWTVYLDALGLVITGTLPVNMTTQGFENKTMLK 480
Db 421 INTQEVLYIGRPMVLAGDKAKOVQWTVYLDALGLVITGTLPVNMTTQGFENKTMLK 480
QY 481 NOLILGVNGVDSLBDIKRLPRFLCPNGYFAIDPMGYVLLIHPNLOPKPKSOEPTL 540
Db 481 NOLILGVNGVDSLBDIKRLPRFLCPNGYFAIDPMGYVLLIHPNLOPKPKSOEPTL 540
QY 541 DFLDAELENDIKVEIRNKKMIDGSESEKTFRLVKSQDERYIDKGNRYTWTVPNGTDSL 600
Db 541 DFLDAELENDIKVEIRNKKMIDGSESEKTFRLVKSQDERYIDKGNRYTWTVPNGTDSL 600
QY 601 ALVLTYSFYIYIKAKLEETIIOARSKKGMKMOSETLKPDPNEESYTTIARDCNDIKI 660
Db 601 ALVLTYSFYIYIKAKLEETIIOARSKKGMKMOSETLKPDPNEESYTTIARDCNDIKI 660
QY 661 SDNNTFELNNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVONVSKONIKGVAR 720
Db 661 SDNNTFELNNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVONVSKONIKGVAR 720
QY 721 FVYTGCGITRYVPRKAGENWQENPETYEDSYKRSLDNDNYFTAPYNNKSGPAYESGI 780
Db 721 FVYTGCGITRYVPRKAGENWQENPETYEDSYKRSLDNDNYFTAPYNNKSGPAYESGI 780
QY 781 MYSKAVEITYOGKLLKPAVVGKIDVNSMIENFTKSTIRDCAGVYCDCKRNSDVMCVI 840
Db 781 MYSKAVEITYOGKLLKPAVVGKIDVNSMIENFTKSTIRDCAGVYCDCKRNSDVMCVI 840
QY 841 LDDGFFLLMANHDDYTNIGREFGEIDPSLMRHLVNSIVAFNKSVDYOSVCEPAARQ 900
Db 841 LDDGFFLLMANHDDYTNIGREFGEIDPSLMRHLVNSIVAFNKSVDYOSVCEPAARQ 900
QY 901 GAGHSAYVPSVADILQIGWMTAAWSILOOFLSLTFPRLLEAWEDEDDFTASLSKQ 960
Db 901 GAGHSAYVPSVADILQIGWMTAAWSILOOFLSLTFPRLLEAWEDEDDFTASLSKQ 960
QY 961 SCITQOTQFFPNDKSPFSGVLDGNCGRIFRGEKLMNTNLIIFWESKGTCPDCTRLI 1020
Db 961 SCITQOTQFFPNDKSPFSGVLDGNCGRIFRGEKLMNTNLIIFWESKGTCPDCTRLI 1020
QY 1021 QAEQTSDEGNPCDMVK 1036
Db 1021 QAEQTSDEGNPCDMVK 1036

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GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSER: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
FILING DATE: May 31, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-455-543A-52

Query Match 100.0%; Score 5443; DB 1; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAACGLATLTLTFLQSLILGSSSEPPPSAVTIKSWDKMOEPLVTLAKTASGVNOLYDI 60
Db 1 MAACGLATLTLTFLQSLILGSSSEPPPSAVTIKSWDKMOEPLVTLAKTASGVNOLYDI 60

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 10, 2003, 14:13:55 ; Search time 11.4906 Seconds

(without alignments)  
2652.785 Million cell updates/sec

Title: US-10-090-827-14

Perfect score: 5443  
Sequence: 1 MAAGCLALTLTFLQSLILIG.....RLIQAQETSDGPNPCDMVK 1036

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents\_AA.\*

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3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PCRTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	5443	100.0	1091	2	US-08-223-305C-52
4	5443	100.0	1091	2	US-08-311-363-25
5	5439	99.9	1091	3	US-08-713-118-4
6	5439	99.9	1091	4	US-08-452-007-4
7	5403.5	99.3	1086	1	US-08-455-543A-54
8	5403.5	99.3	1086	2	US-08-223-305C-54
9	5386.5	99.0	1084	1	US-08-455-543A-56
10	5386.5	99.0	1084	2	US-08-223-305C-56
11	5367	98.6	1103	1	US-08-455-543A-53
12	5367	98.6	1103	2	US-08-223-305C-53
13	5347	98.2	1079	1	US-08-455-543A-55
14	5347	98.2	1079	2	US-08-223-305C-55
15	5229.5	96.1	1106	1	US-08-435-675B-5
16	5229.5	96.1	1106	2	US-08-435-675B-5
17	4978.5	91.5	1086	6	US-08-336-257A-8
18	2907.5	53.4	1145	4	US-09-470-443-2
19	2907.5	53.4	1145	4	US-09-470-443-4
20	2886.5	53.0	1076	4	US-09-470-443-6
21	2581.5	47.4	508	1	US-08-435-675B-6
22	182	3.3	885	3	US-09-074-579-5
23	182	3.3	885	4	US-09-388-774-5
24	159.5	2.9	946	3	US-09-074-579-3
25	159.5	2.9	946	4	US-09-388-774-3
26	158.5	2.9	894	4	US-09-071-035-248
27	158.5	2.9	962	4	US-09-071-035-246

28	158.5	2.9	962	4	US-09-071-035-250	Sequence 250, App
29	158.5	2.9	962	4	US-09-071-035-254	Sequence 254, App
30	158.5	2.9	962	4	US-09-071-035-470	Sequence 470, App
31	158.5	2.9	962	4	US-09-071-035-474	Sequence 474, App
32	158.5	2.9	962	4	US-09-071-035-478	Sequence 478, App
33	154.5	2.8	946	4	US-09-546-153-1	Sequence 1, Appl1
34	154	2.8	903	1	US-08-021-601-12	Sequence 12, Appl1
35	154	2.8	903	1	US-08-082-849B-12	Sequence 12, Appl1
36	154	2.8	903	5	PCT-US94-01624-12	Sequence 12, Appl1
37	152.5	2.8	789	1	US-08-471-033-32	Sequence 32, Appl1
38	152.5	2.8	789	2	US-08-471-044-32	Sequence 32, Appl1
39	152.5	2.8	789	2	US-08-463-483A-32	Sequence 32, Appl1
40	152.5	2.8	789	2	US-08-471-046A-32	Sequence 32, Appl1
41	152.5	2.8	789	2	US-08-470-566B-32	Sequence 32, Appl1
42	152.5	2.8	789	2	US-08-838-219B-4	Sequence 32, Appl1
43	152.5	2.8	789	2	US-08-469-334-32	Sequence 32, Appl1
44	152.5	2.8	789	3	US-09-300-529-32	Sequence 32, Appl1
45	152.5	2.8	789	3	US-09-233-336A-4	Sequence 4, Appl1

## ALIGNMENTS

RESULT 1  
US-07-745-206A-25  
Sequence 25, Application US/07745206A  
Patent No. 5429921

## GENERAL INFORMATION:

APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: McCue, Ann  
APPLICANT: Feldman, Daniel  
TITLE OF INVENTION: Human Calcium Channel Compositions and  
TITLE OF INVENTION: Methods  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Fitch, Even, Tabin & Flannery  
STREET: 135 S. LaSalle  
CITY: Chicago  
STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60603

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07745,206A  
FILING DATE: 19910815  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Feder, Scott B  
REFERENCE/DOCKET NUMBER: 51504  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-372-7842  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1091 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-745-206A-25

Query Match 100.0%; Score 5443; DB 1; Length 1091;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLALTLTFLQSLIGSPSPSPATYIKSWDKMOEDLVTLAKTAGVNOALVDI 60  
DB 1 MAAGCLALTLTFLQSLIGSPSPSPATYIKSWDKMOEDLVTLAKTAGVNOALVDI 60



Tue Feb 11 13:47:51 2003

us-10-090-827-13.raii

Page 15

Search completed: February 10, 2003, 14:23:26  
Job time : 16.291 secs

QY	1	MAAGLILTLILFSS--LLIGPSSSEPPSAVYIKSWYKXMDLTYLAKTASNGOLY	58
Db	1	MAAGRIAMTLILQAMLILIGPSSSEPPSAVYIKSWYKXMDLTYLAKTASNGOLY	60
QY	59	DIYEKYODLYVEPNNAHQVEIARDIEKLISNRSAIYSLALEAKVOAAHOWREDA	118
Db	61	DIYEKYODLYVEPNNAHQVEIARDIEKLISNRSAIYSLALEAKVOAAHOWREDA	120
QY	119	SNEVYYNAKDDLPKEDKSDSPGSOIRIKPVEIDANGCROISYOHAAVHPPDIYSGST	178
Db	121	SNEVYYNAKDDLPKEDKSDSPGSOIRIKPVEIDANGCROISYOHAAVHPPDIYSGST	180
QY	179	VINELNMTSALDEWFKKNREDBPSILMQVEGSATGLARAYPASPWNDSRTPKIDLYDY	238
Db	181	VINELNMTSALDLYVKKNREDBPSILMQVEGSATGLARAYPASPWNDSRTPKIDLYDY	240
QY	239	RRRPYTOGAASPRKMDLILYVSSVSGLTLKILRTSVSMLETLISDDPEVNAVSPNSNA	298
Db	241	RRRPYTOGAASPRKMDLILYVSSVSGLTLKILRTSVSMLETLISDDPEVNAVSPNSNA	300
QY	299	QVSGFOHLYOANVRNKKVYLKDAVNNITAGIDYKKGFEAFEOILLANTVNSRANCKIT	358
Db	301	QVSGFOHLYOANVRNKKVYLKDAVNNITAGIDYKKGFEAFEOILLANTVNSRANCKIT	360
QY	359	MLFTDGEERAOEIFNKYNKDKRYVRFSGVGHNTERGEIOMACENKGYEYIPISTIGA	418
Db	361	MLFTDGEERAOEIFAKYNKDKRYVRFSGVGHNYDRGPLOMACENKGYEYIPISTIGA	420
QY	419	IRINHOEVLVILGSRPMYLAGKAKAOYOWTIVYLDALLEGVITGTLPVNITIGOPFNKTN	478
Db	421	IRINHOEVLVILGSRPMYLAGKAKAOYOWTIVYLDALLEGVITGTLPVNITIGOPFNKTN	480
QY	479	LKNQILIGVMGVDSLIEDIKILTRPFLCPNGYFAIDPBGVYLLHPNLOPK-----	530
Db	481	LKNQILIGVMGVDSLIEDIKILTRPFLCPNGYFAIDPBGVYLLHPNLOPKIGVPT	540
QY	531	-----NPKSOEPTILDFDAELENDIKVEIRNKMIDGSESEKTFRTLVSODER	579
Db	541	INLRKRREPNVONPKSOEPTILDFDAELENDIKVEIRNKMIDGSESEKTFRTLVSODER	600
QY	580	YIDKGNRPYTWTPANGDY--SLAVLPTYSFEYYIAKLEETIIOARSKKMKDSEPTLKP	638
Db	601	YIDKGNRPYTWTPANGDYSLAVLPTYSFEYYIAKLEETIIOAR-----SETLKP	653
QY	639	DNFESGYTPTAPRDYCNDLIKISDNTEFLINNEEIDRKTTPNPSNADLILRYLDAG	698
Db	654	DNFESGYTPTAPRDYCSDLKPSDNTEFLINNEEIDRKTTPNPSCNTDLILRYLDAG	713
QY	699	FTNELYOWYMSKONINIGVAFAPVYDGGITTRYPRKAGENNQENPEYEDSFYKRSIDN	758
Db	714	FTNELYOWYMSKONINIGVAFAPVYDGGITTRYPRKAGENNQENPEYEDSFYKRSIDN	773
QY	759	DNVYETAIFYFNKSGPAGYESGIMWSKAVEIYIOGKLKLAUVGIRKDVNSWLENTTKTISI	818
Db	774	DNVYETAIFYFNKSGPAGYESGIMWSKAVEIYIOGKLKLAUVGIRKDVNSWLENTTKTISI	833
QY	819	RDPCAGPYCCKRNSDVMCVILDDGGFLIMANHDTYNOIGRFGEDIPDSILMRHLYNIS	878
Db	834	RDPCAGPYCCKRNSDVMCVILDDGGFLIMANHDTYNOIGRFGEDIPDSILMRHLYNIS	893
QY	879	VYAFNKSXYDVOSVEPGAAROGGHRSAVVRVADILDIGMWTAAASIIQOFLLSIT	938
Db	894	VYAFNKSXYDVOSVEPGAAROGGHRSAVVRVADILDIGMWTAAASIIQOFLLSIT	953
QY	939	FPRLLEAVEMEDDFTASLSKOSGITEQOTYFPDNDNSKSFSGVLLDGCNCSIRIHEKELMN	998
Db	954	FPRLLEAVEMEDDFTASMSKOSGITEQOTYFPDNDNSKSFSGVLLDGCNCSIRIHEKELMN	1013
QY	999	TNLIFFIWEESGTCPCDTRL 1018	
Db	1014	TNLIFFIWEESGTCPCDTRL 1033	



NAME: Seidman, Stephanie L.  
 REGISTRATION NUMBER: 33,779  
 REFERENCE/DOCKET NUMBER: 52516 (P519739)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619)238-0999  
 TELEFAX: (619)238-0062  
 INFORMATION FOR SEQ ID NO: 55:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1079 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-223-305C-55

Query Match 98.2%; Score 5250; DB 2; Length 1079;  
 Best Local Similarity 98.7%; Pred. No. 0;  
 Matches 1005; Conservative 0; Mismatches 1; Indels 12; Gaps 2;

QY 1 MAAGCLLALTLTLFOSLLIGPSSEFPSPAVTIKSWDKMODLVTLAKTASGVNQLVDI 60  
 DB 1 MAAGCLLALTLTLFOSLLIGPSSEFPSPAVTIKSWDKMODLVTLAKTASGVNQLVDI 60  
 QY 61 YEKYODLYVEPNNAQOLVEIARDIEKLSNRKALVSLAEAKYQAAHQRDEPASN 120  
 DB 61 YEKYODLYVEPNNAQOLVEIARDIEKLSNRKALVSLAEAKYQAAHQRDEPASN 120  
 QY 121 EYVYNAKDDLDPEKNDSEPGSORIKPVFIEDANGROISYQAAVHIPTDIYESTIVL 180  
 DB 121 EYVYNAKDDLDPEKNDSEPGSORIKPVFIEDANGROISYQAAVHIPTDIYESTIVL 180  
 QY 121 EYVYNAKDDLDPEKNDSEPGSORIKPVFIEDANGROISYQAAVHIPTDIYESTIVL 180  
 DB 121 EYVYNAKDDLDPEKNDSEPGSORIKPVFIEDANGROISYQAAVHIPTDIYESTIVL 180  
 QY 181 NELNMTSALDEVFKKRNREDPSLIMOVGSAAGLARYPASPWNVSRIPIKIDLYDVR 240  
 DB 181 NELNMTSALDEVFKKRNREDPSLIMOVGSAAGLARYPASPWNVSRIPIKIDLYDVR 240  
 QY 241 RPYIIOGAASPKDMLILDVSGVSGTLKLRISVSEKLETLSDDDVYNVASFNSNAD 300  
 DB 241 RPYIIOGAASPKDMLILDVSGVSGTLKLRISVSEKLETLSDDDVYNVASFNSNAD 300  
 QY 301 VSCFQHLVQANRNKKVYLKDAVNNTAKGIDYKKGFSFAEQLLNYSRANCKIIML 360  
 DB 301 VSCFQHLVQANRNKKVYLKDAVNNTAKGIDYKKGFSFAEQLLNYSRANCKIIML 360  
 QY 361 FPDGGEERAOELFNKYNKDKVRVRFSGOVNERGPIOMWACNKKYVEIPISIGAIR 420  
 DB 361 FPDGGEERAOELFNKYNKDKVRVRFSGOVNERGPIOMWACNKKYVEIPISIGAIR 420  
 QY 421 INTQEYLDVLRPNVLADKAKAOVMTNVDALDELGLVITGTLPEVFNITGOFEKTKTLK 480  
 DB 421 INTQEYLDVLRPNVLADKAKAOVMTNVDALDELGLVITGTLPEVFNITGOFEKTKTLK 480  
 QY 481 NOLIIIGWGVVSLDIDKRLPRFLPCNGYFAIDPNGVYLLHPNLOPK-----EPVTL 535  
 DB 481 NOLIIIGWGVVSLDIDKRLPRFLPCNGYFAIDPNGVYLLHPNLOPK-----EPVTL 535  
 QY 541 DELDAELENDIKVELIRNKMIAGESEKTFRTLVKSQDERYTDKGRRTYTWPNVGTDSL 600  
 DB 541 DELDAELENDIKVELIRNKMIAGESEKTFRTLVKSQDERYTDKGRRTYTWPNVGTDSL 600  
 QY 601 ALVLPYTSFYIIRAKLEETITQARSKGKMDSETLKPDNFEESGYTFIAPRDCNDLKI 660  
 DB 601 ALVLPYTSFYIIRAKLEETITQARSKGKMDSETLKPDNFEESGYTFIAPRDCNDLKI 660  
 QY 661 SDNNTFEFLNNEFDKTPNNPSCMDLIRVILLDAGFTNELVQNTWSKKNIGYKAR 720  
 DB 661 SDNNTFEFLNNEFDKTPNNPSCMDLIRVILLDAGFTNELVQNTWSKKNIGYKAR 720  
 QY 721 FVYTDGIGITRYYPKAGENMOENPETYEDSYKKSILNDNNTVFAFPNKSGBPAYSIGI 780  
 DB 721 FVYTDGIGITRYYPKAGENMOENPETYEDSYKKSILNDNNTVFAFPNKSGBPAYSIGI 780  
 QY 781 MYSKAVEIYIOGKLKLPAAVGIKIDVNSWIENTFTKTSIRPCAGPVDCCKRNSDVMDCVI 840  
 DB 781 MYSKAVEIYIOGKLKLPAAVGIKIDVNSWIENTFTKTSIRPCAGPVDCCKRNSDVMDCVI 840

DB 769 MYSKAVEIYIOGKLKLPAAVGIKIDVNSWIENTFTKTSIRPCAGPVDCCKRNSDVMDCVI 828  
 QY 841 LDDGFFLLMANHDDYTNOIGRFFGRIIDPSLMRHVNI SVYAFNKSXYQASVCEGAPKQ 900  
 DB 829 LDDGFFLLMANHDDYTNOIGRFFGRIIDPSLMRHVNI SVYAFNKSXYQASVCEGAPKQ 888  
 QY 901 GAGHRSAYVPSVADILQIGMWATAAAMSILQOFLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
 DB 889 GAGHRSAYVPSVADILQIGMWATAAAMSILQOFLSLTFPRLLEAVEMEDDDFTASLSKQ 948  
 QY 961 SCITEQTYFFDNDNSKSSGYLDCGNCRIIFHGEKIMNTNLIIFIMVESKGTCPDTRL 1018  
 DB 949 SCITEQTYFFDNDNSKSSGYLDCGNCRIIFHGEKIMNTNLIIFIMVESKGTCPDTRL 1006

## RESULT 15

US-08-435-675B-5  
 Sequence 5, Application US/08435675B  
 Patent No. 5710250

## GENERAL INFORMATION:

APPLICANT: Ellis, Steven Bradley  
 APPLICANT: Williams, Mark E.  
 APPLICANT: Harpold, Michael Miller  
 APPLICANT: Schwartz, Arnold  
 APPLICANT: Brenner, Robert  
 TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller & McClain  
 STREET: 1660 Union Street  
 CITY: San Diego  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 92101-2926

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
 COMPUTER: IBM compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/435,675B  
 FILING DATE: 05-MAY-1995  
 CLASSIFICATION: 435

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/314,083  
 FILING DATE: 28-SEP-1994  
 APPLICATION NUMBER: US 07/914,231  
 FILING DATE: 13-JUL-1992  
 APPLICATION NUMBER: US 07/603,751  
 FILING DATE: 08-NOV-1990

ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie L.  
 REGISTRATION NUMBER: 33,779  
 REFERENCE/DOCKET NUMBER: 6362-53193  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619-238-0999  
 TELEFAX: 619-238-0062  
 TELEX:

## INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1106 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-435-675B-5

Query Match 96.1%; Score 5137.5; DB 1; Length 1106;  
 Best Local Similarity 94.8%; Pred. No. 0;  
 Matches 986; Conservative 13; Mismatches 12; Indels 29; Gaps 4;

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APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-455-543A-55

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Query Match          98.2% Score 5250: DB 1: Length 1079:
Best Local Similarity 98.7% Pred. No. 0:
Matches 1005; Conservative 0; Mismatches 1; Indels 12; Gaps 2;

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QY 1 MAAGCLLALTLTLFOSLLIGPSSSEPPSAVTIKSWDKMOEDLVTLAKTAGVNDYDI 60
DB 1 MAAGCLLALTLTLFOSLLIGPSSSEPPSAVTIKSWDKMOEDLVTLAKTAGVNDYDI 60
QY 61 YEKYQDLVYEPNNAQVLEIARDIEKLISNSKALVSLAEKVAQAHQWREDFASN 120
DB 61 YEKYQDLVYEPNNAQVLEIARDIEKLISNSKALVSLAEKVAQAHQWREDFASN 120
QY 121 EYVYNAKDLDEPKNDSPGSRIRKPVLEIDANEGROISYQAAVHPTDIEGSTYL 180
DB 121 EYVYNAKDLDEPKNDSPGSRIRKPVLEIDANEGROISYQAAVHPTDIEGSTYL 180
QY 181 NELNMTSALDEVYKKNREDDPSLLMQVFGSATGLARYPASPWNDSRTPNKIDLYVRR 240
DB 181 NELNMTSALDEVYKKNREDDPSLLMQVFGSATGLARYPASPWNDSRTPNKIDLYVRR 240
QY 241 RPYVIGGAASPKDMLILVYSGVSGLTIKLRTSVSEMLETISDDDFNVNVSFNSNAD 300
DB 241 RPYVIGGAASPKDMLILVYSGVSGLTIKLRTSVSEMLETISDDDFNVNVSFNSNAD 300
QY 301 VSCFOHLVQANVANKVLDVANNITAKGITDYKGFSAFEDLLNYSRANCKNTIML 360
DB 301 VSCFOHLVQANVANKVLDVANNITAKGITDYKGFSAFEDLLNYSRANCKNTIML 360
QY 361 FTDGGERAQETFNKYNKKKRVFRFSVGHNYERGPLOMACENKGYEIPISGAIK 420
DB 361 FTDGGERAQETFNKYNKKKRVFRFSVGHNYERGPLOMACENKGYEIPISGAIK 420
QY 421 INTQEVLDVYGRPMVLAGDKAKOVNTNYLDALGLVITGLTPVFNTTGGFENKTNK 480
DB 421 INTQEVLDVYGRPMVLAGDKAKOVNTNYLDALGLVITGLTPVFNTTGGFENKTNK 480
QY 481 NOLITGVMGVDSLEDIKRITPRTLCPPNGYFAIDPNQVYLHPHLOKKNKSOEPTVL 540
DB 481 NOLITGVMGVDSLEDIKRITPRTLCPPNGYFAIDPNQVYLHPHLOKKNKSOEPTVL 540
QY 541 DFLDALENDIKVEIRNKMIDGSGEKTRTLVKSODEYIDKGNRTYTPVNGTDYSL 600
DB 541 DFLDALENDIKVEIRNKMIDGSGEKTRTLVKSODEYIDKGNRTYTPVNGTDYSL 600
QY 596 ATALPYSFYIIKAKLEETITQARY-----SEILKPNFEESGYTFLAPRYCNDLKI 648
DB 596 ATALPYSFYIIKAKLEETITQARY-----SEILKPNFEESGYTFLAPRYCNDLKI 648
QY 661 SDNNTEELINENFEIDRKTPNNNSCANLIRVLLDAGFTNELVQYWSKONIKGVKAR 720
DB 649 SDNNTEELINENFEIDRKTPNNNSCANLIRVLLDAGFTNELVQYWSKONIKGVKAR 708

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QY 721 FVVTDCGITRVPKKEAGENMOENDEYEDSFYKRSLLDNNDVFTAPYFNKSGGAYESGI 780
DB 709 FVVTDCGITRVPKKEAGENMOENDEYEDSFYKRSLLDNNDVFTAPYFNKSGGAYESGI 768
QY 781 MYSKAVEIYIOGKLLKRAVVGKIDVNSWLENFTKTSIRDPACAPVDCCKRNSYMDCVI 840
DB 769 MYSKAVEIYIOGKLLKRAVVGKIDVNSWLENFTKTSIRDPACAPVDCCKRNSYMDCVI 828
QY 841 LDDGFFLMAHNDYTNQIGRFGEIDPSLMRHLVNSYAFNKSXYOSVCEPGAAPKQ 900
DB 829 LDDGFFLMAHNDYTNQIGRFGEIDPSLMRHLVNSYAFNKSXYOSVCEPGAAPKQ 888
QY 901 GAGHSAYVPSVADILQIGWMTAAAMSIIOQLFLSLTFPRLLAEVEMEDDFTASLSKQ 960
DB 889 GAGHSAYVPSVADILQIGWMTAAAMSIIOQLFLSLTFPRLLAEVEMEDDFTASLSKQ 948
QY 961 SCITEQTOYFFDNDKSKSPSYLDGNCNRIFPHGKLMNTNLIPLMVSCKTCCPDTRL 1018
DB 949 SCITEQTOYFFDNDKSKSPSYLDGNCNRIFPHGKLMNTNLIPLMVSCKTCCPDTRL 1006

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RESULT 14
US-08-223-305C-55
Sequence 55, Application US/08223305C
Patent No. 5851824
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESSES:
ADDRESS: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/223,305C
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:

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FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 52516 (P519739)  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1103 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-223-305C-53

Query Match 98.6%; Score 5270; DB 2; Length 1103;  
Best Local Similarity 97.4%; Pred. No. 0;  
Matches 1010; Conservative 0; Mismatches 1; Indels 26; Gaps 2;

QY 1 MAAGCLLALTLFLFSLIGSPSEPPSAVTIKSWDMKMODLYTLAKTASGVNQLVDI 60  
DB 1 MAAGCLLALTLFLFSLIGSPSEPPSAVTIKSWDMKMODLYTLAKTASGVNQLVDI 60  
QY 61 YEKYODLYVEPNNAKQLEIARDIEKLNSRKALVSLAEAKYQAADHMDREFASN 120  
DB 61 YEKYODLYVEPNNAKQLEIARDIEKLNSRKALVSLAEAKYQAADHMDREFASN 120  
QY 121 EYVYVNAKDDLPKENDSPGSGQRKPVFIEDANFGROIYQHAHVHPIDYEGSTVL 180  
DB 121 EYVYVNAKDDLPKENDSPGSGQRKPVFIEDANFGROIYQHAHVHPIDYEGSTVL 180  
QY 181 NELNLTSADEYFKKREEDPSLLQVGSATGLARYYPASPMVNSTPKIDLYDPR 240  
DB 181 NELNLTSADEYFKKREEDPSLLQVGSATGLARYYPASPMVNSTPKIDLYDPR 240  
QY 241 RPYIYQGAASPKDMLLVDSVSGSLTLKLRISVSEMLETISDDDPVNVASFNSNQD 300  
DB 241 RPYIYQGAASPKDMLLVDSVSGSLTLKLRISVSEMLETISDDDPVNVASFNSNQD 300  
QY 301 VSCFQHLVQANRNKKVYLKADVNNTAKGIDYKKGSFAEQLLNYSRANCKIIML 360  
DB 301 VSCFQHLVQANRNKKVYLKADVNNTAKGIDYKKGSFAEQLLNYSRANCKIIML 360  
QY 361 FTDGGEERAQELFNKYNKDKRVRFVSGHNERGPIOMACENKGYEIEISGAIR 420  
DB 361 FTDGGEERAQELFNKYNKDKRVRFVSGHNERGPIOMACENKGYEIEISGAIR 420  
QY 421 INTQYLDVLRPNVLADKAKQVQWTVNYDALELGIVITGLPVFNITGOFENKTULK 480  
DB 421 INTQYLDVLRPNVLADKAKQVQWTVNYDALELGIVITGLPVFNITGOFENKTULK 480  
QY 481 NQILIGVGVVSLIEDIKRLPRFLCPNGYFAIDPNGVYLHPNLOPKIGVIGIPTIN 540  
DB 481 NQILIGVGVVSLIEDIKRLPRFLCPNGYFAIDPNGVYLHPNLOPKIGVIGIPTIN 540  
QY 531 -----NPKSOEPTVLDPLDALENDIKVEIRNKKIDSESEKTPRTLYKQDEXYI 581  
DB 531 -----NPKSOEPTVLDPLDALENDIKVEIRNKKIDSESEKTPRTLYKQDEXYI 581  
QY 541 LKRRPNQNKRSOEPVTLADLEDALENDIKVEIRNKKIDSESEKTPRTLYKQDEXYI 600  
DB 541 LKRRPNQNKRSOEPVTLADLEDALENDIKVEIRNKKIDSESEKTPRTLYKQDEXYI 600  
QY 582 DKGNTTYTWTGVNGTDSLALVLPYTSFYIKAKLEETITQARSKKGMKSETLKPDNF 641  
DB 582 DKGNTTYTWTGVNGTDSLALVLPYTSFYIKAKLEETITQARSKKGMKSETLKPDNF 641  
QY 601 DKGNTTYTWTGVNGTDSLALVLPYTSFYIKAKLEETITQARSKKGMKSETLKPDNF 653  
DB 601 DKGNTTYTWTGVNGTDSLALVLPYTSFYIKAKLEETITQARSKKGMKSETLKPDNF 653  
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DB 642 EESGTYTAPBDYCNLDKISDNTEFLNNEFIDKRTPNPNSCNADLINRVLLDAGFTN 701  
QY 654 EESGTYTAPBDYCNLDKISDNTEFLNNEFIDKRTPNPNSCNADLINRVLLDAGFTN 713  
DB 654 EESGTYTAPBDYCNLDKISDNTEFLNNEFIDKRTPNPNSCNADLINRVLLDAGFTN 713

QY 702 ELVQNTWSKOKNIKGVKARFVVTDOGITRVYPKKEAGENWQENPETYEDSFYKRLSDNDY 761  
DB 702 ELVQNTWSKOKNIKGVKARFVVTDOGITRVYPKKEAGENWQENPETYEDSFYKRLSDNDY 761  
QY 714 ELVQNTWSKOKNIKGVKARFVVTDOGITRVYPKKEAGENWQENPETYEDSFYKRLSDNDY 773  
DB 714 ELVQNTWSKOKNIKGVKARFVVTDOGITRVYPKKEAGENWQENPETYEDSFYKRLSDNDY 773  
QY 762 VETAPYFNKSGGAVESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIEFRTSTIRDP 821  
DB 762 VETAPYFNKSGGAVESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIEFRTSTIRDP 821  
QY 774 VETAPYFNKSGGAVESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIEFRTSTIRDP 833  
DB 774 VETAPYFNKSGGAVESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIEFRTSTIRDP 833  
QY 822 CAGPYCDCKRNSDWDVCDYLLDDGFLMANHDDYTNOIGRFFGEIDSLMRHLVNSIYA 881  
DB 822 CAGPYCDCKRNSDWDVCDYLLDDGFLMANHDDYTNOIGRFFGEIDSLMRHLVNSIYA 881  
QY 834 CAGPYCDCKRNSDWDVCDYLLDDGFLMANHDDYTNOIGRFFGEIDSLMRHLVNSIYA 893  
DB 834 CAGPYCDCKRNSDWDVCDYLLDDGFLMANHDDYTNOIGRFFGEIDSLMRHLVNSIYA 893  
QY 882 FNKSTIDYSCVCPGAAPKQAGHRSAYVSVADILQIGMATAAAMSILQOFLSLTFPR 941  
DB 882 FNKSTIDYSCVCPGAAPKQAGHRSAYVSVADILQIGMATAAAMSILQOFLSLTFPR 941  
QY 894 FNKSYDYSCVCPGAAPKQAGHRSAYVSVADILQIGMATAAAMSILQOFLSLTFPR 953  
DB 894 FNKSYDYSCVCPGAAPKQAGHRSAYVSVADILQIGMATAAAMSILQOFLSLTFPR 953  
QY 942 LLEAVEMEDDFTASLSKOSITBOTOYFPNDKSSSGVLDGCGSRIFHGEKAMTNL 1001  
DB 942 LLEAVEMEDDFTASLSKOSITBOTOYFPNDKSSSGVLDGCGSRIFHGEKAMTNL 1001  
QY 954 LLEAVEMEDDFTASLSKOSITBOTOYFPNDKSSSGVLDGCGSRIFHGEKAMTNL 1013  
DB 954 LLEAVEMEDDFTASLSKOSITBOTOYFPNDKSSSGVLDGCGSRIFHGEKAMTNL 1013  
QY 1002 IFIMVESKGTCPDTRL 1018  
DB 1002 IFIMVESKGTCPDTRL 1018  
QY 1014 IFIMVESKGTCPDTRL 1030  
DB 1014 IFIMVESKGTCPDTRL 1030

## RESULT 13

US-08-455-543A-55

Sequence 55, Application US/08455543A

Patent No. 5792846

## GENERAL INFORMATION:

APPLICANT: Harpold, Michael

APPLICANT: Ellis, Steven

APPLICANT: Williams, Mark

APPLICANT: Feldman, Daniel

APPLICANT: McCue, Ann

APPLICANT: Brenner, Robert

TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

NUMBER OF INVENTIONS: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller &amp; McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/455,543A

FILING DATE: May 31, 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/223,305

FILING DATE: April 4, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/868,354

FILING DATE: April 10, 1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/745,206

FILING DATE: 15-AUG-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/620,250

FILING DATE: 30-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/482,384

FILING DATE: 20-FEB-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/603,751

FILING DATE: 04-APR-1989

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/US89/01408  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/176,899  
 FILING DATE: 04-APR-1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie L.  
 REGISTRATION NUMBER: 33,779  
 REFERENCE/DOCKET NUMBER: 6362-52517  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619)238-0999  
 TELEFAX: (619)238-0062  
 INFORMATION FOR SEQ ID NO: 53:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1103 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-455-543A-53

Query Match 98.6%; Score 5270; DB 1; Length 1103;  
 Best Local Similarity 97.4%; Pred. No. 0;  
 Matches 1010; Conservative 0; Mismatches 1; Indels 26; Gaps 2;

QY 1 MAAGCLLALTLTLEFOSLLIGPSSSEPPSAVTKSWVDKMOEDVLTATAGVNOVDI 60  
 DB 1 MAAGCLLALTLTLEFOSLLIGPSSSEPPSAVTKSWVDKMOEDVLTATAGVNOVDI 60  
 QY 61 YEKYQDLTYEPNNARQVEIARIDEKLLSNRSKALVSLAEKVAHQHREDFASN 120  
 DB 61 YEKYQDLTYEPNNARQVEIARIDEKLLSNRSKALVSLAEKVAHQHREDFASN 120  
 QY 121 EYVYNAKDDLPEDKNDSEPGSORIPVTEEDANFGROISYQAAVHTDYEESTIYL 180  
 DB 121 EYVYNAKDDLPEDKNDSEPGSORIPVTEEDANFGROISYQAAVHTDYEESTIYL 180  
 QY 181 NELNMTSALDEVEFKKREDEPSSLMOVFGSANGIARYPASPVNDSPKNTIDYDVR 240  
 DB 181 NELNMTSALDEVEFKKREDEPSSLMOVFGSANGIARYPASPVNDSPKNTIDYDVR 240  
 QY 241 RPYWIGGAASPKDMLILVYSGSVGLTKLIRTSVSEMLETSLDDDFVNAVSFNSMAD 300  
 DB 241 RPYWIGGAASPKDMLILVYSGSVGLTKLIRTSVSEMLETSLDDDFVNAVSFNSMAD 300  
 QY 301 VSCFOHLVQANVRKRVLDVANNITAKGITDYKKGFSAFQDLNNTYNSRANCKIIML 360  
 DB 301 VSCFOHLVQANVRKRVLDVANNITAKGITDYKKGFSAFQDLNNTYNSRANCKIIML 360  
 QY 361 FTDGGERAQLFNKYNKKKVFPRFSVQGNHYERGPIQMMACENKGGYIEIPSGAIR 420  
 DB 361 FTDGGERAQLFNKYNKKKVFPRFSVQGNHYERGPIQMMACENKGGYIEIPSGAIR 420  
 QY 421 INTQEVLDVGRPMVLADGAKAKOVQNTNYLDALDELGLVITGTLPEVNTTGGFENKTNL 480  
 DB 421 INTQEVLDVGRPMVLADGAKAKOVQNTNYLDALDELGLVITGTLPEVNTTGGFENKTNL 480  
 QY 481 NOILIVMGVDSLEDIKRLTPRTLCPRNGYFAIDPNNGYVLLHPMLQK----- 530  
 DB 481 NOILIVMGVDSLEDIKRLTPRTLCPRNGYFAIDPNNGYVLLHPMLQK----- 530  
 QY 531 -----NPKSQEVTLDLDAELENDIKVEIRKMKIDGEGEKTFTLVKSODERYI 581  
 DB 541 LKRRRNINQPKSQEVTLDLDAELENDIKVEIRKMKIDGEGEKTFTLVKSODERYI 600  
 QY 582 DKGNRTYTWTPVNGTDYSLALVLPYSPFYIAKALEETITQARSKGKKMDESLKPDNF 641  
 DB 601 DKGNRTYTWTPVNGTDYSLALVLPYSPFYIAKALEETITQARSKGKKMDESLKPDNF 653  
 QY 642 EESGYTFIAPRODCNDLKISDNTTEFLNFEITDKRTNNPNCNDLIRNYLLDAGFTN 701  
 DB 642 EESGYTFIAPRODCNDLKISDNTTEFLNFEITDKRTNNPNCNDLIRNYLLDAGFTN 701

DB 654 EESGYTFIAPRODCNDLKISDNTTEFLNFEITDKRTNNPNCNDLIRNYLLDAGFTN 713  
 QY 702 ELVQYNMCKOKINIGVAKARFVDTGGITRVYPKAGEWMOENPETYEDSYKKSLDNDY 761  
 DB 714 ELVQYNMCKOKINIGVAKARFVDTGGITRVYPKAGEWMOENPETYEDSYKKSLDNDY 773  
 QY 762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGIKIDVNSMIENFTKTSIRD 821  
 DB 774 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGIKIDVNSMIENFTKTSIRD 833  
 QY 822 CAGPYCCKRNSDVMDCYIIDDGSEFLMANHDYDNTNIGRFFGIDPSLKRHLVNSIYVA 881  
 DB 834 CAGPYCCKRNSDVMDCYIIDDGSEFLMANHDYDNTNIGRFFGIDPSLKRHLVNSIYVA 893  
 QY 882 FNSYDYOSCEPGAAPKQAGHRSAYVPSVADILQIGMWATAAAMSILQOFLSLTFPR 941  
 DB 894 FNSYDYOSCEPGAAPKQAGHRSAYVPSVADILQIGMWATAAAMSILQOFLSLTFPR 953  
 QY 942 LLEAVEMEDDFTASLSKQSCITEOTOYFEDNDSKFSGVLDCGNCRIFFHGEKLMNTNL 1001  
 DB 954 LLEAVEMEDDFTASLSKQSCITEOTOYFEDNDSKFSGVLDCGNCRIFFHGEKLMNTNL 1013  
 QY 1002 IFIMWESKGTCPDTRL 1018  
 DB 1014 IFIMWESKGTCPDTRL 1030

## RESULT 12

US-08-223-305C-53  
 Sequence 53, Application US/08223305C

Patent No. 5851824

GENERAL INFORMATION:

APPLICANT: Harpold, Michael

APPLICANT: Ellis, Steven

APPLICANT: Williams, Mark

APPLICANT: Feldman, Daniel

APPLICANT: McCue, Ann

TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller & McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSD Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/223,305C

FILING DATE: April 4, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/868,354

FILING DATE: April 10, 1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/745,206

FILING DATE: 15-AUG-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/620,250

FILING DATE: 30-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/482,384

FILING DATE: 20-FEB-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/603,751

FILING DATE: 04-APR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US89/01408

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/603,751  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/US89/01408  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/176,899  
 FILING DATE: 04-APR-1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie L.  
 REGISTRATION NUMBER: 33,779  
 REFERENCE/DOCKET NUMBER: 52516 (P519739)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619)238-0999  
 TELEFAX: (619)238-0062  
 INFORMATION FOR SEQ ID NO: 56:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1084 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-223-305C-56

Query Match 98.9%; Score 5289.5; DB 2; Length 1084;  
 Best Local Similarity 99.2%; Pred. No. 0;  
 Matches 1010; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 1 MAAGCLLTLTLFOSLIGSPSEPPSATYIKSWVKMGEDLVTLAKTASGVNQLVDI 60  
 DB 1 MAAGCLLTLTLFOSLIGSPSEPPSATYIKSWVKMGEDLVTLAKTASGVNQLVDI 60  
 QY 61 YEKYODLYVEBNNAQVETIARDIEKLNSRSKALVSLAEKVOAQMREDFASN 120  
 DB 61 YEKYODLYVEBNNAQVETIARDIEKLNSRSKALVSLAEKVOAQMREDFASN 120  
 QY 121 EYVYNNADDDPEKNDSEPSQRIKPYFIEDANFROIYQHAHVHPTDIEGSTIVL 180  
 DB 121 EYVYNNADDDPEKNDSEPSQRIKPYFIEDANFROIYQHAHVHPTDIEGSTIVL 180  
 QY 121 EYVYNNADDDPEKNDSEPSQRIKPYFIEDANFROIYQHAHVHPTDIEGSTIVL 180  
 DB 121 EYVYNNADDDPEKNDSEPSQRIKPYFIEDANFROIYQHAHVHPTDIEGSTIVL 180  
 QY 181 NELNNTSALDEYFKKREDEPSLIMQVGSATGLARYYPASPDWNSPTPKIDLYDRR 240  
 DB 181 NELNNTSALDEYFKKREDEPSLIMQVGSATGLARYYPASPDWNSPTPKIDLYDRR 240  
 QY 181 NELNNTSALDEYFKKREDEPSLIMQVGSATGLARYYPASPDWNSPTPKIDLYDRR 240  
 DB 181 NELNNTSALDEYFKKREDEPSLIMQVGSATGLARYYPASPDWNSPTPKIDLYDRR 240  
 QY 241 RFWYIOGAASPKDMLIVDVSGSVGLTKLIRTSVSEMLETSLDDDFVNAVSNANOD 300  
 DB 241 RFWYIOGAASPKDMLIVDVSGSVGLTKLIRTSVSEMLETSLDDDFVNAVSNANOD 300  
 QY 301 VSCFHLVQAVNRKKVYKADAVNNITAKGITDYKKGSFAFEQOLINVSANCKIIML 360  
 DB 301 VSCFHLVQAVNRKKVYKADAVNNITAKGITDYKKGSFAFEQOLINVSANCKIIML 360  
 QY 301 VSCFHLVQAVNRKKVYKADAVNNITAKGITDYKKGSFAFEQOLINVSANCKIIML 360  
 DB 301 VSCFHLVQAVNRKKVYKADAVNNITAKGITDYKKGSFAFEQOLINVSANCKIIML 360  
 QY 361 FPDGGEERAOEFNKYNKDKRVRFPSVGOHNERGDIOMMACENKYYEISIGAIR 420  
 DB 361 FPDGGEERAOEFNKYNKDKRVRFPSVGOHNERGDIOMMACENKYYEISIGAIR 420  
 QY 421 INTQETLDVLRPNVLADKAKOVOMTVYLDALIELGLVITGLTPVFNTIQGFENKTULK 480  
 DB 421 INTQETLDVLRPNVLADKAKOVOMTVYLDALIELGLVITGLTPVFNTIQGFENKTULK 480  
 QY 421 INTQETLDVLRPNVLADKAKOVOMTVYLDALIELGLVITGLTPVFNTIQGFENKTULK 480  
 DB 421 INTQETLDVLRPNVLADKAKOVOMTVYLDALIELGLVITGLTPVFNTIQGFENKTULK 480  
 QY 481 NOLIGVGVSVLEDIRLRLPRFLTCNGYYFAIDPNGVYLLHPNLOPKNPKSQEPVTL 540  
 DB 481 NOLIGVGVSVLEDIRLRLPRFLTCNGYYFAIDPNGVYLLHPNLOPKNPKSQEPVTL 540  
 QY 541 DFLDAELNDIKVEIRNMKIDGEGSEKFTLVKSODERYIDKGRYTWTPVNGTQSL 600  
 DB 541 DFLDAELNDIKVEIRNMKIDGEGSEKFTLVKSODERYIDKGRYTWTPVNGTQSL 600  
 QY 601 ALVLDPTYSFYIKAKLEETITQARSKKGMDSFTLKPDNFEESGYTFIARDYCNDLKI 660  
 DB 601 ALVLDPTYSFYIKAKLEETITQARSKKGMDSFTLKPDNFEESGYTFIARDYCNDLKI 660  
 QY 601 ALVLDPTYSFYIKAKLEETITQARSKKGMDSFTLKPDNFEESGYTFIARDYCNDLKI 660  
 DB 601 ALVLDPTYSFYIKAKLEETITQARSKKGMDSFTLKPDNFEESGYTFIARDYCNDLKI 660

QY 661 SDNTEFLNFEIDRKTPNPNSCNADLINRVLLDAGFTNELVQYWSKOKNIKGVKAR 720  
 DB 654 SDNTEFLNFEIDRKTPNPNSCNADLINRVLLDAGFTNELVQYWSKOKNIKGVKAR 713  
 QY 721 FVYTDGGITRYVYKREAGENNQENPETYEDSFYKRSLDNDNYVTATYFNSKSGAYESGI 780  
 DB 714 FVYTDGGITRYVYKREAGENNQENPETYEDSFYKRSLDNDNYVTATYFNSKSGAYESGI 773  
 QY 781 MVSRAVEITYOGKLLKPAVVGIRKIDVNSWTEFTKTSIRPDCAGPDCCKRNSDVMDCYI 840  
 DB 774 MVSRAVEITYOGKLLKPAVVGIRKIDVNSWTEFTKTSIRPDCAGPDCCKRNSDVMDCYI 833  
 QY 841 LDDGFLMANHDDYTNOIGRFFGEIDPSLMRLVNSVYAFKNSYDQSVCEPGAAPKQ 900  
 DB 834 LDDGFLMANHDDYTNOIGRFFGEIDPSLMRLVNSVYAFKNSYDQSVCEPGAAPKQ 893  
 QY 901 GAGHRSAYVPSVADIIQIGWATRAAASIIQOFLSLTFPRLLEAVEMEDDFTASLSKQ 960  
 DB 894 GAGHRSAYVPSVADIIQIGWATRAAASIIQOFLSLTFPRLLEAVEMEDDFTASLSKQ 953  
 QY 961 SCITEOTQYFEFNDKSKFSGLDGCNCSRIFGHEKLMNTLIFIMVESKGTCPDTRL 1018  
 DB 954 SCITEOTQYFEFNDKSKFSGLDGCNCSRIFGHEKLMNTLIFIMVESKGTCPDTRL 1011

RESULT 11  
 US-08-455-543A-53  
 Sequence 53, Application US/08455543A  
 Patent No. 5792846  
 GENERAL INFORMATION:  
 APPLICANT: Harpold, Michael  
 APPLICANT: Ellis, Steven  
 APPLICANT: Williams, Mark  
 APPLICANT: Feldman, Daniel  
 APPLICANT: McCue, Ann  
 APPLICANT: Brenner, Robert  
 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
 NUMBER OF SEQUENCES: 57  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Brown, Martin, Haller & McClain  
 STREET: 1660 Union Street  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92101-2926  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/455,543A  
 FILING DATE: May 31, 1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/223,305  
 FILING DATE: April 4, 1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/868,354  
 FILING DATE: April 10, 1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/745,206  
 FILING DATE: 15-AUG-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/620,250  
 FILING DATE: 30-NOV-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/482,384  
 FILING DATE: 20-FEB-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/603,751  
 FILING DATE: 04-APR-1989

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0062
TELEFAX: (619)238-0062
INFORMATION FOR SEQ. ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 1084 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-455-543A-56

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Query Match          98.9%; Score 5289.5; DB 1; Length 1084;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1010; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

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QY 1 MAAGCLLALTLTLFOSLLIPSSSEPPSAVTIKSWDKKQEDLVTLAASGVNQLVDI 60
DB 1 MAAGCLLALTLTLFOSLLIPSSSEPPSAVTIKSWDKKQEDLVTLAASGVNQLVDI 60
QY 61 YEKYQDLTYEPNNARQIVIAARDIEKLISNSKALVSLAEKVVQAAHQREDFASN 120
DB 61 YEKYQDLTYEPNNARQIVIAARDIEKLISNSKALVSLAEKVVQAAHQREDFASN 120
QY 121 EYVYNAKADLDPEKNDSEGSORIKVPFIEDANFGROISYQAAHIFPDIEGSTIYL 180
DB 121 EYVYNAKADLDPEKNDSEGSORIKVPFIEDANFGROISYQAAHIFPDIEGSTIYL 180
QY 181 NEIINMTSALDEVFKKREDDPSILMOWFGSANGTGLARYPASPVWDSRTPNKIDLYDVR 240
DB 181 NEIINMTSALDEVFKKREDDPSILMOWFGSANGTGLARYPASPVWDSRTPNKIDLYDVR 240
QY 241 RPYWYIGGAASPKMMLLVVYSGVSGITLKITRSVSEMLETISDDDFPVNVAFSNNAD 300
DB 241 RPYWYIGGAASPKMMLLVVYSGVSGITLKITRSVSEMLETISDDDFPVNVAFSNNAD 300
QY 301 VSCFOHLVQANVANKKYLKDAVANNITAKGITDYKKGFSAFBOPLLNYNVRANCKNIML 360
DB 301 VSCFOHLVQANVANKKYLKDAVANNITAKGITDYKKGFSAFBOPLLNYNVRANCKNIML 360
QY 361 FTDGGERAOEIFNKNKDKKVVFRFVSGQHNBERGPIOMMACENKGGYIEIPISGAIR 420
DB 361 FTDGGERAOEIFNKNKDKKVVFRFVSGQHNBERGPIOMMACENKGGYIEIPISGAIR 420
QY 421 INTQEVLDVYGRPMVLAGDKAKOVQNTNYLDALEGLVITGTLVPFNITGQFENKTNK 480
DB 421 INTQEVLDVYGRPMVLAGDKAKOVQNTNYLDALEGLVITGTLVPFNITGQFENKTNK 480
QY 481 NOLILGVMGVDSLEEDIKRLTPRETCPNGYPAIDPNGVYLHPVLOKPKRSOPVTL 540
DB 481 NOLILGVMGVDSLEEDIKRLTPRETCPNGYPAIDPNGVYLHPVLOKPKRSOPVTL 540
QY 541 DFLDAELNDIKVEIRNMKIDGESGKTRFTLVKSODERYIDKGNRTYWTVPVNGTDSL 600

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DB 541 DFLDAELNDIKVEIRNMKIDGESGKTRFTLVKSODERYIDKGNRTYWTVPVNGTDSL 600
QY 601 ALVLPYSFYYIKAKLEETITQARSKKGMKMDSEFIKPDNFEESGYPIARDCNDLKI 660
DB 601 ALVLPYSFYYIKAKLEETITQARSKKGMKMDSEFIKPDNFEESGYPIARDCNDLKI 660
QY 661 SDNTEFLNFEFIDRKTTPNNPSCNADLIRVLLDAGFTNELVQNTWSKOKNIKGVAKR 720
DB 661 SDNTEFLNFEFIDRKTTPNNPSCNADLIRVLLDAGFTNELVQNTWSKOKNIKGVAKR 720
QY 721 EYVYDGGITRYIPKAGGNWQBNPEYDSTFKNSLDNDNVYFAFPKNSGPGAYESGI 780
DB 721 EYVYDGGITRYIPKAGGNWQBNPEYDSTFKNSLDNDNVYFAFPKNSGPGAYESGI 780
QY 774 FVYITGGITRYIPKAGGNWQBNPEYDSTFKNSLDNDNVYFAFPKNSGPGAYESGI 773
DB 774 FVYITGGITRYIPKAGGNWQBNPEYDSTFKNSLDNDNVYFAFPKNSGPGAYESGI 773
QY 781 MYSKAVEIYIOGKLKLPVAVGKIDVNSWIEFNTKTSIRDPACAPVDCCKRNSDVMOCVI 840
DB 781 MYSKAVEIYIOGKLKLPVAVGKIDVNSWIEFNTKTSIRDPACAPVDCCKRNSDVMOCVI 840
QY 841 LDDGFFLMAHNDYTNOIGRFFGEIDPSLMRHLVNISSVAFNKSSTYQSYCEPGAAPKQ 900
DB 841 LDDGFFLMAHNDYTNOIGRFFGEIDPSLMRHLVNISSVAFNKSSTYQSYCEPGAAPKQ 900
QY 894 GAGHSATVPSYADILQIGMNTAAANSILQOFLISTFPRLDAVEMEDDFTASLSKQ 960
DB 894 GAGHSATVPSYADILQIGMNTAAANSILQOFLISTFPRLDAVEMEDDFTASLSKQ 960
QY 961 SCITEOTOYFPDNDKSPSGVLDGNCRIIFHEKIMNTNLIIFIMVSKGCPDFTL 1018
DB 961 SCITEOTOYFPDNDKSPSGVLDGNCRIIFHEKIMNTNLIIFIMVSKGCPDFTL 1018

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US-08-223-305C-56
Sequence 56, Application US/08223305C

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PATENT NO. 3851824
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESS: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/223,305C
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990

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PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/745,206  
 FILING DATE: 15-AUG-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/620,250  
 FILING DATE: 30-NOV-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/482,384  
 FILING DATE: 20-FEB-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/603,751  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: NO PCT/US89/01408  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/176,899  
 FILING DATE: 04-APR-1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie L.  
 REGISTRATION NUMBER: 33,779  
 REFERENCE/DOCKET NUMBER: 52516 (P519739)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619)238-0062  
 TELEFAX: (619)238-0062  
 INFORMATION FOR SEQ ID NO: 54:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1086 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-223-305C-54

Query Match 99.3%; Score 5306.5; DB 2: Length 1086;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 1013: Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 MAAGCLALTLTLFOSLLIGPSSEPPPSAVT I KSWDKMEDLVTAKTASGVNQLVDI 60  
 DB 1 MAAGCLALTLTLFOSLLIGPSSEPPPSAVT I KSWDKMEDLVTAKTASGVNQLVDI 60  
 QY 61 YKYODLTVEPNNAKQVEIARIEKLLNSKALVSLAEKQVAAQWREDFASN 120  
 DB 61 YKYODLTVEPNNAKQVEIARIEKLLNSKALVSLAEKQVAAQWREDFASN 120  
 QY 121 EYVYNNARDDLDPEKNDESPGSORIKPFYIEDANFGROISYQHAAPHPTDIYEGSTIVL 180  
 DB 121 EYVYNNARDDLDPEKNDESPGSORIKPFYIEDANFGROISYQHAAPHPTDIYEGSTIVL 180  
 QY 161 NELNMTSALDEVFKKRNREDSLSLMQVGSATGLARYYPASPWDNSRTPPKIDLYDVR 240  
 DB 161 NELNMTSALDEVFKKRNREDSLSLMQVGSATGLARYYPASPWDNSRTPPKIDLYDVR 240  
 QY 241 RPYWYOGAASPRDMLIVDVSGSVGLTKLIRTSVSMLETTISDDDFVNVASNSNAOD 300  
 DB 241 RPYWYOGAASPRDMLIVDVSGSVGLTKLIRTSVSMLETTISDDDFVNVASNSNAOD 300  
 QY 301 VSCFOHLVQAVNRKKVYLKDAVNNITAKGITDYKKGFSFAEQLLNTVSPANCKTIML 360  
 DB 301 VSCFOHLVQAVNRKKVYLKDAVNNITAKGITDYKKGFSFAEQLLNTVSPANCKTIML 360  
 QY 361 FTDDGEERAQEIFPKYKNDKRVFRFSVGOHNERGPIQMACENKGYEIPISGAIR 420  
 DB 361 FTDDGEERAQEIFPKYKNDKRVFRFSVGOHNERGPIQMACENKGYEIPISGAIR 420  
 QY 421 INFOEYLDVLRPWYLAGDKAKQVOMTVYDALDELIGVITGTLPTVNTIGQFENKTNLK 480  
 DB 421 INFOEYLDVLRPWYLAGDKAKQVOMTVYDALDELIGVITGTLPTVNTIGQFENKTNLK 480  
 QY 481 NOLIGVGVDSLEDIKRLTPRETLCPNGYFAIDPBGVYLHPNLOPKRKSQDEPVTL 540  
 DB 481 NOLIGVGVDSLEDIKRLTPRETLCPNGYFAIDPBGVYLHPNLOPKRKSQDEPVTL 540

DB 481 NOLIGVGVDSLEDIKRLTPRETLCPNGYFAIDPBGVYLHPNLOPKRKSQDEPVTL 535  
 QY 541 DFLDAELENDIKVEIRNMIDGEGEKTRFLVVSODERTYDKNNRYYTWPVNGDTYSL 600  
 DB 536 DFLDAELENDIKVEIRNMIDGEGEKTRFLVVSODERTYDKNNRYYTWPVNGDTYSL 595  
 QY 601 ALVLPYTSFYIYIKAKLEETITQARSKKGMKDSSTLKPDPNEEGSYTFIAPROVCDNLKI 660  
 DB 596 ALVLPYTSFYIYIKAKLEETITQARSKKGMKDSSTLKPDPNEEGSYTFIAPROVCDNLKI 655  
 QY 661 SDNNTFELNNEFDIKRTPNPNPCNADLNRVLLDAGFTNELVQVWYSKOKNIKGVKAR 720  
 DB 656 SDNNTFELNNEFDIKRTPNPNPCNADLNRVLLDAGFTNELVQVWYSKOKNIKGVKAR 715  
 QY 721 FVWTDGGITRYPKBAGNMOENPETEDSYKSLNDNVYVFAFPKNSGCGATYSGI 780  
 DB 716 FVWTDGGITRYPKBAGNMOENPETEDSYKSLNDNVYVFAFPKNSGCGATYSGI 775  
 QY 781 MYSKAVEIYIGKLLKPAVVGIRKIDVNSWIENFTKTSIRPCAGPVCDCKRNSPDMCVI 840  
 DB 776 MYSKAVEIYIGKLLKPAVVGIRKIDVNSWIENFTKTSIRPCAGPVCDCKRNSPDMCVI 835  
 QY 841 LDDGFLMANHDDYTNOIGRFGEIDPSLMRLVNISYVAFNKSYDYQSVCEPGAAPKQ 900  
 DB 836 LDDGFLMANHDDYTNOIGRFGEIDPSLMRLVNISYVAFNKSYDYQSVCEPGAAPKQ 895  
 QY 901 GAGHRSAYVPSADIILIGWMTAAWSIILOQFLSLTFRLLLEAVMEDDDTASLSKO 960  
 DB 896 GAGHRSAYVPSADIILIGWMTAAWSIILOQFLSLTFRLLLEAVMEDDDTASLSKO 955  
 QY 961 SCITEOTQYEFENDSKSFGSLDGCNCSRIFHGEKLANMLIFIMYESKGTCCDTRL 1018  
 DB 956 SCITEOTQYEFENDSKSFGSLDGCNCSRIFHGEKLANMLIFIMYESKGTCCDTRL 1013

RESULT 9  
 US-08-455-543A-56  
 Sequence 56, Application US/08455543A  
 Patent No. 5792846  
 GENERAL INFORMATION:  
 APPLICANT: Harpold, Michael  
 APPLICANT: Ellis, Steven  
 APPLICANT: Williams, Mark  
 APPLICANT: Feldman, Daniel  
 APPLICANT: McCue, Ann  
 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
 NUMBER OF SEQUENCES: 57  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Brown, Martin, Haller & McClain  
 STREET: 1660 Union Street  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92101-2926  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/455,543A  
 FILING DATE: May 31, 1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/223,305  
 FILING DATE: April 4, 1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/868,354  
 FILING DATE: April 10, 1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/745,206  
 FILING DATE: 15-AUG-1991

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 1086 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-455-543A-54

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Query Match          99.3%; Score 5306.5; DB 1; Length 1086;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1013; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

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QY 1 MAAGCLLALTLTFLFOSLLTGPSSSEPPPSAVTIKSWVDKMOEDLVTLAKTASGVNQLVDI 60
DB 1 MAAGCLLALTLTFLFOSLLTGPSSSEPPPSAVTIKSWVDKMOEDLVTLAKTASGVNQLVDI 60
QY 61 YERYODLYTEPNNAQVEIAARDIEKLLSNRSKALVSLAEAEKVQAHHQWREDFASN 120
DB 61 YERYODLYTEPNNAQVEIAARDIEKLLSNRSKALVSLAEAEKVQAHHQWREDFASN 120
QY 121 EYVYNAKDDLPEKNDSEPGSORIKRVFEDANFGROISYQAANAHIPTDIESTIYL 180
DB 121 EYVYNAKDDLPEKNDSEPGSORIKRVFEDANFGROISYQAANAHIPTDIESTIYL 180
QY 121 EYVYNAKDDLPEKNDSEPGSORIKRVFEDANFGROISYQAANAHIPTDIESTIYL 180
DB 121 EYVYNAKDDLPEKNDSEPGSORIKRVFEDANFGROISYQAANAHIPTDIESTIYL 180
QY 181 NELNWTSALEDEVFKKNEEDPSILMOVFGSATGLARYPASPVWDNSRTPNKIDLDVRR 240
DB 181 NELNWTSALEDEVFKKNEEDPSILMOVFGSATGLARYPASPVWDNSRTPNKIDLDVRR 240
QY 181 NELNWTSALEDEVFKKNEEDPSILMOVFGSATGLARYPASPVWDNSRTPNKIDLDVRR 240
DB 181 NELNWTSALEDEVFKKNEEDPSILMOVFGSATGLARYPASPVWDNSRTPNKIDLDVRR 240
QY 241 RPYVIOGAASPKDMLILVDVSGVSGITLKLIRTSVSEMLETSLDDDFVNVASFNSNAOD 300
DB 241 RPYVIOGAASPKDMLILVDVSGVSGITLKLIRTSVSEMLETSLDDDFVNVASFNSNAOD 300
QY 301 VSCFOHLYOVANVNNKAYLKAANNITAKGTTDKKGSFPEFEOULLYNNVSRANCKITIML 360
DB 301 VSCFOHLYOVANVNNKAYLKAANNITAKGTTDKKGSFPEFEOULLYNNVSRANCKITIML 360
QY 361 FTGGERAEIEFNKYKDKKVVFRFVSQOHNYERQPIOMMACENKGGYYEIPISGATIR 420
DB 361 FTGGERAEIEFNKYKDKKVVFRFVSQOHNYERQPIOMMACENKGGYYEIPISGATIR 420

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QY 421 INFOEYLDVGRPMVLADGKAKQVQWNTNVYLDALGLVITGLTPVENINGOENKTNLK 480
DB 421 INFOEYLDVGRPMVLADGKAKQVQWNTNVYLDALGLVITGLTPVENINGOENKTNLK 480
QY 481 NOLLIGWGVVSLIEDIKRLTPRTLCPNGYFFAIDPNGVYLLHPNIQPNKPSOEYVL 540
DB 481 NOLLIGWGVVSLIEDIKRLTPRTLCPNGYFFAIDPNGVYLLHPNIQPNKPSOEYVL 540
QY 541 DELAELENDIKVELRNKMDIGSEGEKTFRLVVSODERYIDKGNRTYMTVPNGTQYSL 600
DB 541 DELAELENDIKVELRNKMDIGSEGEKTFRLVVSODERYIDKGNRTYMTVPNGTQYSL 600
QY 601 ALVLPYSFYIYKAKLEETITQARKSKGKMDSETLAPDNFEESGYTFIAPRDYCNLDKI 660
DB 601 ALVLPYSFYIYKAKLEETITQARKSKGKMDSETLAPDNFEESGYTFIAPRDYCNLDKI 660
QY 661 SDNNTTEFLNNEFIDKRTPNPNPCNADLNRVLLDAGFTNELVQNWWSQOKNIKVKAR 720
DB 661 SDNNTTEFLNNEFIDKRTPNPNPCNADLNRVLLDAGFTNELVQNWWSQOKNIKVKAR 720
QY 721 FVVTGGITRIVPKRAGEENMOENPETYEDSFYKRSNDNDNVFTAPYFNKSGPARESGI 780
DB 721 FVVTGGITRIVPKRAGEENMOENPETYEDSFYKRSNDNDNVFTAPYFNKSGPARESGI 780
QY 776 FVYIDGGITRIVPKRAGEENMOENPETYEDSFYKRSNDNDNVFTAPYFNKSGPARESGI 775
DB 776 FVYIDGGITRIVPKRAGEENMOENPETYEDSFYKRSNDNDNVFTAPYFNKSGPARESGI 775
QY 841 LDDGFFLLMANHDDYTNOIGRFPGHIDPSLMRHLVNSVYAFNKSXYOASCEGGAAPKQ 900
DB 841 LDDGFFLLMANHDDYTNOIGRFPGHIDPSLMRHLVNSVYAFNKSXYOASCEGGAAPKQ 900
QY 895 LDDGFFLLMANHDDYTNOIGRFPGHIDPSLMRHLVNSVYAFNKSXYOASCEGGAAPKQ 895
DB 895 LDDGFFLLMANHDDYTNOIGRFPGHIDPSLMRHLVNSVYAFNKSXYOASCEGGAAPKQ 895
QY 901 GAGHSATVPSVADILQIGMWATAAANSILQOFLSLTFPRLLEAVEMEDDFTASLSKQ 960
DB 901 GAGHSATVPSVADILQIGMWATAAANSILQOFLSLTFPRLLEAVEMEDDFTASLSKQ 960
QY 956 SCITEQOTQYFFDNDKSKSFSGVLDGNCGRIFHGEKLMNTNLIPTMVESKGTCPDTRL 1013
DB 956 SCITEQOTQYFFDNDKSKSFSGVLDGNCGRIFHGEKLMNTNLIPTMVESKGTCPDTRL 1013

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RESULT 8
US-08-223-305C-54
Sequence 54, Application US/08223305C
Patent No. 5851824
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASCAL Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/223,305C
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992

```



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US-09-452-007-4
; Sequence 4, Application US/09452007
; Patent No. 6140485
; GENERAL INFORMATION:
; APPLICANT: Franco, Rodrigo
; APPLICANT: Sun Chen, Ai Ru
; APPLICANT: Sney, David J.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL
; TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/452.007
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/713.118
; FILING DATE: 16-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mata, Elizabeth W.
; REGISTRATION NUMBER: 38,236
; REFERENCE/DOCKET NUMBER: ACC96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1091 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-452-007-4

Query Match          99.9%; Score 5342; DB 4; Length 1091;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1017; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAGCLLALITLTFOSLIGSSSEPPSAVTIKSWDKQEDLVTLAKTASGVNQLVDI 60
DB 1 MAAGCLLALITLTFOSLIGSSSEPPSAVTIKSWDKQEDLVTLAKTASGVNQLVDI 60
QY 61 YEKYODLYTEPNNAQOLVEIAARDIEKLSNRKALVSLALEAKYQAAHOMREDFASN 120
DB 61 YEKYODLYTEPNNAQOLVEIAARDIEKLSNRKALVSLALEAKYQAAHOMREDFASN 120
QY 121 EYVYVNAKDDIDPEKNSPEPSQRIKVFYTEDANFGROISTQAAVHIPTDIYEGSTIVL 180
DB 121 EYVYVNAKDDIDPEKNSPEPSQRIKVFYTEDANFGROISTQAAVHIPTDIYEGSTIVL 180
QY 181 NELWMTSALDEVFKNREDEPSILMOYFGSATGLARYPASPWNDSRTNKTIDLYVRR 240
DB 181 NELWMTSALDEVFKNREDEPSILMOYFGSATGLARYPASPWNDSRTNKTIDLYVRR 240
QY 241 RPWTIOGASFEKMDLIVDYSGVSGVLTLLKLRISVSEMLETSDDFVAVASNSNAOD 300
DB 241 RPWTIOGASFEKMDLIVDYSGVSGVLTLLKLRISVSEMLETSDDFVAVASNSNAOD 300
QY 301 VSCFOHLVQAVNRKKYLAKAVNNITAKGTTDYKKGSSFAFEOLLVNSBRANCKITIML 360
DB 301 VSCFOHLVQAVNRKKYLAKAVNNITAKGTTDYKKGSSFAFEOLLVNSBRANCKITIML 360
QY 361 FTDGEERAQEIFNKYKKDKKVRFRFVSQOHNYERGPIDMMAECENKGYEYIIPISGAIR 420

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DB 361 FTDGEERAQEIFNKYKKDKKVRFRFVSQOHNYERGPIDMMAECENKGYEYIIPISGAIR 420
QY 421 INFOYIDVYGRPMVLAGDAKAKOVMTNVLDALEGLVITGLTPFNITGCFENKTNK 480
DB 421 INFOYIDVYGRPMVLAGDAKAKOVMTNVLDALEGLVITGLTPFNITGCFENKTNK 480
QY 481 NOLILGVMDVSLIEDIKRLTPREFTLCPNGYPAIDPNCYVLLHPMLQPKNPSQEPVTL 540
DB 481 NOLILGVMDVSLIEDIKRLTPREFTLCPNGYPAIDPNCYVLLHPMLQPKNPSQEPVTL 540
QY 541 DFLDAELENDIKVEIRKMKIDSGEGKTYFTLVKSODERYIDKGNFTYWTVPNGTDSL 600
DB 541 DFLDAELENDIKVEIRKMKIDSGEGKTYFTLVKSODERYIDKGNFTYWTVPNGTDSL 600
QY 601 ALVLPYSEFYIKAKLEETTOARSKKGGKJOSSETLAKPNFEESGTYTAPRDYCDLKI 660
DB 601 ALVLPYSEFYIKAKLEETTOARSKKGGKJOSSETLAKPNFEESGTYTAPRDYCDLKI 660
QY 661 SDNNTTEFLNFEIDRKTPNPNPCNADLIRVLDAGFTNELVQYWSKOKNIKGVKAR 720
DB 661 SDNNTTEFLNFEIDRKTPNPNPCNADLIRVLDAGFTNELVQYWSKOKNIKGVKAR 720
QY 721 FVYTDGCTIRVYKKEAGENMOENPEYEDSFYKRSIDNDNVYFTAPYFNKSGPAYESGI 780
DB 721 FVYTDGCTIRVYKKEAGENMOENPEYEDSFYKRSIDNDNVYFTAPYFNKSGPAYESGI 780
QY 781 MVSRAVEITYOGKLLPAYVGIKIDVNSMTENTKTSINDPCAGPDCCKRSDVWDCYI 840
DB 781 MVSRAVEITYOGKLLPAYVGIKIDVNSMTENTKTSINDPCAGPDCCKRSDVWDCYI 840
QY 841 LDDGFLMANHNDYTNQICRFEIDPSLMRLVNIISVAFNRKSDYOSVCEPAAPO 900
DB 841 LDDGFLMANHNDYTNQICRFEIDPSLMRLVNIISVAFNRKSDYOSVCEPAAPO 900
QY 901 GAGHRSAVYPSVADIIQIGMATTAAMSILQOFLSLTEPRLLLEAVEMDDFTASLSQ 960
DB 901 GAGHRSAVYPSVADIIQIGMATTAAMSILQOFLSLTEPRLLLEAVEMDDFTASLSQ 960
QY 961 SCITEOYEFNDKSKFSGVLDGNCSTRIFGEXIMTNLFIWVESGTCPCCTRL 1018
DB 961 SCITEOYEFNDKSKFSGVLDGNCSTRIFGEXIMTNLFIWVESGTCPCCTRL 1018

RESULT 7
US-08-455-543A-54
; Sequence 54, Application US/0845543A
; Patent No. 5792846
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESS: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455.543A
; FILING DATE: May 31, 1995

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QY 601 ALVLPYSFYIKAKLEETITQARSKGKMKDSETLKPDNFEESGYTFIAPDYCNDLKI 660  
 DB 601 ALVLPYSFYIKAKLEETITQARSKGKMKDSETLKPDNFEESGYTFIAPDYCNDLKI 660  
 QY 661 SDNTEFLNFEIDRKTNNPNSCNADLINRVLLDAGFTNELVQNYMSKOKINIGVKAR 720  
 DB 661 SDNTEFLNFEIDRKTNNPNSCNADLINRVLLDAGFTNELVQNYMSKOKINIGVKAR 720  
 QY 721 FVYTDGTRVYPRKAGENMOENPETEYEDSFYKSLDNDNYFTAPYFNKSGPAYESGI 780  
 DB 721 FVYTDGTRVYPRKAGENMOENPETEYEDSFYKSLDNDNYFTAPYFNKSGPAYESGI 780  
 QY 781 MYSKAVEIYIOGKLKPAVVGIKIDVNSWIENTFTSIRDPACAGVCCCKRNSDVMDCVI 840  
 DB 781 MYSKAVEIYIOGKLKPAVVGIKIDVNSWIENTFTSIRDPACAGVCCCKRNSDVMDCVI 840  
 QY 841 LDDGFLMANHDDYTNOIGRFEIDPSLMRHLVNI SVAFNKSVDYQSVCEGPAARQ 900  
 DB 841 LDDGFLMANHDDYTNOIGRFEIDPSLMRHLVNI SVAFNKSVDYQSVCEGPAARQ 900  
 QY 901 GAGHSAYPSVADILQIGWMTAAASLLOQFLSLTFPRLLLEVEMEDDFTASLSKQ 960  
 DB 901 GAGHSAYPSVADILQIGWMTAAASLLOQFLSLTFPRLLLEVEMEDDFTASLSKQ 960  
 QY 961 SCITEQTOYFFPDNDKSFSGVLDGCGNCSRI FHGEKLMNTNLI FIMVESKGTCPDTRL 1018  
 DB 961 SCITEQTOYFFPDNDKSFSGVLDGCGNCSRI FHGEKLMNTNLI FIMVESKGTCPDTRL 1018

## RESULT 5

US-08-713-118-4  
 ; Sequence 4, Application us/08713118  
 ; Patent No. 6040436

## GENERAL INFORMATION:

APPLICANT: Franco, Rodrigo  
 APPLICANT: Sun Chen, Ai Ru  
 APPLICANT: Suey, David J.  
 TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL  
 TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
 STREET: Two Millitia Drive  
 CITY: Lexington  
 STATE: MA  
 COUNTRY: USA

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/713,118  
 FILING DATE: 16-SEP-1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mata, Elizabeth W.  
 REGISTRATION NUMBER: 38,236  
 REFERENCE/DOCKET NUMBER: ACC96-01  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-861-6240  
 TELEFAX: 617-861-9540  
 INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1091 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-713-118-4

Query Match

99.9%; Score 5342; DB 3; Length 1091;

Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1017; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAACCLALITLTLEFOSLILPPSSSEPPSAVTTIKSWYDKQOEDLYTLAKTASGVNOLVDI 60  
 DB 1 MAACCLALITLTLEFOSLILPPSSSEPPSAVTTIKSWYDKQOEDLYTLAKTASGVNOLVDI 60  
 QY 61 YEKQODLYTEPPNAROLVETIARDIEKLNSKALVSLALBAEKVOAAHQREDFASN 120  
 DB 61 YEKQODLYTEPPNAROLVETIARDIEKLNSKALVSLALBAEKVOAAHQREDFASN 120  
 QY 121 EYVYNAKDDLDPEKNDSEPSORIKPVFTEDANFGQOISYQAAVHIPTDIYEGSTYVL 180  
 DB 121 EYVYNAKDDLDPEKNDSEPSORIKPVFTEDANFGQOISYQAAVHIPTDIYEGSTYVL 180  
 QY 181 NELWMTSALDEVFKNKEEDPSLIMQVFGSATGLARYYPASPVWDNSRTPNKIDLYDVR 240  
 DB 181 NELWMTSALDEVFKNKEEDPSLIMQVFGSATGLARYYPASPVWDNSRTPNKIDLYDVR 240  
 QY 241 RPYVIOGAASPKDMILIVDSGSVSGTLTKLIRTSVEMLETLSDDDFVAVASFNSAOD 300  
 DB 241 RPYVIOGAASPKDMILIVDSGSVSGTLTKLIRTSVEMLETLSDDDFVAVASFNSAOD 300  
 QY 301 VSCFOHLVQANVRNKKVILKDAVNNITAKGITDYKKGSFAPEOLLNYSRANCKIIML 360  
 DB 301 VSCFOHLVQANVRNKKVILKDAVNNITAKGITDYKKGSFAPEOLLNYSRANCKIIML 360  
 QY 361 FTDDGEERAOIEFNKYKDKKVRVRFPSVGOHNREPRIDOMMACENKGYEETIPSTGIR 420  
 DB 361 FTDDGEERAOIEFNKYKDKKVRVRFPSVGOHNREPRIDOMMACENKGYEETIPSTGIR 420  
 QY 421 INFOEYLDVIGRPMVNLADGKAKQVQWNTNVYLDALDELGI VITGTLPVFNITGOENKTNLK 480  
 DB 421 INFOEYLDVIGRPMVNLADGKAKQVQWNTNVYLDALDELGI VITGTLPVFNITGOENKTNLK 480  
 QY 481 NQILIGWGVDSLEDIRKLTPTLCPNGYYPRAIDNGVYLLHPNLOPNPKSOPBYTL 540  
 DB 481 NQILIGWGVDSLEDIRKLTPTLCPNGYYPRAIDNGVYLLHPNLOPNPKSOPBYTL 540  
 QY 541 DELFAELNDIKVIRNKMIDEGSEKTFRTLYVSOBERIYDKGNRTYTTPVNGDTYSL 600  
 DB 541 DELFAELNDIKVIRNKMIDEGSEKTFRTLYVSOBERIYDKGNRTYTTPVNGDTYSL 600  
 QY 601 ALVLPYSFYIKAKLEETITQARSKGKMKDSETLKPDNFEESGYTFIAPDYCNDLKI 660  
 DB 601 ALVLPYSFYIKAKLEETITQARSKGKMKDSETLKPDNFEESGYTFIAPDYCNDLKI 660  
 QY 661 SDNTEFLNFEIDRKTNNPNSCNADLINRVLLDAGFTNELVQNYMSKOKINIGVKAR 720  
 DB 661 SDNTEFLNFEIDRKTNNPNSCNADLINRVLLDAGFTNELVQNYMSKOKINIGVKAR 720  
 QY 721 FVYTDGTRVYPRKAGENMOENPETEYEDSFYKSLDNDNYFTAPYFNKSGPAYESGI 780  
 DB 721 FVYTDGTRVYPRKAGENMOENPETEYEDSFYKSLDNDNYFTAPYFNKSGPAYESGI 780  
 QY 781 MYSKAVEIYIOGKLKPAVVGIKIDVNSWIENTFTSIRDPACAGVCCCKRNSDVMDCVI 840  
 DB 781 MYSKAVEIYIOGKLKPAVVGIKIDVNSWIENTFTSIRDPACAGVCCCKRNSDVMDCVI 840  
 QY 841 LDDGFLMANHDDYTNOIGRFEIDPSLMRHLVNI SVAFNKSVDYQSVCEGPAARQ 900  
 DB 841 LDDGFLMANHDDYTNOIGRFEIDPSLMRHLVNI SVAFNKSVDYQSVCEGPAARQ 900  
 QY 901 GAGHSAYPSVADILQIGWMTAAASLLOQFLSLTFPRLLLEVEMEDDFTASLSKQ 960  
 DB 901 GAGHSAYPSVADILQIGWMTAAASLLOQFLSLTFPRLLLEVEMEDDFTASLSKQ 960  
 QY 961 SCITEQTOYFFPDNDKSFSGVLDGCGNCSRI FHGEKLMNTNLI FIMVESKGTCPDTRL 1018  
 DB 961 SCITEQTOYFFPDNDKSFSGVLDGCGNCSRI FHGEKLMNTNLI FIMVESKGTCPDTRL 1018

RESULT 6

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181 NELNMTSALDEVFKKNEEDPSLIMOVGSAIGLARIYFASPMWVNSRTPKNTIDLYDVR 240
QY 241 RPYWIOGAASPKDMLILVDVSGSVGLTLKLRISVSEMLETSDDDFVNVASFNSNAD 300
DB 241 RPYWIOGAASPKDMLILVDVSGSVGLTLKLRISVSEMLETSDDDFVNVASFNSNAD 300
QY 301 VSCFOHLVQANVRNKKVLDKAVNNITAGITDYKKGFSFEBOLLNVNSRANCKIIML 360
DB 301 VSCFOHLVQANVRNKKVLDKAVNNITAGITDYKKGFSFEBOLLNVNSRANCKIIML 360
QY 361 FTDGEERAOEIFNKYKNDKRVFRFSGOHYERGPLOMACENKGYEETPSIGAIR 420
DB 361 FTDGEERAOEIFNKYKNDKRVFRFSGOHYERGPLOMACENKGYEETPSIGAIR 420
QY 421 INTQEYLDVLRPNVLAGDKAKOVMTNVDALDELGLVITGTLPEVNTIGQFENKTNLK 480
DB 421 INTQEYLDVLRPNVLAGDKAKOVMTNVDALDELGLVITGTLPEVNTIGQFENKTNLK 480
QY 481 NOLLIGWGVDSLEDIKRLTPRTFLCPNGYFAIDPBGVYLHPNLOPKNPKSQEPVTL 540
DB 481 NOLLIGWGVDSLEDIKRLTPRTFLCPNGYFAIDPBGVYLHPNLOPKNPKSQEPVTL 540
QY 541 DFLDAELENDIKVEIRNKMIDGSEGEKFTLVKSODERYIDKGNRTYTWTVPVNGTDSL 600
DB 541 DFLDAELENDIKVEIRNKMIDGSEGEKFTLVKSODERYIDKGNRTYTWTVPVNGTDSL 600
QY 601 ALVLPYSFYIKAKLETTIQARSKKGMDSFTLKPDNEESGYEIAIPDYCNLDKI 660
DB 601 ALVLPYSFYIKAKLETTIQARSKKGMDSFTLKPDNEESGYEIAIPDYCNLDKI 660
QY 661 SPNNTEFLINFEETDRTPNPNPCNADLINRVLLDAGFTNELVONYSKKNIKGVAR 720
DB 661 SPNNTEFLINFEETDRTPNPNPCNADLINRVLLDAGFTNELVONYSKKNIKGVAR 720
QY 721 FVYVGTGITRVYKPEAGENMOENPEYEDSFYKRSILDNDNVFTAPYFNKSGPGAYESGI 780
DB 721 FVYVGTGITRVYKPEAGENMOENPEYEDSFYKRSILDNDNVFTAPYFNKSGPGAYESGI 780
QY 781 MYSKAVEITYIOGKLKPAVVGIKIDVNSMIENFTKTSIRDPGACVGCCKRNSDMCVI 840
DB 781 MYSKAVEITYIOGKLKPAVVGIKIDVNSMIENFTKTSIRDPGACVGCCKRNSDMCVI 840
QY 841 LDDGFFLLMANHDDYTNQIGREFEIDPSLMHHTVINSVAFNKSVDYQSVCEPAAKQ 900
DB 841 LDDGFFLLMANHDDYTNQIGREFEIDPSLMHHTVINSVAFNKSVDYQSVCEPAAKQ 900
QY 901 GAGHRSAYVPSADILQIGMWATAAWSILQOFLSLTFPRLLEAVEMEDDFTASLSKQ 960
DB 901 GAGHRSAYVPSADILQIGMWATAAWSILQOFLSLTFPRLLEAVEMEDDFTASLSKQ 960
QY 961 SCITEQOTQFEDNDKSFSGVLDGNCRIHFGKELMNTNLIETWESKGTCPDTRL 1018
DB 961 SCITEQOTQFEDNDKSFSGVLDGNCRIHFGKELMNTNLIETWESKGTCPDTRL 1018

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RESULT 4  
US-08-311-363-25

; Sequence 25, Application US/08311363

; Patent No. 5876958

; GENERAL INFORMATION:

; APPLICANT: Harpold, Michael

; APPLICANT: Ellis, Steven

; APPLICANT: Williams, Mark

; APPLICANT: Feldman, Daniel

; APPLICANT: McCue, Ann

; APPLICANT: Brenner, Robert

; TITLE OF INVENTION: Human Calcium Channel Compositions and

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brown, Martin, Haller & McClain

; STREET: 1660 Union Street

```

CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,363
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-51506
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-311-363-25

Query Match 100.0%; Score 5346; DB 2; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAACCLALTLTLTQSLIGPSSSEPPSAVTIKSWDKQCELVTLAKTASGVNLDVI 60
DB 1 MAACCLALTLTLTQSLIGPSSSEPPSAVTIKSWDKQCELVTLAKTASGVNLDVI 60
QY 61 YEKYQDLYVEPNNAQRLVEIARADIEKLSNRSKALVSLAEKVOAHQREDPASN 120
DB 61 YEKYQDLYVEPNNAQRLVEIARADIEKLSNRSKALVSLAEKVOAHQREDPASN 120
QY 121 EYVYNNAKDLDPEKKNSEBGSQRIKPVFIEDANFGQISYQAAVHIPIIDIEGSTIYL 180
DB 121 EYVYNNAKDLDPEKKNSEBGSQRIKPVFIEDANFGQISYQAAVHIPIIDIEGSTIYL 180
QY 181 NELNMTSALDEVFKKNEEDPSLIMOVGSAIGLARIYFASPMWVNSRTPKNTIDLYDVR 240
DB 181 NELNMTSALDEVFKKNEEDPSLIMOVGSAIGLARIYFASPMWVNSRTPKNTIDLYDVR 240
QY 241 RPYWIOGAASPKDMLILVDVSGSVGLTLKLRISVSEMLETSDDDFVNVASFNSNAD 300
DB 241 RPYWIOGAASPKDMLILVDVSGSVGLTLKLRISVSEMLETSDDDFVNVASFNSNAD 300
QY 301 VSCFOHLVQANVRNKKVLDKAVNNITAGITDYKKGFSFEBOLLNVNSRANCKIIML 360
DB 301 VSCFOHLVQANVRNKKVLDKAVNNITAGITDYKKGFSFEBOLLNVNSRANCKIIML 360
QY 361 FTDGEERAOEIFNKYKNDKRVFRFSGOHYERGPLOMACENKGYEETPSIGAIR 420
DB 361 FTDGEERAOEIFNKYKNDKRVFRFSGOHYERGPLOMACENKGYEETPSIGAIR 420
QY 421 INTQEYLDVLRPNVLAGDKAKOVMTNVDALDELGLVITGTLPEVNTIGQFENKTNLK 480
DB 421 INTQEYLDVLRPNVLAGDKAKOVMTNVDALDELGLVITGTLPEVNTIGQFENKTNLK 480
QY 481 NOLLIGWGVDSLEDIKRLTPRTFLCPNGYFAIDPBGVYLHPNLOPKNPKSQEPVTL 540
DB 481 NOLLIGWGVDSLEDIKRLTPRTFLCPNGYFAIDPBGVYLHPNLOPKNPKSQEPVTL 540
QY 541 DFLDAELENDIKVEIRNKMIDGSEGEKFTLVKSODERYIDKGNRTYTWTVPVNGTDSL 600
DB 541 DFLDAELENDIKVEIRNKMIDGSEGEKFTLVKSODERYIDKGNRTYTWTVPVNGTDSL 600

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QY 121 EVVYNAKDDLDPEKNDSESGRIKPVLETDANFGROISYOHAAVHPTDIYEGSTIVL 180
DB 121 EVVYNAKDDLDPEKNDSESGRIKPVLETDANFGROISYOHAAVHPTDIYEGSTIVL 180
QY 181 NELNMTSALDEVEFKKREDEPSSLIMQVFGSATGLARYYPASPWVNSRTPNKIDLYDVR 240
DB 181 NELNMTSALDEVEFKKREDEPSSLIMQVFGSATGLARYYPASPWVNSRTPNKIDLYDVR 240
QY 241 RFWYIOGAASPKDMLILVYVSGVSGLTJLKTSTVSEKLETLSDDDFNVASFSNMAOD 300
DB 241 RFWYIOGAASPKDMLILVYVSGVSGLTJLKTSTVSEKLETLSDDDFNVASFSNMAOD 300
QY 301 VSCFOHLVOANVRNKKVYLKDAVNNITAKGITDYKKGFSAFEPOLLNVNVRANCKNIML 360
DB 301 VSCFOHLVOANVRNKKVYLKDAVNNITAKGITDYKKGFSAFEPOLLNVNVRANCKNIML 360
QY 361 FPDGGERAOEIFNKNKKNKKVAVFVSQHNHYERGPLOMMAECENKGYEIEPSIGAIR 420
DB 361 FPDGGERAOEIFNKNKKNKKVAVFVSQHNHYERGPLOMMAECENKGYEIEPSIGAIR 420
QY 421 INFOEYLDVLRPMVLGAKAKOVNTNYLDALDELGLVITGTLPVNTTGOEENKTNLK 480
DB 421 INFOEYLDVLRPMVLGAKAKOVNTNYLDALDELGLVITGTLPVNTTGOEENKTNLK 480
QY 481 NQIILGVMGVDSLEDIKRLTPFTLCPNGYFAIDPNCYVLLHPNLQPKNRSQEPVTL 540
DB 481 NQIILGVMGVDSLEDIKRLTPFTLCPNGYFAIDPNCYVLLHPNLQPKNRSQEPVTL 540
QY 541 DFLDALDELNDIKVEIKNNKIDSESGEKTIRITVKSODEYIDKGNKTYTWTVNGTDSL 600
DB 541 DFLDALDELNDIKVEIKNNKIDSESGEKTIRITVKSODEYIDKGNKTYTWTVNGTDSL 600
QY 601 ALVLPYSEFYIKAKLEETITQARSKKGMKXOSETLKPNEFESGTFAPRDYCNDKI 660
DB 601 ALVLPYSEFYIKAKLEETITQARSKKGMKXOSETLKPNEFESGTFAPRDYCNDKI 660
QY 661 SDNTEFLNPFNEIDRKTTPNPNPCNADLINRYLLDAGFTNELVOYMSKONIKGVKAR 720
DB 661 SDNTEFLNPFNEIDRKTTPNPNPCNADLINRYLLDAGFTNELVOYMSKONIKGVKAR 720
QY 721 FVYTOGCTIRVYPKKAGEWMOENPEYEDSFYKRSIDNUNYVFTAPYFKSGPAGYESGI 780
DB 721 FVYTOGCTIRVYPKKAGEWMOENPEYEDSFYKRSIDNUNYVFTAPYFKSGPAGYESGI 780
QY 781 MYSKAEIYIOGKLKPAVVGIKIDVNSWIEFTKTSIDPCAGPVCDCRKSNDWDCYI 840
DB 781 MYSKAEIYIOGKLKPAVVGIKIDVNSWIEFTKTSIDPCAGPVCDCRKSNDWDCYI 840
QY 841 LDDGGFLMANHDDYTNQIGREFGETIDPSLMRHLVNI SYVAFNKSXYDOSVCEPGAAPRO 900
DB 841 LDDGGFLMANHDDYTNQIGREFGETIDPSLMRHLVNI SYVAFNKSXYDOSVCEPGAAPRO 900
QY 901 GAGHRSAYVSVADILQIGWMAATAAAMSTLQOFLSLTFPRLEAVEEMDDPFTSLSKQ 960
DB 901 GAGHRSAYVSVADILQIGWMAATAAAMSTLQOFLSLTFPRLEAVEEMDDPFTSLSKQ 960
QY 961 SCITTEOTYFFPNDKSFSGVLDCCGNCSTIFGEGKLMNTNLFIVESKGTCPDTRL 1018
DB 961 SCITTEOTYFFPNDKSFSGVLDCCGNCSTIFGEGKLMNTNLFIVESKGTCPDTRL 1018

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RESULT 3  
US-08-223-305C-52  
Sequence 52, Application US/08223305C

Patent No. 5651824  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert

```

TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESS: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/223,305C
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 52516 (P519739)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
US-08-223-305C-52

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Query Match 100.0%; Score 5346; DB 2; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MAAGCLALTLTLPQSLIGPSEPPPSAVTISKWDKMQEDLVTLAKTASGVNQLVDI 60
QY 61 YEKYQDLTYVEPNNAQOLVEIARDIEKLSSNSKALVSLALEAEKYQAAHQWREDFASN 120
DB 61 YEKYQDLTYVEPNNAQOLVEIARDIEKLSSNSKALVSLALEAEKYQAAHQWREDFASN 120
QY 121 EVVYNAKDDLDPEKNDSESGRIKPVLETDANFGROISYOHAAVHPTDIYEGSTIVL 180
DB 121 EVVYNAKDDLDPEKNDSESGRIKPVLETDANFGROISYOHAAVHPTDIYEGSTIVL 180
QY 181 NELNMTSALDEVEFKKREDEPSSLIMQVFGSATGLARYYPASPWVNSRTPNKIDLYDVR 240

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QY 61 YEKYODLYTEPNNAQOLVEIARDIEKLSNRKALVSLAEAKVOAHOHREDPASN 120
Db 61 YEKYODLYTEPNNAQOLVEIARDIEKLSNRKALVSLAEAKVOAHOHREDPASN 120
QY 121 EVVYVNAKDDLPKNDSEPSQRIKPYEIEDANFGROIYOHAAVHPTDYESTIVL 180
Db 121 EVVYVNAKDDLPKNDSEPSQRIKPYEIEDANFGROIYOHAAVHPTDYESTIVL 180
QY 181 NELNMTSALDEVFKKNNREDDPSLLMQVFGSATGLARYYPASPWVNSRTPKIDLYVR 240
Db 181 NELNMTSALDEVFKKNNREDDPSLLMQVFGSATGLARYYPASPWVNSRTPKIDLYVR 240
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Db 241 RPYVIOGASAPKMDLILVDVSGVSLTKLIRTSVSEMLFTLSDDDVNNAFSPSNAD 300
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Db 301 VSCFOHLVQANRNKKVLDKAVNNITAGITDYKKGFSAFEOQLNVTNVRANCKIIML 360
QY 361 FTDGGEERAQOEIENKYNKDKAVRFVRSVGOHNYERGPIONMACENKGYEIPSGAIR 420
Db 361 FTDGGEERAQOEIENKYNKDKAVRFVRSVGOHNYERGPIONMACENKGYEIPSGAIR 420
QY 421 INTQYLYLVGRPMVLADGAKAQOVMTVYLDALGLVITGILPVENITGOFEKKTMLK 480
Db 421 INTQYLYLVGRPMVLADGAKAQOVMTVYLDALGLVITGILPVENITGOFEKKTMLK 480
QY 481 NOLILGVAVDLSLBDIKRLPRTLCNGYFAIDPNGYVLLHNNLOPKMKPSOEPVL 540
Db 481 NOLILGVAVDLSLBDIKRLPRTLCNGYFAIDPNGYVLLHNNLOPKMKPSOEPVL 540
QY 541 DFLDALENDIKVEIRNKMIDGSEGEKTFRLVKSQDERYIDKGNRTYWTVPNGTDSL 600
Db 541 DFLDALENDIKVEIRNKMIDGSEGEKTFRLVKSQDERYIDKGNRTYWTVPNGTDSL 600
QY 601 ALVLTYSFYYIKAKLEETIQOARSKKGMKDSKTLKPDNFEESGYTFIARDONOLKI 660
Db 601 ALVLTYSFYYIKAKLEETIQOARSKKGMKDSKTLKPDNFEESGYTFIARDONOLKI 660
QY 661 SDNNTFELNNEFIDRTPNPNPSCNADLINRVLLDAGFTNELVQVYMSKONIKGVAR 720
Db 661 SDNNTFELNNEFIDRTPNPNPSCNADLINRVLLDAGFTNELVQVYMSKONIKGVAR 720
QY 721 FVYVYGGITRYPKRAGENMOENPTTYDSYKSLDNNTVFTAPYFNKSGPAYESGI 780
Db 721 FVYVYGGITRYPKRAGENMOENPTTYDSYKSLDNNTVFTAPYFNKSGPAYESGI 780
QY 781 MYSKAVEIYIOGKILKPAVVGIKIDVNSWIMNFTKSTRDPCAGPVCCCKRNSVMDCVI 840
Db 781 MYSKAVEIYIOGKILKPAVVGIKIDVNSWIMNFTKSTRDPCAGPVCCCKRNSVMDCVI 840
QY 841 LDDGGFLLMANHDDYTNOIGRFGFIDPSLMRHLVNIISVAFNKSVDYOSCEGAPAKO 900
Db 841 LDDGGFLLMANHDDYTNOIGRFGFIDPSLMRHLVNIISVAFNKSVDYOSCEGAPAKO 900
QY 901 GAGHSATVPSVADILQIGMATAAAMSILQOFLISTFPLLEAVEMEDDFTASLSKQ 960
Db 901 GAGHSATVPSVADILQIGMATAAAMSILQOFLISTFPLLEAVEMEDDFTASLSKQ 960
QY 961 SCITFOOTYFPDNDKSPSGVLDGNCGRIFHGEKIMNTNLIIFIMVBSKGCPCDTRL 1018
Db 961 SCITFOOTYFPDNDKSPSGVLDGNCGRIFHGEKIMNTNLIIFIMVBSKGCPCDTRL 1018

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RESULT 2  
US-08-455-543A-52

; Sequence 52, Application US/08455543A

; Patent No. 5792846

; GENERAL INFORMATION:

; APPLICANT: Harpold, Michael

; APPLICANT: Ellis, Steven

; APPLICANT: Williams, Mark

```

APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESS: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
FILING DATE: May 31, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-455-543A-52

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Query Match 100.0%; Score 5346; DB 1; Length 1091;

Best local Similarity 100.0%; Pred. No. 0;

Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MAAGCLALTLTIFOSLILGPSSEPPPSAVYTKSVYDKMOEDLVTLAKTAGVNOVDI 60
Db 1 MAAGCLALTLTIFOSLILGPSSEPPPSAVYTKSVYDKMOEDLVTLAKTAGVNOVDI 60
QY 61 YEKYODLYTEPNNAQOLVEIARDIEKLSNRKALVSLAEAKVOAHOHREDPASN 120
Db 61 YEKYODLYTEPNNAQOLVEIARDIEKLSNRKALVSLAEAKVOAHOHREDPASN 120

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 10, 2003, 14:13:55 ; Search time 11.291 seconds  
(without alignments)  
2652.785 Million cell updates/sec

Title: US-10-090-827-13

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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

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5: /cgn2\_6/prodata/1/1aa/PCRU.COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/backfilest1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5346	100.0	1091	1	US-07-745-206A-25
2	5346	100.0	1091	1	US-08-455-543A-52
3	5346	100.0	1091	2	US-08-223-305C-52
4	5346	100.0	1091	2	US-08-311-363-25
5	5342	99.9	1091	3	US-08-713-118-4
6	5342	99.9	1091	4	US-09-452-007-4
7	5306.5	99.3	1086	1	US-08-455-543A-54
8	5306.5	99.3	1086	2	US-08-223-305C-54
9	5289.5	98.9	1084	1	US-08-455-543A-56
10	5289.5	98.9	1084	2	US-08-223-305C-56
11	5270	98.6	1103	1	US-08-455-543A-53
12	5270	98.6	1103	2	US-08-223-305C-53
13	5250	98.2	1079	1	US-08-455-543A-55
14	5250	98.2	1079	2	US-08-223-305C-55
15	5137.5	96.1	1106	1	US-08-435-675B-5
16	5119.5	95.8	1106	1	US-08-336-257A-8
17	4913	91.9	1086	6	5386025-8
18	2872.5	53.7	1145	4	US-09-470-443-2
19	2872.5	53.7	1145	4	US-09-470-443-4
20	2851.5	53.3	1076	4	US-09-470-443-6
21	2581.5	48.3	508	1	US-08-435-675B-6
22	182	3.4	885	3	US-09-074-579-5
23	182	3.4	885	3	US-09-388-774-5
24	159.5	3.0	946	3	US-09-074-579-3
25	159.5	3.0	946	4	US-09-388-774-3
26	158.5	3.0	894	4	US-09-071-035-248
27	158.5	3.0	962	4	US-09-071-035-246

28	158.5	3.0	962	4	US-09-071-035-250	Sequence 250, App
29	158.5	3.0	962	4	US-09-071-035-254	Sequence 254, App
30	158.5	3.0	962	4	US-09-071-035-470	Sequence 470, App
31	158.5	3.0	962	4	US-09-071-035-474	Sequence 474, App
32	158.5	3.0	962	4	US-09-071-035-478	Sequence 478, App
33	154.5	2.9	946	4	US-09-546-153-1	Sequence 1, Appl1
34	154	2.9	903	1	US-08-021-601-12	Sequence 12, Appl1
35	154	2.9	903	1	US-08-082-849B-12	Sequence 12, Appl1
36	154	2.9	903	5	PCT-US94-01624-12	Sequence 12, Appl1
37	152.5	2.9	789	1	US-08-471-033-32	Sequence 32, Appl1
38	152.5	2.9	789	2	US-08-471-044-32	Sequence 32, Appl1
39	152.5	2.9	789	2	US-08-463-483A-32	Sequence 32, Appl1
40	152.5	2.9	789	2	US-08-471-046A-32	Sequence 32, Appl1
41	152.5	2.9	789	2	US-08-470-566B-32	Sequence 32, Appl1
42	152.5	2.9	789	2	US-08-838-219B-4	Sequence 4, Appl1
43	152.5	2.9	789	2	US-08-469-334-32	Sequence 32, Appl1
44	152.5	2.9	789	3	US-09-300-529-32	Sequence 32, Appl1
45	152.5	2.9	789	3	US-09-233-336A-4	Sequence 4, Appl1

#### ALIGNMENTS

RESULT 1  
US-07-745-206A-25  
Sequence 25, Application US/07745206A  
Patent No. 5429921

#### GENERAL INFORMATION:

APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: McCue, Ann  
APPLICANT: Feldman, Daniel  
TITLE OF INVENTION: Human Calcium Channel Compositions and  
TITLE OF INVENTION: Methods  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fitch, Even, Tabin & Flannery  
STREET: 135 S. LaSalle  
CITY: Chicago  
STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60603

#### COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07745,206A  
FILING DATE: 19910815  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Feder, Scott B  
REFERENCE/DOCKET NUMBER: 51504  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-372-7842  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1091 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-745-206A-25

Query Match 100.0%; Score 5346; DB 1; Length 1091;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLALTLTLPISLIGPSSEPPSAVTIKSWDKMOEDLVTLAKTASGVNOLVDI 60  
DB 1 MAAGCLALTLTLPISLIGPSSEPPSAVTIKSWDKMOEDLVTLAKTASGVNOLVDI 60







## RESULT 14

US-08-223-305C-55

Sequence 55, Application US/08223305C

Patent No. 5851824

GENERAL INFORMATION:

APPLICANT: Harpold, Michael

APPLICANT: Ellis, Steven

APPLICANT: Williams, Mark

APPLICANT: Feldman, Daniel

APPLICANT: McCue, Ann

APPLICANT: Brenner, Robert

TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

METHODS

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller &amp; McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: PasteSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/223,305C

FILING DATE: April 4, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/868,354

FILING DATE: April 10, 1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/745,206

FILING DATE: 15-AUG-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/620,250

FILING DATE: 30-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/482,384

FILING DATE: 20-FEB-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/603,751

FILING DATE: 04-APR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US89/01408

FILING DATE: 04-APR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/176,899

FILING DATE: 04-APR-1988

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L.

REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 52516 (P519739)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619)238-0999

TELEFAX: (619)238-0062

INFORMATION FOR SEQ ID NO: 55:

SEQUENCE CHARACTERISTICS:

LENGTH: 1079 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

US-08-223-305C-55

Query Match 98.3% Score 5503: DB 2: Length 1079;

Best Local Similarity 98.8% Pred. No. 0;

Matches 1050; Conservative 0; Mismatches 1; Indels 12; Gaps 2;

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OY 1

MAAGCLALTLTLFQSLIGPSSSEPPSAVTIKSWDKMGEDLVTLAKTASGVNQLVDI 60

Db 1 MAAGCLALTLTLFQSLIGPSSSEPPSAVTIKSWDKMGEDLVTLAKTASGVNQLVDI 60

OY 61 YEKYODLYTVEPNNAKROLVEIAARDIEKLNSRKALVSLALEAKYQAAHOMWEDASN 120

Db 61 YEKYODLYTVEPNNAKROLVEIAARDIEKLNSRKALVSLALEAKYQAAHOMWEDASN 120

OY 121 EYVYNAKDDLPKNDSEPSGRIKPYFIEDANFGROIYQHAVAHIPTDIYGSTIVL 180

Db 121 EYVYNAKDDLPKNDSEPSGRIKPYFIEDANFGROIYQHAVAHIPTDIYGSTIVL 180

OY 121 EYVYNAKDDLPKNDSEPSGRIKPYFIEDANFGROIYQHAVAHIPTDIYGSTIVL 180

Db 121 EYVYNAKDDLPKNDSEPSGRIKPYFIEDANFGROIYQHAVAHIPTDIYGSTIVL 180

OY 181 NELMNTSLDVEFKKNEEDPSLLMOYFGSATGLARYPASPVYDNRTPNKIDLYDVR 240

Db 181 NELMNTSLDVEFKKNEEDPSLLMOYFGSATGLARYPASPVYDNRTPNKIDLYDVR 240

OY 241 RPYIYOGAASPKDMLLYDVSGSVGLTKLIRTSVEMLETTSDDDFVAVASFSNAOD 300

Db 241 RPYIYOGAASPKDMLLYDVSGSVGLTKLIRTSVEMLETTSDDDFVAVASFSNAOD 300

OY 301 VSCFOHLVQANVRNKKVYLKDAVNNITAKGTDYKGFSAFEQILNYSRANCKITML 360

Db 301 VSCFOHLVQANVRNKKVYLKDAVNNITAKGTDYKGFSAFEQILNYSRANCKITML 360

OY 361 FTDGGEERAQIEFNKKYKDKKVRFRSVQHNTERGPIDMACENKGYIETPSIGAIR 420

Db 361 FTDGGEERAQIEFNKKYKDKKVRFRSVQHNTERGPIDMACENKGYIETPSIGAIR 420

OY 421 INTQYLDVIGRPVWLAGDKAKOVQNTNYLDALIELGLVYTGTLPVNTIGQENKTNK 480

Db 421 INTQYLDVIGRPVWLAGDKAKOVQNTNYLDALIELGLVYTGTLPVNTIGQENKTNK 480

OY 481 NQILIGVWVDVSLIEDIKRLTPRETLCPNGYFAIDPBGVYLHPNLQPKNSQEPVTL 540

Db 481 NQILIGVWVDVSLIEDIKRLTPRETLCPNGYFAIDPBGVYLHPNLQPKNSQEPVTL 540

OY 541 DELDAELNDIKVEIRKMKIDGEGEKTFTLYKSQDERIDGKNRTYTPVNGTDYSL 600

Db 541 DELDAELNDIKVEIRKMKIDGEGEKTFTLYKSQDERIDGKNRTYTPVNGTDYSL 600

OY 596 ALVLPYTSFYIKAKLEETITQARSKGKMKDSEFTLKPDNFESGTYFLAPRYCNDIKI 660

Db 596 ALVLPYTSFYIKAKLEETITQARSKGKMKDSEFTLKPDNFESGTYFLAPRYCNDIKI 660

OY 661 SDNTEFLNFEIDRKTNNPSNADLNRVLLDAGFTNELVQYWSKOKNIKGVKAR 720

Db 661 SDNTEFLNFEIDRKTNNPSNADLNRVLLDAGFTNELVQYWSKOKNIKGVKAR 720

OY 721 FVYTDGGITRYYPREAGENQENPEYEDSFYKRSLDNDNYVTATYFNKSGGAYESGI 780

Db 721 FVYTDGGITRYYPREAGENQENPEYEDSFYKRSLDNDNYVTATYFNKSGGAYESGI 780

OY 769 FVYTDGGITRYYPREAGENQENPEYEDSFYKRSLDNDNYVTATYFNKSGGAYESGI 768

Db 769 FVYTDGGITRYYPREAGENQENPEYEDSFYKRSLDNDNYVTATYFNKSGGAYESGI 768

OY 781 MVSNAVEIYIOGKLLKPAVVGIRKIDVNSWJENFTKTSIRPCGAPYCDCKRNSDVADCI 840

Db 781 MVSNAVEIYIOGKLLKPAVVGIRKIDVNSWJENFTKTSIRPCGAPYCDCKRNSDVADCI 840

OY 841 LDDGGLFLMANHDDYTNOIGRFFGEIDPSLMRLVINSYVAFNKSVDYOSVCEPGAAPQ 900

Db 841 LDDGGLFLMANHDDYTNOIGRFFGEIDPSLMRLVINSYVAFNKSVDYOSVCEPGAAPQ 900

OY 829 LDDGGLFLMANHDDYTNOIGRFFGEIDPSLMRLVINSYVAFNKSVDYOSVCEPGAAPQ 888

Db 829 LDDGGLFLMANHDDYTNOIGRFFGEIDPSLMRLVINSYVAFNKSVDYOSVCEPGAAPQ 888

OY 901 GAGHRSAYVPSVADIIIOIGWMTAAAMSIIQOFLSLTPRRLLEAVEMDDDTASLSKQ 960

Db 901 GAGHRSAYVPSVADIIIOIGWMTAAAMSIIQOFLSLTPRRLLEAVEMDDDTASLSKQ 960

OY 961 SCITEQTOYFFNDSDSKSFSGLDGCNCSRIFHEKELMNTNLPIFVYESKGTGCDPRLLI 1020

Db 961 SCITEQTOYFFNDSDSKSFSGLDGCNCSRIFHEKELMNTNLPIFVYESKGTGCDPRLLI 1020

OY 1021 QAEQTSQGPVPCVMYKQPRIRKGPVDCPDNNVLEDTYDCGGVS 1063

Db 1021 QAEQTSQGPVPCVMYKQPRIRKGPVDCPDNNVLEDTYDCGGVS 1063

RESULT 15

## RESULT 13

US-08-455-543A-55

Sequence 55. Application US/08455543A

Patent No. 5792846

GENERAL INFORMATION:

APPLICANT: Harpold, Michael

APPLICANT: Ellis, Steven

APPLICANT: Williams, Mark

APPLICANT: Feldman, Daniel

APPLICANT: McCue, Ann

APPLICANT: Brenner, Robert

TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

METHODS

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Brown, Martin, Haller &amp; McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/455,543A

FILING DATE: May 31, 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/223,305

FILING DATE: April 4, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/868,354

FILING DATE: April 10, 1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/745,206

FILING DATE: 15-AUG-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/620,250

FILING DATE: 30-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/603,751

FILING DATE: 04-APR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US89/01408

FILING DATE: 04-APR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/176,899

FILING DATE: 04-APR-1988

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L.

REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 6362-52517

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619)238-0999

TELEFAX: (619)238-0062

INFORMATION FOR SEQ ID NO: 55:

SEQUENCE CHARACTERISTICS:

LENGTH: 1079 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

US-08-455-543A-55

Query Match

Best Local Similarity

Matches 1050; Conservative

98.3%; Score 5503; DB 1; Length 1079;

98.8%; Pred. No. 0;

0; Mismatches

1; Indels

12; Gaps

2;

QY 1 MAAGCLLALTLTLFOSLLIGPSSEEPSPAYTIKSWDKMODLVTLLAKTASGVNOIYDI 60

DB 1 MAGCLLALTLTLFOSLLIGPSSEEPSPAYTIKSWDKMODLVTLLAKTASGVNOIYDI 60

QY 61 YEKYODLYTVEPNNAKQVLEIAARDIEKLLSNRSKALVSLLEAKYQAAHQMEDFASN 120

DB 61 YEKYODLYTVEPNNAKQVLEIAARDIEKLLSNRSKALVSLLEAKYQAAHQMEDFASN 120

QY 121 EYVYYNAKDDLDPEKNDSEPSQRIKPVFIEDANFGROIYQAAVH1PTDIYGGSTIVL 180

DB 121 EYVYYNAKDDLDPEKNDSEPSQRIKPVFIEDANFGROIYQAAVH1PTDIYGGSTIVL 180

QY 181 NELNMTSALDEYFKKRNREDSLLMVGSAATGLARYYPASPWVNSRTPKIDLYVRR 240

DB 181 NELNMTSALDEYFKKRNREDSLLMVGSAATGLARYYPASPWVNSRTPKIDLYVRR 240

QY 241 RPYITOGAASPMDLILVDVSGVSGTLTKLIRTSVSEMLETSLDDDFVNVASFNSNAD 300

DB 241 RPYITOGAASPMDLILVDVSGVSGTLTKLIRTSVSEMLETSLDDDFVNVASFNSNAD 300

QY 301 VSCFOHLYOANVRNKKVLDKAVNNTAKGTDYKKGSFARFOLNINVSANCKIIML 360

DB 301 VSCFOHLYOANVRNKKVLDKAVNNTAKGTDYKKGSFARFOLNINVSANCKIIML 360

QY 361 FTDGGEERAQELFNKYNKDKKRVFRFVGQHNTERGPIOMACENKGYEIPSIGAIR 420

DB 361 FTDGGEERAQELFNKYNKDKKRVFRFVGQHNTERGPIOMACENKGYEIPSIGAIR 420

QY 421 INTQEYLDVLRPMVLAADKAKOVOMTNYLDALDELGLVITGLPVENITQGFENKTLK 480

DB 421 INTQEYLDVLRPMVLAADKAKOVOMTNYLDALDELGLVITGLPVENITQGFENKTLK 480

QY 481 NOLLIGWGVVYSLEDIRLTPRFTLCPNGYFFALDPNGYVLLHPNLOPKPKQOEPTL 540

DB 481 NOLLIGWGVVYSLEDIRLTPRFTLCPNGYFFALDPNGYVLLHPNLOPKPKQOEPTL 540

QY 541 DFLDAELENDIKVEIRNKMIDGSEGEKTFRLVKSQDRYIDKGRITWTVPNGTDSL 600

DB 541 DFLDAELENDIKVEIRNKMIDGSEGEKTFRLVKSQDRYIDKGRITWTVPNGTDSL 600

QY 596 ALVLPYSEYIYIKAKLEETITQARY-----SEFLKPDNEESGYTIAIPDYCNLDKI 648

DB 596 ALVLPYSEYIYIKAKLEETITQARY-----SEFLKPDNEESGYTIAIPDYCNLDKI 648

QY 661 SNNTEFLINFEFIDRKTNNPSCNADLINRVLDAGFTLDELVOYNTWSKOKNIKGVAKR 720

DB 661 SNNTEFLINFEFIDRKTNNPSCNADLINRVLDAGFTLDELVOYNTWSKOKNIKGVAKR 720

QY 721 FVYTDGGITRVYPKEAGENWQENPETYEDSFYKRSILDNDNYVTAPYENKSGPAYESGI 780

DB 721 FVYTDGGITRVYPKEAGENWQENPETYEDSFYKRSILDNDNYVTAPYENKSGPAYESGI 780

QY 769 MYSKAVEIYIOGKLLKPAVGIKIDVNSMIEFTTSTRDPCAGVCCCKRNSDMCVI 840

DB 769 MYSKAVEIYIOGKLLKPAVGIKIDVNSMIEFTTSTRDPCAGVCCCKRNSDMCVI 840

QY 841 LDDGGFLMANHDDTNOIGRFGEIDPSLMHLNINIVYAFNKSVDYQSCPCGAAPKQ 900

DB 841 LDDGGFLMANHDDTNOIGRFGEIDPSLMHLNINIVYAFNKSVDYQSCPCGAAPKQ 900

QY 901 GAGHSAYVSVADILIOGWMTAAAMSTLQOFLSLTFPRLLAEVEMEDDFTASLSKQ 960

DB 901 GAGHSAYVSVADILIOGWMTAAAMSTLQOFLSLTFPRLLAEVEMEDDFTASLSKQ 960

QY 949 SCITTEQTOYFFNDNDSKSGVLDGNCGRIFRGEKLMNTNLIIFIVESKGTGCPDTRILLI 1008

DB 949 SCITTEQTOYFFNDNDSKSGVLDGNCGRIFRGEKLMNTNLIIFIVESKGTGCPDTRILLI 1008

QY 1021 QAEQTSIDGPNPCDMVKOPRYRKGPVCPDNNVLEIYTCGGVS 1063

DB 1009 QAEQTSIDGPNPCDMVKOPRYRKGPVCPDNNVLEIYTCGGVS 1051

Sequence 53, Application US/08223305C  
Patent No. 5851824  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/223,305C  
FILING DATE: April 4, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 52516 (P519739)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1103 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-223-305C-53

Query Match 98.6%; Score 5523; DB 2; length 1103;  
Best Local Similarity 97.5%; Pred. No. 0;  
Matches 1055; Conservative 0; Mismatches 1; Indels 26; Gaps 2;

QY 1 MAAGCLALTLTLFQSLIGPSSEPPSAVTIKSWVDKQEDLVTLAKTAGVNLVDI 60  
DB 1 MAAGCLALTLTLFQSLIGPSSEPPSAVTIKSWVDKQEDLVTLAKTAGVNLVDI 60

QY 61 YEKYQDLYVEPNNAARLVETLAARDIEKLLSNNSKALVSLALAEKVOAHOQREDPASN 120  
DB 61 YEKYQDLYVEPNNAARLVETLAARDIEKLLSNNSKALVSLALAEKVOAHOQREDPASN 120  
QY 121 EVVYNNAKDDLPKKNSEPGSORIKRPVTEIDANFGQISYOHAAVHIPDIEGSTIYL 180  
DB 121 EVVYNNAKDDLPKKNSEPGSORIKRPVTEIDANFGQISYOHAAVHIPDIEGSTIYL 180  
QY 181 NELNMTSALDEVEFKKNEDEPSSLMOVFGSATGLARYPPASPVWDSKRPNNKIDLYDVR 240  
DB 181 NELNMTSALDEVEFKKNEDEPSSLMOVFGSATGLARYPPASPVWDSKRPNNKIDLYDVR 240  
QY 241 RPYTIQGAAPKMDLILVDVSGSVGLTKLIRTSVSEMLFTLSDDDFVAVSPNSAOD 300  
DB 241 RPYTIQGAAPKMDLILVDVSGSVGLTKLIRTSVSEMLFTLSDDDFVAVSPNSAOD 300  
QY 301 VSCFOHLVOANVRKRVKLVKAVNNITAKGTDVKKGSFAEQLLNNVSRACNKTIML 360  
DB 301 VSCFOHLVOANVRKRVKLVKAVNNITAKGTDVKKGSFAEQLLNNVSRACNKTIML 360  
QY 361 FTDGEERAQEIFNKYKNDKRVFRFVSQOHNERGPIDMACENKGYEIPISGAIR 420  
DB 361 FTDGEERAQEIFNKYKNDKRVFRFVSQOHNERGPIDMACENKGYEIPISGAIR 420  
QY 421 INTQETLDVIGRPVYLAGDAKQOVQWTVYLDLGLGLVITGTLVPVFNITQGEENKTNL 480  
DB 421 INTQETLDVIGRPVYLAGDAKQOVQWTVYLDLGLGLVITGTLVPVFNITQGEENKTNL 480  
QY 481 NOLLGVAGVDSLEDIKRLPRFTLCPNGYFPAIDNGVLLHPNLOPK----- 530  
DB 481 NOLLGVAGVDSLEDIKRLPRFTLCPNGYFPAIDNGVLLHPNLOPK----- 530  
QY 531 -----NPKSQEPTLDELDALENDIKVEIRNMIGESGEKFTFLVKSODERYI 581  
DB 531 -----NPKSQEPTLDELDALENDIKVEIRNMIGESGEKFTFLVKSODERYI 581  
QY 582 DKGRTYTWPNVNGTDSLALVLPYSFYIKAKLETTIQAASKKGMKMDSTLKPDNF 641  
DB 601 DKGRTYTWPNVNGTDSLALVLPYSFYIKAKLETTIQAASKKGMKMDSTLKPDNF 641  
QY 642 EESGYTFLAPRDYNDKISDNNTFELNNEFLNDRTPNNPSCNADLIRVLLDGFN 701  
DB 654 EESGYTFLAPRDYNDKISDNNTFELNNEFLNDRTPNNPSCNADLIRVLLDGFN 701  
QY 702 ELVQNMYSKOKINIGVAREVYTDGITRYYPKEAGENMOENPETYEDSFYKRSIDNDY 761  
DB 714 ELVQNMYSKOKINIGVAREVYTDGITRYYPKEAGENMOENPETYEDSFYKRSIDNDY 761  
QY 762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLKPAVVGIKIDVNSWLENFTKTSIRDP 821  
DB 774 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLKPAVVGIKIDVNSWLENFTKTSIRDP 821  
QY 822 CAGPVCCKRNSDVMDCVIILDDGFLMANHDDYTNIGFPEIDPSLMRHLVNSVYA 881  
DB 834 CAGPVCCKRNSDVMDCVIILDDGFLMANHDDYTNIGFPEIDPSLMRHLVNSVYA 881  
QY 882 FNSKYDYQVCEPGAAPKOGAGHRSAYVPSVADILQGMATAAASIIQOFLSLTFPR 941  
DB 894 FNSKYDYQVCEPGAAPKOGAGHRSAYVPSVADILQGMATAAASIIQOFLSLTFPR 941  
QY 942 LLEAVEMEDDDFTASLSKQSCITBQTOYFFDNDKSGSGVLDGCNCSRIIPHGEKLMNTNL 1001  
DB 954 LLEAVEMEDDDFTASLSKQSCITBQTOYFFDNDKSGSGVLDGCNCSRIIPHGEKLMNTNL 1001  
QY 1002 IFIMVESKGTCPDPTRLILIAEQTSDPNCMDVYKQRYRKGDPVCFDNNVLEDTYDCG 1061  
DB 1014 IFIMVESKGTCPDPTRLILIAEQTSDPNCMDVYKQRYRKGDPVCFDNNVLEDTYDCG 1061  
QY 1062 VS 1063  
DB 1074 VS 1075

APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,543A  
FILING DATE: May 31, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/223,305  
FILING DATE: April 4, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: NO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-52517  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1103 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-455-543A-53

Query Match 98.6%; Score 5523; DB 1; Length 1103;  
Best Local Similarity 97.5%; Pred. No. 0;  
Matches 1055; Conservative 0; Mismatches 1; Indels 26; Gaps 2;

QY 1 MAAGCLLALTLTFLGSLIGPSSEEPFSAVTIKSWDKMOEDLVTLAATAGVQVQVLDI 60  
DB 1 MAAGCLLALTLTFLGSLIGPSSEEPFSAVTIKSWDKMOEDLVTLAATAGVQVQVLDI 60  
QY 61 YEKYODLYTVEPNNAQQLVEIARDIEKLNSRKALVSLAEAEVQAAHQWREDFASN 120

DB 61 YEKYODLYTVEPNNAQQLVEIARDIEKLNSRKALVSLAEAEVQAAHQWREDFASN 120  
QY 121 EYVYNNADDDLDPEKNDSEPGSQRKIPFIEDANGROISQHAAYHPTDIIYEGSTIVL 180  
DB 121 EYVYNNADDDLDPEKNDSEPGSQRKIPFIEDANGROISQHAAYHPTDIIYEGSTIVL 180  
QY 181 NELNMTSALDEYFKKKNREDEPSLQMVGSAATGLARYYPASPMVNSRTPKIDLYDVR 240  
DB 181 NELNMTSALDEYFKKKNREDEPSLQMVGSAATGLARYYPASPMVNSRTPKIDLYDVR 240  
QY 241 RPYITOGAASPDKMLILVDGSGVSGTLKILRTSVSEMLETLSDDEPVNVAFNSNAOD 300  
DB 241 RPYITOGAASPDKMLILVDGSGVSGTLKILRTSVSEMLETLSDDEPVNVAFNSNAOD 300  
QY 301 VSCFHLVQANVRNKKVLDKAVNNITTAGITDYKKGSFAEQLNINVASANKIIML 360  
DB 301 VSCFHLVQANVRNKKVLDKAVNNITTAGITDYKKGSFAEQLNINVASANKIIML 360  
QY 361 FTDGGEERAQEIFNKNKDKKRVFRFVGQHNTERGP IQMACEKNGYIEIPSIGAIR 420  
DB 361 FTDGGEERAQEIFNKNKDKKRVFRFVGQHNTERGP IQMACEKNGYIEIPSIGAIR 420  
QY 421 INFOEYLDVLRPMVLADGKAKQVQWNTVYLDALGLVITGTLDPVNTIGQFENKTNLK 480  
DB 421 INFOEYLDVLRPMVLADGKAKQVQWNTVYLDALGLVITGTLDPVNTIGQFENKTNLK 480  
QY 481 NQILIGWGVVSLSDIKRLTPRPLCPNGYYPALDPNGYVLLHPNLOPK----- 530  
DB 481 NQILIGWGVVSLSDIKRLTPRPLCPNGYYPALDPNGYVLLHPNLOPKIGVIGPTIN 540  
QY 531 -----NPKSOPVTLDFLDAELENDIKVEIRNKKIDSESEKFTRTLVKSODERYI 581  
DB 541 LKRRPNINQNKRSQSPRYLDFLDAELENDIKVEIRNKKIDSESEKFTRTLVKSODERYI 600  
QY 582 DKGAFYTWTPVNGTDSLALVLPYSPYYIKAKLEETITQARSKKGMKDSFLKPDNF 641  
DB 601 DKGAFYTWTPVNGTDSLALVLPYSPYYIKAKLEETITQARSKKGMKDSFLKPDNF 653  
QY 642 EESGTFIAPRDYCNLDKISDNNTFELNFEFLDRKTPNPNPSCNADLINVLDAEFTN 701  
DB 654 EESGTFIAPRDYCNLDKISDNNTFELNFEFLDRKTPNPNPSCNADLINVLDAEFTN 713  
QY 702 ELVQYWSKORNIKGVKARFVVTGDIRVYPKAGEWMOENPEYEDSFYKRSLDNDY 761  
DB 714 ELVQYWSKORNIKGVKARFVVTGDIRVYPKAGEWMOENPEYEDSFYKRSLDNDY 773  
QY 762 VFTAPYFNKSGPGAYESGIMSKAVEIYIOGKLLKPAVVGIKIDVNSMIENFTKTSIRDP 821  
DB 774 VFTAPYFNKSGPGAYESGIMSKAVEIYIOGKLLKPAVVGIKIDVNSMIENFTKTSIRDP 833  
QY 822 CAGPYCDCKRNSDVMDVCTILDGGLMANHDDVTNOIGREFGIDSLMHRHVNISVYA 881  
DB 834 CAGPYCDCKRNSDVMDVCTILDGGLMANHDDVTNOIGREFGIDSLMHRHVNISVYA 893  
QY 882 FNKSYDQSVCEPGAAPKOGAGHRSAYVSVADILQIGWMTAAWMSILQOFLSLTFPR 941  
DB 894 FNKSYDQSVCEPGAAPKOGAGHRSAYVSVADILQIGWMTAAWMSILQOFLSLTFPR 953  
QY 942 LLEAVEMEDDPTASLSKQSCITEQTYFFPNDKSKSGVLDGCGNCRIFHGEKLMNTNL 1001  
DB 954 LLEAVEMEDDPTASLSKQSCITEQTYFFPNDKSKSGVLDGCGNCRIFHGEKLMNTNL 1013  
QY 1002 IFIMVESKGTCPDPTRLILQAEQTSDDGNPCDMVKOPRYRKGPRVCPDNVNLDEYTPCGG 1061  
DB 1014 IFIMVESKGTCPDPTRLILQAEQTSDDGNPCDMVKOPRYRKGPRVCPDNVNLDEYTPCGG 1073  
QY 1062 VS 1063  
DB 1074 VS 1075

RESULT 12  
US-08-223-305C-53

APPLICANT: Harpold, Michael  
 APPLICANT: Ellis, Steven  
 APPLICANT: Williams, Mark  
 APPLICANT: Feldman, Daniel  
 APPLICANT: McCue, Ann  
 APPLICANT: Brenner, Robert  
 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
 TITLE OF INVENTION: METHODS  
 NUMBER OF SEQUENCES: 57  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Brown, Martin, Haller & McClain  
 STREET: 1660 Union Street  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92101-2926  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/223,305C  
 FILING DATE: April 4, 1994  
 APPLICATION DATA:  
 APPLICATION NUMBER: 07/868,354  
 FILING DATE: April 10, 1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/745,206  
 FILING DATE: 15-AUG-1991  
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 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/176,899  
 FILING DATE: 04-APR-1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie L.  
 REGISTRATION NUMBER: 33,779  
 REFERENCE/DOCKET NUMBER: 52516 (P519739)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619)238-0999  
 TELEFAX: (619)238-0062  
 INFORMATION FOR SEQ ID NO: 56:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1084 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-223-305C-56

Query Match 99.0%; Score 5542.5; DB 2; Length 1084;  
 Best Local Similarity 99.2%; Pred. No. 0;  
 Matches 1055; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 1 MAAGCLALITLTFOSLLIGSSSEPPSAVTIKSWDMQMEDLVTLAKTASGVNQLVDI 60  
 DB 1 MAAGCLALITLTFOSLLIGSSSEPPSAVTIKSWDMQMEDLVTLAKTASGVNQLVDI 60  
 QY 61 YEKYODLTVEPNNAKQVEITARDIEKLLNSRKALYSIALLEAKVQAHQWREDFASN 120  
 DB 61 YEKYODLTVEPNNAKQVEITARDIEKLLNSRKALYSIALLEAKVQAHQWREDFASN 120

QY 121 EVVYVNAKDDLDPEKNDSEPSQRIKPVFIEDANFGROIYQHAAVHIPTDIYGSSTVL 180  
 DB 121 EVVYVNAKDDLDPEKNDSEPSQRIKPVFIEDANFGROIYQHAAVHIPTDIYGSSTVL 180  
 QY 181 NELNMTSALDEVYFKKNREEDPSLLMQVFGSATGLARYYPASPMYDNSTPKIDLYDVR 240  
 DB 181 NELNMTSALDEVYFKKNREEDPSLLMQVFGSATGLARYYPASPMYDNSTPKIDLYDVR 240  
 QY 241 RPYWYOGAASPMDMLIVDYSVSGSLTKLIRTSVSEMLETSDDEYVNAFNSNAD 300  
 DB 241 RPYWYOGAASPMDMLIVDYSVSGSLTKLIRTSVSEMLETSDDEYVNAFNSNAD 300  
 QY 301 VSCFQHLVQANRNKKVLDKDAVNNITAGITDYKGFSEFQOLLNVSRANKNTIML 360  
 DB 301 VSCFQHLVQANRNKKVLDKDAVNNITAGITDYKGFSEFQOLLNVSRANKNTIML 360  
 QY 361 FTDGEERAQOEIFNKYKNDKAVRFRESVGOHNERGPIOMACENKGYEYFISGAIR 420  
 DB 361 FTDGEERAQOEIFNKYKNDKAVRFRESVGOHNERGPIOMACENKGYEYFISGAIR 420  
 QY 421 INTQYLDVIGRPVYLADGAKQVQNTVYLDALLEGVITGTLPRVNTIQFENKTNLK 480  
 DB 421 INTQYLDVIGRPVYLADGAKQVQNTVYLDALLEGVITGTLPRVNTIQFENKTNLK 480  
 QY 481 NQLLIGVGVVSLIEDIRLTPRETLCPNGYFFAIDPBGVYLLPNNLOPKPKSQEPVTL 540  
 DB 481 NQLLIGVGVVSLIEDIRLTPRETLCPNGYFFAIDPBGVYLLPNNLOPKPKSQEPVTL 540  
 QY 541 DFLDALELNDIKVELRNKMDIGESGEKTEFRLVKSQDERYIDKGNRTYTWTVPVGTDSL 600  
 DB 541 DFLDALELNDIKVELRNKMDIGESGEKTEFRLVKSQDERYIDKGNRTYTWTVPVGTDSL 600  
 QY 601 ALVLPYTSFYIYKAKLEETITQARSKKGMKDSFTLKPDPNEESGYFTIAPROVCNCLKI 660  
 DB 601 ALVLPYTSFYIYKAKLEETITQARSKKGMKDSFTLKPDPNEESGYFTIAPROVCNCLKI 660  
 QY 661 SDNNTFELNFEIDRKTNNPNSCNDLNRVLIDAGFTNELVQYVNSKOKNIKGYKAR 720  
 DB 661 SDNNTFELNFEIDRKTNNPNSCNDLNRVLIDAGFTNELVQYVNSKOKNIKGYKAR 720  
 QY 721 FVYVMDGKITRYPKRAGNMENPEYEDSFYKSLDNDNVYFAPYFNSKSGPATESGI 780  
 DB 721 FVYVMDGKITRYPKRAGNMENPEYEDSFYKSLDNDNVYFAPYFNSKSGPATESGI 780  
 QY 781 MYSKAVEIYIOGKLLKPAVVGIRKIDVNSWIEFNTKTSIRPCAGPVCDCKRNSVMDCVI 840  
 DB 781 MYSKAVEIYIOGKLLKPAVVGIRKIDVNSWIEFNTKTSIRPCAGPVCDCKRNSVMDCVI 840  
 QY 841 LDGCGFLMANHDDYTNOIGRFGELIDPSLMRHLVNI SVYAFNKSXYDQSVCEGAPKQ 900  
 DB 841 LDGCGFLMANHDDYTNOIGRFGELIDPSLMRHLVNI SVYAFNKSXYDQSVCEGAPKQ 900  
 QY 901 GAGHRSAYVPSVADILIOIGWATTAAMSIIQOPLSLTFPRLLLEYAVMEDDDPTASLSKO 960  
 DB 901 GAGHRSAYVPSVADILIOIGWATTAAMSIIQOPLSLTFPRLLLEYAVMEDDDPTASLSKO 960  
 QY 961 SCITEQYQYFEDNDSKSFSGVLDGCGNSRIEFGHEKILNTNLIIFWESKGTCCDTRLIL 1020  
 DB 961 SCITEQYQYFEDNDSKSFSGVLDGCGNSRIEFGHEKILNTNLIIFWESKGTCCDTRLIL 1020  
 QY 1021 QABOTSGPNPCDMVKOPRRYKGPVDCFDNNVLEDYTDGCGVS 1063  
 DB 1021 QABOTSGPNPCDMVKOPRRYKGPVDCFDNNVLEDYTDGCGVS 1063  
 QY 1014 QABOTSGPNPCDMVKOPRRYKGPVDCFDNNVLEDYTDGCGVS 1056  
 DB 1014 QABOTSGPNPCDMVKOPRRYKGPVDCFDNNVLEDYTDGCGVS 1056

RESULT 11  
 US-08-455-543A-53  
 Sequence 53; Application US/08455543A  
 Patent No. 5792846  
 GENERAL INFORMATION:  
 APPLICANT: Harpold, Michael  
 APPLICANT: Ellis, Steven

APPLICANT: Ellis, Steven  
 APPLICANT: Williams, Mark  
 APPLICANT: Feldman, Daniel  
 APPLICANT: McCue, Ann  
 APPLICANT: Brenner, Robert  
 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
 NUMBER OF SEQUENCES: 57  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Brown, Martin, Haller & McClain  
 STREET: 1660 Union Street  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92101-2926  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/455,543A  
 FILING DATE: May 31, 1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/223,305  
 FILING DATE: April 4, 1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/868,354  
 FILING DATE: April 10, 1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/745,206  
 FILING DATE: 15-AUG-1991  
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 APPLICATION NUMBER: US 07/482,384  
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 APPLICATION NUMBER: WO PCT/US89/01408  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/176,899  
 FILING DATE: 04-APR-1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie L.  
 REGISTRATION NUMBER: 33,779  
 REFERENCE/DOCKET NUMBER: 6362-52517  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619)238-0999  
 TELEFAX: (619)238-0062  
 INFORMATION FOR SEQ ID NO: 56:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1084 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-455-543A-56

Query Match 99.0%; Score 5542.5; DB 1; Length 1084;  
 Best Local Similarity 99.2%; Pred. No. 0;  
 Matches 1053; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 1 MAACCLATLTTLTFLPOSILIGSPSEPPSAVTIKSWDKQOEDLVTLAKTASGVNQLVDI 60  
 DB 1 MAACCLATLTTLTFLPOSILIGSPSEPPSAVTIKSWDKQOEDLVTLAKTASGVNQLVDI 60  
 QY 61 YEKYODLYVEPNNAQOLVETIARDIEKLNSRSKALVSIALAEKVOAAHQWREDFASN 120

DB 61 YEKYODLYVEPNNAQOLVETIARDIEKLNSRSKALVSIALAEKVOAAHQWREDFASN 120  
 QY 121 EYVYNNADDDDDPEKNDSEPSORIKPYFIEDANPGRQISVOAAVHPDIDYEGSTIVL 180  
 DB 121 EYVYNNADDDDDPEKNDSEPSORIKPYFIEDANPGRQISVOAAVHPDIDYEGSTIVL 180  
 QY 181 NELNNTSALDEVFKKREDEPSILMQVGSATGLARYPPASPMYDNRTPKIDLYVRR 240  
 DB 181 NELNNTSALDEVFKKREDEPSILMQVGSATGLARYPPASPMYDNRTPKIDLYVRR 240  
 QY 241 RPYWTOGAASPKMDLILVDVSGSVGLTKLIRTSVSEMETLSDDDFVNVAFTNSNAD 300  
 DB 241 RPYWTOGAASPKMDLILVDVSGSVGLTKLIRTSVSEMETLSDDDFVNVAFTNSNAD 300  
 QY 301 VSCFOHVOANRNKKVLLKDAVNNITAGLIDYKGFSEFAEQLNVAANCKIIML 360  
 DB 301 VSCFOHVOANRNKKVLLKDAVNNITAGLIDYKGFSEFAEQLNVAANCKIIML 360  
 QY 361 PTDGGEERAQELFNKNYNNDKKRVFRFSVGOHNERGPIQWAGENKGYEIPISGAIR 420  
 DB 361 PTDGGEERAQELFNKNYNNDKKRVFRFSVGOHNERGPIQWAGENKGYEIPISGAIR 420  
 QY 421 INTQETLDVLRPNVLAGDKAKOVQWTVYLDALGLVITGILPEVNTQOFENKTNLK 480  
 DB 421 INTQETLDVLRPNVLAGDKAKOVQWTVYLDALGLVITGILPEVNTQOFENKTNLK 480  
 QY 481 NOLILGVNGVDVSLIEDIRLPRFTLCNGYFAIDPNGYVLLHPNLOPKKSOEPTVL 540  
 DB 481 NOLILGVNGVDVSLIEDIRLPRFTLCNGYFAIDPNGYVLLHPNLOPKKSOEPTVL 540  
 QY 541 DELDALENDIKVEIRNKKIDEGSEKTEFTLVKSODERYIDKGNRTYTWTPVNGTDSL 600  
 DB 541 DELDALENDIKVEIRNKKIDEGSEKTEFTLVKSODERYIDKGNRTYTWTPVNGTDSL 600  
 QY 601 ALVLPYTSYTYIKAKLEETIYQARSKKGMDSFLKADNPEESYTTIARDCNDIKI 660  
 DB 601 ALVLPYTSYTYIKAKLEETIYQARSKKGMDSFLKADNPEESYTTIARDCNDIKI 660  
 QY 661 SDNTEFFLNFEFIDRKTNNPNSCNADILNVLDAFETNELVONYMSKOKNIKGVAR 720  
 DB 661 SDNTEFFLNFEFIDRKTNNPNSCNADILNVLDAFETNELVONYMSKOKNIKGVAR 720  
 QY 721 FVYTDGGITRVPYKPEGEMWQENPETYEDSFYKRSILDNDVNYFTAPYFNKSGPGAYESGI 780  
 DB 721 FVYTDGGITRVPYKPEGEMWQENPETYEDSFYKRSILDNDVNYFTAPYFNKSGPGAYESGI 780  
 QY 781 MYSKAVEITYIGKRLKRPAYVGIKIDVNSWIEFTTSTRDPCAGVCCCKRNSDMDCVI 840  
 DB 781 MYSKAVEITYIGKRLKRPAYVGIKIDVNSWIEFTTSTRDPCAGVCCCKRNSDMDCVI 840  
 QY 841 LDDGGFLMANHDDYTNOIGRFGEIDPSILMHLVINSYVAFNKSVDYQSCPEGAABQ 900  
 DB 841 LDDGGFLMANHDDYTNOIGRFGEIDPSILMHLVINSYVAFNKSVDYQSCPEGAABQ 900  
 QY 901 GAGHRSAYVSVADIIQIGWMAATAAWSILQOFLSLTFPRLLAEVEMEDDFTASLSKQ 960  
 DB 901 GAGHRSAYVSVADIIQIGWMAATAAWSILQOFLSLTFPRLLAEVEMEDDFTASLSKQ 960  
 QY 961 SCTTEOTQYFFDNDKSFSGVLDGNCSTRIFGEKLMNTNLFINVESKGTQPCOTRLLI 1020  
 DB 961 SCTTEOTQYFFDNDKSFSGVLDGNCSTRIFGEKLMNTNLFINVESKGTQPCOTRLLI 1020  
 QY 1021 QAEQTSIDGPNPCDMVYKOPRYRKGPVYCFNNVLEDTYDCGVS 1063  
 DB 1021 QAEQTSIDGPNPCDMVYKOPRYRKGPVYCFNNVLEDTYDCGVS 1063  
 QY 1014 QAEQTSIDGPNPCDMVYKOPRYRKGPVYCFNNVLEDTYDCGVS 1056  
 DB 1014 QAEQTSIDGPNPCDMVYKOPRYRKGPVYCFNNVLEDTYDCGVS 1056

RESULT 10  
 US-08-223-305C-56  
 ; Sequence 56, Application US/08223305C  
 ; Patent No. 5851824  
 ; GENERAL INFORMATION:

GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: Moeue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
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FILING DATE: 30-NOV-1990  
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APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
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PRIOR APPLICATION DATA:  
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PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 52516 (P519739)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1086 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-223-305C-54

Query Match 99.3% Score 5559.5; DB 2: Length 1086;  
Best Local Similarity 99.3% Pred. No. 0;  
Matches 1058; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 MAACCLATLTTLTQSLIGPSSSEPPSAVTITKSWVDKMOEDLYTLAKTASGVNOLYDI 60  
DB 1 MAACCLATLTTLTQSLIGPSSSEPPSAVTITKSWVDKMOEDLYTLAKTASGVNOLYDI 60  
QY 61 YEKYQDLYTVEPNNAQOLVEIARIDIEKLISNRKALVSLALEAKVQAOAHQWREDFASN 120  
|||||

DB 61 YEKYQDLYTVEPNNAQOLVEIARIDIEKLISNRKALVSLALEAKVQAOAHQWREDFASN 120  
QY 121 EYVYNNKADLDLPEKNDSEKNSORIKPVFTEDANFGROIYQHAAPHIDIEGSTIYL 180  
DB 121 EYVYNNKADLDLPEKNDSEKNSORIKPVFTEDANFGROIYQHAAPHIDIEGSTIYL 180  
QY 181 NELNMTSALDEVRKKNREEDPSLLMOVFSATGLARYYPASPVWDSRPNNKIDLYDVR 240  
DB 181 NELNMTSALDEVRKKNREEDPSLLMOVFSATGLARYYPASPVWDSRPNNKIDLYDVR 240  
QY 241 RPWYIOGAASPKMLILVDYSGSVGLTKLITTSVSEMLETISDDDFNVASFNSNAOD 300  
DB 241 RPWYIOGAASPKMLILVDYSGSVGLTKLITTSVSEMLETISDDDFNVASFNSNAOD 300  
QY 301 VSCFOHLVQANVENKVKYLDKAVNNITAKGITDYKKGSFPEOLLNYSRANCKITML 360  
DB 301 VSCFOHLVQANVENKVKYLDKAVNNITAKGITDYKKGSFPEOLLNYSRANCKITML 360  
QY 361 FTGGEERAQELFNKYNKDKVVPFRPSVQOHNYERGPLOMACENKGYEELPSIGAIR 420  
DB 361 FTGGEERAQELFNKYNKDKVVPFRPSVQOHNYERGPLOMACENKGYEELPSIGAIR 420  
QY 421 INTQETLDVLRPMVLAGDQAKOVNTNYLDLDELGLVITGLTPFNITGOFENKTNK 480  
DB 421 INTQETLDVLRPMVLAGDQAKOVNTNYLDLDELGLVITGLTPFNITGOFENKTNK 480  
QY 481 NOLILGVGVDSLEIDIKRLTPRFTLCPNGYFAIDPNCVLLHPYLOKPNKSOEPTL 540  
DB 481 NOLILGVGVDSLEIDIKRLTPRFTLCPNGYFAIDPNCVLLHPYLOKPNKSOEPTL 540  
QY 541 DFLDAELENDIKVEIRNKMIDSGEKTEFTLVKSODERYIDKGNFTYTPNGTDSL 600  
DB 541 DFLDAELENDIKVEIRNKMIDSGEKTEFTLVKSODERYIDKGNFTYTPNGTDSL 600  
QY 536 DFLDAELENDIKVEIRNKMIDSGEKTEFTLVKSODERYIDKGNFTYTPNGTDSL 595  
DB 536 DFLDAELENDIKVEIRNKMIDSGEKTEFTLVKSODERYIDKGNFTYTPNGTDSL 595  
QY 601 ALVPTYSFYITAKLEETITQARSKKGMKQSEITLKPNEFSSTGTAPADYCDLKI 660  
DB 596 ALVPTYSFYITAKLEETITQARSKKGMKQSEITLKPNEFSSTGTAPADYCDLKI 655  
QY 661 SDNTEFLNFEFIDRKTPNPNCSNADLINRYLDAGFTNELVQYMSKOKNIKGVAR 720  
DB 656 SDNTEFLNFEFIDRKTPNPNCSNADLINRYLDAGFTNELVQYMSKOKNIKGVAR 715  
QY 721 FVYTDGIRTVYKKEGENKQENPEYEDSFYKRSIDNDNYFTAPYENKSGPAYESGI 780  
DB 716 FVYTDGIRTVYKKEGENKQENPEYEDSFYKRSIDNDNYFTAPYENKSGPAYESGI 775  
QY 781 MYSKAVEITYOGKLKPAYVGIKIDVNSMTENTKTSIRDPACGAPVCDCKRNSDWDCTI 840  
DB 776 MYSKAVEITYOGKLKPAYVGIKIDVNSMTENTKTSIRDPACGAPVCDCKRNSDWDCTI 835  
QY 841 LDDGGFLMANHDDYTNOIGRFEGLIDPSLMRLVNI SYAENKSYDYQSVCEPGAAPRO 900  
DB 836 LDDGGFLMANHDDYTNOIGRFEGLIDPSLMRLVNI SYAENKSYDYQSVCEPGAAPRO 895  
QY 901 GAGHRSAVYPSVADITQIGWMTAAWMSILOFLSLTPRLLAEVEMEDDFTASLSKO 960  
DB 896 GAGHRSAVYPSVADITQIGWMTAAWMSILOFLSLTPRLLAEVEMEDDFTASLSKO 955  
QY 961 SCITEOTYFFENDSKSFSGVLDGNCNCSRIPEGEXKLMNTNLFIFIVESGTCPCPTRLI 1020  
DB 956 SCITEOTYFFENDSKSFSGVLDGNCNCSRIPEGEXKLMNTNLFIFIVESGTCPCPTRLI 1015  
QY 1021 QAEQTSDDGPNPCDMVKOPRYRKGPDPVCFDNNVLYEDYTDGCVS 1063  
DB 1016 QAEQTSDDGPNPCDMVKOPRYRKGPDPVCFDNNVLYEDYTDGCVS 1058

RESULT 9  
US-08-455-543A-56  
Sequence 56, Application US/08455543A  
Patent No. 5792846  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael

APPLICANT: Harpold, Michael  
 APPLICANT: Ellis, Steven  
 APPLICANT: Williams, Mark  
 APPLICANT: Feldman, Daniel  
 APPLICANT: McCue, Ann  
 APPLICANT: Brenner, Robert  
 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
 NUMBER OF SEQUENCES: 57  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Brown, Martin, Haller & McClain  
 STREET: 1660 Union Street  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92101-2926  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/455,543A  
 FILING DATE: May 31, 1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/223,305  
 FILING DATE: April 4, 1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/868,354  
 FILING DATE: April 10, 1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/745,206  
 FILING DATE: 15-AUG-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/620,250  
 FILING DATE: 30-NOV-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/482,384  
 FILING DATE: 20-FEB-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/603,751  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/US89/01408  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/176,899  
 FILING DATE: 04-APR-1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie L.  
 REGISTRATION NUMBER: 33,779  
 REFERENCE/DOCKET NUMBER: 6362-52517  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619)238-0999  
 TELEFAX: (619)238-0062  
 INFORMATION FOR SEQ ID NO: 54:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1086 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-455-543A-54

Query Match 99.3%; Score 5559.5; DB 1; Length 1086;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 1058; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

OY 1 MAAGCIIATLTTLFOSLLTIGSSPEEPSPAVTIKSWDKMOEDLVYLLAKTAGSVNOLYDI 60  
 DB 1 MAAGCIIATLTTLFOSLLTIGSSPEEPSPAVTIKSWDKMOEDLVYLLAKTAGSVNOLYDI 60

OY 61 YEKYODLYTVEBNNAQRLVEIARPIEKLISNRKATVSLALAEKVOAAHQWREDFASN 120  
 DB 61 YEKYODLYTVEBNNAQRLVEIARPIEKLISNRKATVSLALAEKVOAAHQWREDFASN 120  
 OY 121 EVVYVNAKDDLDPEKNDSEPGSQRIPVEIEDANGROISYQAAVHLPTDIYEGSTIVL 180  
 DB 121 EVVYVNAKDDLDPEKNDSEPGSQRIPVEIEDANGROISYQAAVHLPTDIYEGSTIVL 180  
 OY 181 NELNMTSALDEYFKKRNREDESLIMQVGSATGLARYYPAPPMWVNSTPTPKIDLYVRR 240  
 DB 181 NELNMTSALDEYFKKRNREDESLIMQVGSATGLARYYPAPPMWVNSTPTPKIDLYVRR 240  
 OY 241 RPYITOGAASPCKDMLIVDVGSGVGLTKLIRTSVSEMLETISDDPEVNAVSPNSAOD 300  
 DB 241 RPYITOGAASPCKDMLIVDVGSGVGLTKLIRTSVSEMLETISDDPEVNAVSPNSAOD 300  
 OY 301 VSCFOHLYOANVRNKKVLDKAVNNITANGITDYKKGFSFAEBOLLNVNSRANCKITIML 360  
 DB 301 VSCFOHLYOANVRNKKVLDKAVNNITANGITDYKKGFSFAEBOLLNVNSRANCKITIML 360  
 OY 361 FPDGGEERAQETFNKYNKDKVVRPFSVGONHNERGPIOMACENKGYEIPISGAIR 420  
 DB 361 FPDGGEERAQETFNKYNKDKVVRPFSVGONHNERGPIOMACENKGYEIPISGAIR 420  
 OY 421 INTOEYLDVIGRPVLAGDKAKQVOMTVYLDALGLVITGLTPVENITGOFENKTYLK 480  
 DB 421 INTOEYLDVIGRPVLAGDKAKQVOMTVYLDALGLVITGLTPVENITGOFENKTYLK 480  
 OY 481 NOLILGVKGVDSLDIDIKRLPRPPLCPNGYYPALDPNGYVLLHPNLOPKPKKSOEPLYL 540  
 DB 481 NOLILGVKGVDSLDIDIKRLPRPPLCPNGYYPALDPNGYVLLHPNLOPKPKKSOEPLYL 540  
 OY 541 DFLDALENDIKVEIRNKKMIDGEGEKTEPRTLVKSODRRTYIDKGRRTYTPVNGTDSL 600  
 DB 541 DFLDALENDIKVEIRNKKMIDGEGEKTEPRTLVKSODRRTYIDKGRRTYTPVNGTDSL 600  
 OY 596 ALVLPYSEYIYIKAKLEETITQARSKKGMKDSSETLKPNEESGYTPVIAADYCNLDKI 660  
 DB 596 ALVLPYSEYIYIKAKLEETITQARSKKGMKDSSETLKPNEESGYTPVIAADYCNLDKI 660  
 OY 661 SNNTEFLLNNEFEDRKTPNNPSCNADLINRVLLDAQFTNELVONTYWSKKNIKGVKAR 720  
 DB 661 SNNTEFLLNNEFEDRKTPNNPSCNADLINRVLLDAQFTNELVONTYWSKKNIKGVKAR 720  
 OY 715 SDNTEFLLNNEFEDRKTPNNPSCNADLINRVLLDAQFTNELVONTYWSKKNIKGVKAR 715  
 DB 715 SDNTEFLLNNEFEDRKTPNNPSCNADLINRVLLDAQFTNELVONTYWSKKNIKGVKAR 715  
 OY 721 FVYITOGITRVPYKRAGENKMOENPETIEDSPYKRSLLDMNDVYFVPYPNKSGPAYESGI 780  
 DB 721 FVYITOGITRVPYKRAGENKMOENPETIEDSPYKRSLLDMNDVYFVPYPNKSGPAYESGI 780  
 OY 775 FVYITOGITRVPYKRAGENKMOENPETIEDSPYKRSLLDMNDVYFVPYPNKSGPAYESGI 775  
 DB 775 FVYITOGITRVPYKRAGENKMOENPETIEDSPYKRSLLDMNDVYFVPYPNKSGPAYESGI 775  
 OY 781 MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPACGAVCDCKRNSDVCVI 840  
 DB 781 MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPACGAVCDCKRNSDVCVI 840  
 OY 836 LDDGGFLMANHDDYTNOIGREFGIDPSLMHLVNIISVYAFNKSVDYQVSCERGAARKQ 900  
 DB 836 LDDGGFLMANHDDYTNOIGREFGIDPSLMHLVNIISVYAFNKSVDYQVSCERGAARKQ 900  
 OY 901 GAGHSAYVPSYADIIIOGMATTAAMSTILOOFLSTFPRLLEAVEMEDDFTASLSKQ 960  
 DB 901 GAGHSAYVPSYADIIIOGMATTAAMSTILOOFLSTFPRLLEAVEMEDDFTASLSKQ 960  
 OY 956 SCITEGOTYFFPNDKSKFSGVLDCCNCSRIFFGEKIMNTNLIFFIWESEKGCPCDTRLII 1015  
 DB 956 SCITEGOTYFFPNDKSKFSGVLDCCNCSRIFFGEKIMNTNLIFFIWESEKGCPCDTRLII 1015  
 OY 1021 QAEQTSIDGPNPCDMVKQPRYRKGPVYCDNNVLEBYTCCGVS 1063  
 DB 1021 QAEQTSIDGPNPCDMVKQPRYRKGPVYCDNNVLEBYTCCGVS 1063

RESULT 8  
 US-08-223-305C-54  
 ; Sequence 54, Application US/08223305C  
 ; Patent No. 5851824



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Db 781 MVSAAVEIYIOGKLLKPAVYGIKIDVNSWIENFTKTSIRDPGAGPVCDCKRNSDVNDCVI 840
QY 841 LDDGFLMANHDDYTNOIGRPFGEIDPSLMRHLVNSVYAFKNSVDYOSVCEPGAAPKQ 900
Db 841 LDDGFLMANHDDYTNOIGRPFGEIDPSLMRHLVNSVYAFKNSVDYOSVCEPGAAPKQ 900
QY 901 GAGHRSAYVPSVADIIQIGMWATAAAMSIIOQFLSLTFPRLEAVEMEDDPTASLSKQ 960
Db 901 GAGHRSAYVPSVADIIQIGMWATAAAMSIIOQFLSLTFPRLEAVEMEDDPTASLSKQ 960
QY 961 SCITEOTQYFFDNDKSFSGVLDCGNCSTRIFHEKLMNTNLIPIWESKGTGCPDTRLLI 1020
Db 961 SCITEOTQYFFDNDKSFSGVLDCGNCSTRIFHEKLMNTNLIPIWESKGTGCPDTRLLI 1020
QY 1021 QABQTSIDGPNPCDMVKQPRYRKGPDYCFDNNVLEDYTDGCGVS 1063
Db 1021 QABQTSIDGPNPCDMVKQPRYRKGPDYCFDNNVLEDYTDGCGVS 1063

RESULT 6
US-09-452-007-4
; Sequence 4, Application US/09452007
; Patent No. 6140485
; GENERAL INFORMATION:
; APPLICANT: Franco, Rodrigo
; APPLICANT: Sun Chen, Ai Ru
; APPLICANT: Suey, David J.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL
; TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/452,007
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,118
; FILING DATE: 16-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mata, Elizabeth W.
; REGISTRATION NUMBER: 38,236
; REFERENCE/DOCKET NUMBER: ACC96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1091 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-452-007-4

Query Match 99.9%; Score 5595; DB 4; Length 1091;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1062; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAAGCLALTLTLFOSLILGPSSEPPSAVTIKSWDKMEDIVTAKTSGVNOAVDI 60
Db 1 MAAGCLALTLTLFOSLILGPSSEPPSAVTIKSWDKMEDIVTAKTSGVNOAVDI 60
QY 61 YEKYODLTYVEPNNAKQVETIAARDIEKLLNSRKAIVSIALAEAKVOAAHOMREDFASN 120

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Db 61 YEKYODLTYVEPNNAKQVETIAARDIEKLLNSRKAIVSIALAEAKVOAAHOMREDFASN 120
QY 121 EYVYVNAKDDLDPEKNDSEPSQRIKPVFIEDANPGROIYQHAHVHPTDIYGSSTVL 180
Db 121 EYVYVNAKDDLDPEKNDSEPSQRIKPVFIEDANPGROIYQHAHVHPTDIYGSSTVL 180
QY 181 NELMNTSALDEFEKKNREDDPSLLMOVGSATGLARIPASPVWDSNTPKIDLYDVR 240
Db 181 NELMNTSALDEFEKKNREDDPSLLMOVGSATGLARIPASPVWDSNTPKIDLYDVR 240
QY 241 RPYVIOGAASPMDLILVDVSGVSGTLKLRISVSMTLTDLDDDFVAVASNSNAOD 300
Db 241 RPYVIOGAASPMDLILVDVSGVSGTLKLRISVSMTLTDLDDDFVAVASNSNAOD 300
QY 301 VSCFQHLVQANVRNKKVYLKDAVNNITAKITDYKKGSFAFEOILLNVSRANCKIIML 360
Db 301 VSCFQHLVQANVRNKKVYLKDAVNNITAKITDYKKGSFAFEOILLNVSRANCKIIML 360
QY 361 FTDGGEERAQELFNKYNKDKVYVRFSGVGOHNERGPIQMACENKGYEITPSIAIR 420
Db 361 FTDGGEERAQELFNKYNKDKVYVRFSGVGOHNERGPIQMACENKGYEITPSIAIR 420
QY 421 INFOEYLDVLRPNVLAGDKAKQVQWNTNVDALAEGLVITGTLPVNITGOFENKTNLK 480
Db 421 INFOEYLDVLRPNVLAGDKAKQVQWNTNVDALAEGLVITGTLPVNITGOFENKTNLK 480
QY 481 NOLLIGVGVVSLIEDIKRLTPRTLCPNGYYPADIPNGVYLHPNLOPKNPKSQEPVTL 540
Db 481 NOLLIGVGVVSLIEDIKRLTPRTLCPNGYYPADIPNGVYLHPNLOPKNPKSQEPVTL 540
QY 541 DFLDAELENDIKVEIRNKMIDGSEKTEFTLVASOBERYIDKGNRRYTWTPVNGTYSL 600
Db 541 DFLDAELENDIKVEIRNKMIDGSEKTEFTLVASOBERYIDKGNRRYTWTPVNGTYSL 600
QY 601 ALVLPYTSFYIYAKLEETITQARSKKGMKDSFTLKPDEFEESGYFTIAPRYCNDLKI 660
Db 601 ALVLPYTSFYIYAKLEETITQARSKKGMKDSFTLKPDEFEESGYFTIAPRYCNDLKI 660
QY 661 SDNNTEFLNNEFDIKRTPNPNPCNADLINRYLLDAGFNELVQYVWSKOKNIKVKAR 720
Db 661 SDNNTEFLNNEFDIKRTPNPNPCNADLINRYLLDAGFNELVQYVWSKOKNIKVKAR 720
QY 721 FVVTGIGITRYVPEKAGEENQENPETEYEDSFYKRSILDNDYVFTAPFNKSGGAVESGI 780
Db 721 FVVTGIGITRYVPEKAGEENQENPETEYEDSFYKRSILDNDYVFTAPFNKSGGAVESGI 780
QY 781 MVSAAVEIYIOGKLLKPAVYGIKIDVNSWIENFTKTSIRDPGAGPVCDCKRNSDVNDCVI 840
Db 781 MVSAAVEIYIOGKLLKPAVYGIKIDVNSWIENFTKTSIRDPGAGPVCDCKRNSDVNDCVI 840
QY 841 LDDGFLMANHDDYTNOIGRPFGEIDPSLMRHLVNSVYAFKNSVDYOSVCEPGAAPKQ 900
Db 841 LDDGFLMANHDDYTNOIGRPFGEIDPSLMRHLVNSVYAFKNSVDYOSVCEPGAAPKQ 900
QY 901 GAGHRSAYVPSVADIIQIGMWATAAAMSIIOQFLSLTFPRLEAVEMEDDPTASLSKQ 960
Db 901 GAGHRSAYVPSVADIIQIGMWATAAAMSIIOQFLSLTFPRLEAVEMEDDPTASLSKQ 960
QY 961 SCITEOTQYFFDNDKSFSGVLDCGNCSTRIFHEKLMNTNLIPIWESKGTGCPDTRLLI 1020
Db 961 SCITEOTQYFFDNDKSFSGVLDCGNCSTRIFHEKLMNTNLIPIWESKGTGCPDTRLLI 1020
QY 1021 QABQTSIDGPNPCDMVKQPRYRKGPDYCFDNNVLEDYTDGCGVS 1063
Db 1021 QABQTSIDGPNPCDMVKQPRYRKGPDYCFDNNVLEDYTDGCGVS 1063

RESULT 7
US-08-455-543A-54
; Sequence 54, Application US/08455543A
; Patent No. 5792846
; GENERAL INFORMATION:

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QY 421 INFOEYLDVLRPMVLAGDKAKOVOMTNYLDALGLVITGTLDPVFNITGOFENKTNLK 480
DB 421 INFOEYLDVLRPMVLAGDKAKOVOMTNYLDALGLVITGTLDPVFNITGOFENKTNLK 480
QY 481 NOLIIGVMGVDSLEIDIKRLTPRFTLCPNGYFAIDPNGYVLLHPNLQPKNKSQEPVTL 540
DB 481 NOLIIGVMGVDSLEIDIKRLTPRFTLCPNGYFAIDPNGYVLLHPNLQPKNKSQEPVTL 540
QY 541 DFLDAELNDIVKVEIRNKMIDGSEKTRTLVKSODERYIDKGNRTYTWTPVNGTDSL 600
DB 541 DFLDAELNDIVKVEIRNKMIDGSEKTRTLVKSODERYIDKGNRTYTWTPVNGTDSL 600
QY 601 ALVLPYFSFYIKAKLEETITQARSKKGMKDETLKPNFESGYTLAPRDYCNLDKI 660
DB 601 ALVLPYFSFYIKAKLEETITQARSKKGMKDETLKPNFESGYTLAPRDYCNLDKI 660
QY 661 SDNTEFLINFEIDRKTTPNPNPCNADLINRVLLDAGFTNELVONYWSKOKNIKGVKAR 720
DB 661 SDNTEFLINFEIDRKTTPNPNPCNADLINRVLLDAGFTNELVONYWSKOKNIKGVKAR 720
QY 721 FVYTDGTRVYPKEAGENMOENPEYEDSFYKRSIDNDNYFTAFYFNKSGPAGESGI 780
DB 721 FVYTDGTRVYPKEAGENMOENPEYEDSFYKRSIDNDNYFTAFYFNKSGPAGESGI 780
QY 781 MYSKAVEIYIOGKLLPAAVGIKIDVNSWIENTFTKSIDPCGAPYCDCKRNSDVMDCYI 840
DB 781 MYSKAVEIYIOGKLLPAAVGIKIDVNSWIENTFTKSIDPCGAPYCDCKRNSDVMDCYI 840
QY 841 LDDGGLMANHDDYTNOIGRFFGEIDPSLMRLVNIISYAFNKSVDYOSVCEPGAAPRO 900
DB 841 LDDGGLMANHDDYTNOIGRFFGEIDPSLMRLVNIISYAFNKSVDYOSVCEPGAAPRO 900
QY 901 GAGHRSAYVSVADIIQIGWATAAAMSTIIQOFLSLTEPRILEAYEMEDDDETTASLSKO 960
DB 901 GAGHRSAYVSVADIIQIGWATAAAMSTIIQOFLSLTEPRILEAYEMEDDDETTASLSKO 960
QY 961 SCITEQOYFFDNDKSFSGVLDGNCSTRIFHEKELMNTNLIPIWESKQTCPCDTRLLI 1020
DB 961 SCITEQOYFFDNDKSFSGVLDGNCSTRIFHEKELMNTNLIPIWESKQTCPCDTRLLI 1020
QY 1021 QAEOTSDGPNPCDMVKOPRYRKGPVOCFDMNVLEDYTDGCGVS 1063
DB 1021 QAEOTSDGPNPCDMVKOPRYRKGPVOCFDMNVLEDYTDGCGVS 1063

RESULT 5
US-08-713-118-4
; Sequence 4, Application US/08713118
; Patent No. 6040436
; GENERAL INFORMATION:
; APPLICANT: Franco, Rodrigo
; APPLICANT: Sun Chen, Ai Ru
; APPLICANT: Suey, David J.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL
; TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,118
; FILING DATE: 16-SEP-1996
; CLASSIFICATION: 435

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; ATTORNEY/AGENT INFORMATION:
; NAME: Mata, Elizabeth W.
; REGISTRATION NUMBER: 38,236
; REFERENCE/DOCKET NUMBER: ACC96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1091 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-713-118-4

Query Match 99.9%; Score 5595; DB 3; Length 1091;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1062; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLTLFQSLIGPSSSEPPSAVTIKSWDKMOEDLVTLAKTASGVNQLVDI 60
DB 1 MAAGCLLALTLTLFQSLIGPSSSEPPSAVTIKSWDKMOEDLVTLAKTASGVNQLVDI 60
QY 61 YEKYODLYVEBPNNARQLVEIAARDIEKLSNRKALVSLALEAKYQAAHOMREDAFN 120
DB 61 YEKYODLYVEBPNNARQLVEIAARDIEKLSNRKALVSLALEAKYQAAHOMREDAFN 120
QY 121 EYVYNNAKDDLDPKENDSEPSORIKPFIEDANFGROIYQOAAVHPTDIYGSTYVL 180
DB 121 EYVYNNAKDDLDPKENDSEPSORIKPFIEDANFGROIYQOAAVHPTDIYGSTYVL 180
QY 181 NELNMTSALDEVEFKKREDEPSLMOVFGSATGLARYYPASPWNDRTPKIDLYVRR 240
DB 181 NELNMTSALDEVEFKKREDEPSLMOVFGSATGLARYYPASPWNDRTPKIDLYVRR 240
QY 241 RMYTIOGAASPRKMLIYDVSGSVGLTKLIRTSVSMLETLSDDDPVNVAASNSAOD 300
DB 241 RMYTIOGAASPRKMLIYDVSGSVGLTKLIRTSVSMLETLSDDDPVNVAASNSAOD 300
QY 301 VSCFOHLVQANRNNKVLKDAVNNITANGITDYKKGFSFAEQLLNTVNSRANCKIIML 360
DB 301 VSCFOHLVQANRNNKVLKDAVNNITANGITDYKKGFSFAEQLLNTVNSRANCKIIML 360
QY 361 FTDGGEERAQELFNKYNKDKKVRVRFVSGOHNTRBGTIOMACBENKGYTIEISGAR 420
DB 361 FTDGGEERAQELFNKYNKDKKVRVRFVSGOHNTRBGTIOMACBENKGYTIEISGAR 420
QY 421 INFOEYLDVLRPMVLAGDKAKOVOMTNYLDALGLVITGTLDPVFNITGOFENKTNLK 480
DB 421 INFOEYLDVLRPMVLAGDKAKOVOMTNYLDALGLVITGTLDPVFNITGOFENKTNLK 480
QY 481 NOLIIGVMGVDSLEIDIKRLTPRFTLCPNGYFAIDPNGYVLLHPNLQPKNKSQEPVTL 540
DB 481 NOLIIGVMGVDSLEIDIKRLTPRFTLCPNGYFAIDPNGYVLLHPNLQPKNKSQEPVTL 540
QY 541 DFLDAELNDIVKVEIRNKMIDGSEKTRTLVKSODERYIDKGNRTYTWTPVNGTDSL 600
DB 541 DFLDAELNDIVKVEIRNKMIDGSEKTRTLVKSODERYIDKGNRTYTWTPVNGTDSL 600
QY 601 ALVLPYFSFYIKAKLEETITQARSKKGMKDETLKPNFESGYTLAPRDYCNLDKI 660
DB 601 ALVLPYFSFYIKAKLEETITQARSKKGMKDETLKPNFESGYTLAPRDYCNLDKI 660
QY 661 SDNTEFLINFEIDRKTTPNPNPCNADLINRVLLDAGFTNELVONYWSKOKNIKGVKAR 720
DB 661 SDNTEFLINFEIDRKTTPNPNPCNADLINRVLLDAGFTNELVONYWSKOKNIKGVKAR 720
QY 721 FVYTDGTRVYPKEAGENMOENPEYEDSFYKRSIDNDNYFTAFYFNKSGPAGESGI 780
DB 721 FVYTDGTRVYPKEAGENMOENPEYEDSFYKRSIDNDNYFTAFYFNKSGPAGESGI 780
QY 781 MYSKAVEIYIOGKLLPAAVGIKIDVNSWIENTFTKSIDPCGAPYCDCKRNSDVMDCYI 840
DB 781 MYSKAVEIYIOGKLLPAAVGIKIDVNSWIENTFTKSIDPCGAPYCDCKRNSDVMDCYI 840

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Db 61 YEKYODLYTVEPNNAKQVLEIAARDIEKLSSNSKALVSLALEAKYQAAHQRREDFASN 120
QY 121 EYVYNAKDDLPKNDSEPGSQRKIPVETEDANFCRQISYQAAHPIPTDIYEGSTIYL 180
Db 121 EYVYNAKDDLPKNDSEPGSQRKIPVETEDANFCRQISYQAAHPIPTDIYEGSTIYL 180
QY 181 NELNMTSALDEVRKKNNEEDPSILMOVFGSATGLARYPPSPWVDSRTPNKIDLYDVR 240
Db 181 NELNMTSALDEVRKKNNEEDPSILMOVFGSATGLARYPPSPWVDSRTPNKIDLYDVR 240
QY 241 RPYWIOGAASPKDMLILVDVSGSVSGTLTKLIRTSVSEMLETSDDDDFVAVASFNMAOD 300
Db 241 RPYWIOGAASPKDMLILVDVSGSVSGTLTKLIRTSVSEMLETSDDDDFVAVASFNMAOD 300
QY 301 VSCFOHLYOAVNRKKVYLKDAVNNITAKGTTDYKKGFSFAEQLLNVNVRANCKNTIML 360
Db 301 VSCFOHLYOAVNRKKVYLKDAVNNITAKGTTDYKKGFSFAEQLLNVNVRANCKNTIML 360
QY 361 FTDGEERAQEIFNKYKKNKDKKVVFRFVSQGHYERGPLOMACENKGYIYEIPSGAIR 420
Db 361 FTDGEERAQEIFNKYKKNKDKKVVFRFVSQGHYERGPLOMACENKGYIYEIPSGAIR 420
QY 421 INTQETLDVLRPMVLADGKAKQVNTNYLDALDELGLVITGTLPEFNITGOFENKTNLK 480
Db 421 INTQETLDVLRPMVLADGKAKQVNTNYLDALDELGLVITGTLPEFNITGOFENKTNLK 480
QY 481 NOLILVGMCDVSLIEDIKLTPFTLCPNGYFPAIDPNGYVLLHPNLQPRNKSOEPTVL 540
Db 481 NOLILVGMCDVSLIEDIKLTPFTLCPNGYFPAIDPNGYVLLHPNLQPRNKSOEPTVL 540
QY 541 DFLDALENDIKVEIRNKIMIDGESGKTRTLYKSODERYIDKGNNTYWTVPNGDYSL 600
Db 541 DFLDALENDIKVEIRNKIMIDGESGKTRTLYKSODERYIDKGNNTYWTVPNGDYSL 600
QY 601 ALVLPYSEYIYIKAKLEETITQARSKKGMKSETLKPNFESEGYTFAPRDYCNLKI 660
Db 601 ALVLPYSEYIYIKAKLEETITQARSKKGMKSETLKPNFESEGYTFAPRDYCNLKI 660
QY 661 SDNTEFLNPNFIDRKTTPNPNSCADLINVLLDAGTNELVONYMSKONIKGVAR 720
Db 661 SDNTEFLNPNFIDRKTTPNPNSCADLINVLLDAGTNELVONYMSKONIKGVAR 720
QY 721 FVYTDGTRVYPKKAGEMWQENPETEYEDSFYKRSIDNDNYETAPYFKKSGPAGYESGI 780
Db 721 FVYTDGTRVYPKKAGEMWQENPETEYEDSFYKRSIDNDNYETAPYFKKSGPAGYESGI 780
QY 781 MYSKAVEIYIOGKLLKPAVVGIIKIDVNSWIEENFTKTSIRDPGAGVCDCKRNSDVMDCYI 840
Db 781 MYSKAVEIYIOGKLLKPAVVGIIKIDVNSWIEENFTKTSIRDPGAGVCDCKRNSDVMDCYI 840
QY 841 LDDGGFLMANHDDYTNOIGRFEGETIDPSIMRLVNISYAAFNKSYDYQVCEPCAARPO 900
Db 841 LDDGGFLMANHDDYTNOIGRFEGETIDPSIMRLVNISYAAFNKSYDYQVCEPCAARPO 900
QY 901 GAGHSASVYVADILIOGWMATAAAMSTIOQLSLSTFPRLLAEVEMEDDEFTASLSKO 960
Db 901 GAGHSASVYVADILIOGWMATAAAMSTIOQLSLSTFPRLLAEVEMEDDEFTASLSKO 960
QY 961 SCITTOYOTYFFPNDSKSGVLDGCGNSRIHGEKIAMTNIIFIVESKGTCPDTRILLI 1020
Db 961 SCITTOYOTYFFPNDSKSGVLDGCGNSRIHGEKIAMTNIIFIVESKGTCPDTRILLI 1020
QY 1021 QAEQTSDDGNPCDMYKOPRYRKGPDVCFDNNVLEDTYTCGGGVS 1063
Db 1021 QAEQTSDDGNPCDMYKOPRYRKGPDVCFDNNVLEDTYTCGGGVS 1063

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RESULT 4  
 US-08-311-363-25  
 ; Sequence 25, Application US/08311363  
 ; Patent No. 5876598  
 ; GENERAL INFORMATION:

```

? APPLICANT: Harpold, Michael
? APPLICANT: Ellis, Steven
? APPLICANT: Williams, Mark
? APPLICANT: Feldman, Daniel
? APPLICANT: McCue, Ann
? APPLICANT: Brenner, Robert
? TITLE OF INVENTION: Human Calcium Channel Compositions and
? TITLE OF INVENTION: Methods
? NUMBER OF SEQUENCES: 32
? CORRESPONDENCE ADDRESS:
? ADDRESS: Brown, Martin, Haller & McClain
? STREET: 1660 Union Street
? CITY: San Diego
? STATE: California
? COUNTRY: USA
? ZIP: 92101-2926
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent In Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/311,363
? FILING DATE:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/745,206
? FILING DATE: 15-AUG-1991
? ATTORNEY/AGENT INFORMATION:
? NAME: Seidman, Stephanie L.
? REGISTRATION NUMBER: 33,779
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (619)238-0999
? TELEFAX: (619)238-0062
? INFORMATION FOR SEQ ID NO: 25:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1091 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-311-363-25

Query Match 100.0%; Score 5599; DB 2; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 YERYODLYVEPNNAQVLEIARDEIKLSNSKALVSLAEVYQAAHQWREDFASN 120
Db 61 YERYODLYVEPNNAQVLEIARDEIKLSNSKALVSLAEVYQAAHQWREDFASN 120
QY 121 EYVYNAKDDLDPEKNDSESGORIKPVFEJEDNFGKROISYQAAHIPTDIESTIYL 180
Db 121 EYVYNAKDDLDPEKNDSESGORIKPVFEJEDNFGKROISYQAAHIPTDIESTIYL 180
QY 181 NEIWMTSALDEVEFKKNEEDPSLLMOVFGSATGLARYPASPVWDSRPNKIDLYDVR 240
Db 181 NEIWMTSALDEVEFKKNEEDPSLLMOVFGSATGLARYPASPVWDSRPNKIDLYDVR 240
QY 241 RPYVIGASPKDMLLVVSGVSGITLKLITVSSEMETTSDDEPVVAFSNSNAD 300
Db 241 RPYVIGASPKDMLLVVSGVSGITLKLITVSSEMETTSDDEPVVAFSNSNAD 300
QY 301 VSCFOHLYOANVRKVKLKAANNITAKGTDKKGFSFEDLLNVSRAKCNKTIIM 360
Db 301 VSCFOHLYOANVRKVKLKAANNITAKGTDKKGFSFEDLLNVSRAKCNKTIIM 360
QY 361 FTDSGERAEIENKYNKDKKVRFRSVQOHYERGP10MMACENKGYEETPSIGAIR 420
Db 361 FTDSGERAEIENKYNKDKKVRFRSVQOHYERGP10MMACENKGYEETPSIGAIR 420
QY 421 INTQYLDVIGRPVLAGDKAKOVQWNTVYLDALLEGVITGTLVPFNITGQENKTNLK 480
Db 421 INTQYLDVIGRPVLAGDKAKOVQWNTVYLDALLEGVITGTLVPFNITGQENKTNLK 480
QY 481 NQILISGWDVSDIEDIKRLTPRTLCPNGYFAIDPNGVLLHPN10PNPNSOEYVL 540
Db 481 NQILISGWDVSDIEDIKRLTPRTLCPNGYFAIDPNGVLLHPN10PNPNSOEYVL 540
QY 541 DFLDAELENDIKVEIRKMKIDGESGEKTFRTLVKSODERTIDKGNRTYTPVNGTDYSL 600
Db 541 DFLDAELENDIKVEIRKMKIDGESGEKTFRTLVKSODERTIDKGNRTYTPVNGTDYSL 600
QY 601 ALVLPYTSFYIRAKLEETITQARSKKGGKMDSETLKPDPNEESGTFIAPROYCNDLKI 660
Db 601 ALVLPYTSFYIRAKLEETITQARSKKGGKMDSETLKPDPNEESGTFIAPROYCNDLKI 660
QY 661 SDNTEFLNPNFNEIDKRTNPNPCNDL1NRVLLDAGFNELVQNTWMSKOKNIKVKAR 720
Db 661 SDNTEFLNPNFNEIDKRTNPNPCNDL1NRVLLDAGFNELVQNTWMSKOKNIKVKAR 720
QY 721 FVVTGIGITRVPKAGEENQENPEYEDSFYKRSILDNDVYFTAPYFNKSGGAYESGI 780
Db 721 FVVTGIGITRVPKAGEENQENPEYEDSFYKRSILDNDVYFTAPYFNKSGGAYESGI 780
QY 781 MVSRAVEIYIOGKLLKRAVYGIKIDVNSK1ENFTKTSIRBPACAPVDCRNSDVMDCVI 840
Db 781 MVSRAVEIYIOGKLLKRAVYGIKIDVNSK1ENFTKTSIRBPACAPVDCRNSDVMDCVI 840
QY 841 LDDGGFLMANHNDYTNQIGFGEIDPS1MRHLVNS1VYAFNKSYSYOSVCEPGAAPKQ 900
Db 841 LDDGGFLMANHNDYTNQIGFGEIDPS1MRHLVNS1VYAFNKSYSYOSVCEPGAAPKQ 900
QY 901 GAGHRSAYVPSVADIIQIGMMAT1AAASIIQOFLSLTPRLLAEAVEMEDDFTASLSKQ 960
Db 901 GAGHRSAYVPSVADIIQIGMMAT1AAASIIQOFLSLTPRLLAEAVEMEDDFTASLSKQ 960
QY 961 SCITEQOYFFDNDKSFSGVLDGNGSR1FHEKLMNTULIF1MWSKGTCPDTRLII 1020
Db 961 SCITEQOYFFDNDKSFSGVLDGNGSR1FHEKLMNTULIF1MWSKGTCPDTRLII 1020
QY 1021 QABQTSQPNPCDMYKOPRYRKGPVCFDNNVLEDYTDGCGVS 1063
Db 1021 QABQTSQPNPCDMYKOPRYRKGPVCFDNNVLEDYTDGCGVS 1063

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RESULT 3  
 US-08-223-305C-52  
 ; Sequence 52, Application US/08223305C

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; Patent No. 5851824
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McQue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/223,305C
; FILING DATE: April 4, 1994
; APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 20-FEB-1990
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 52516 (P519739)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1091 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-223-305C-52

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Query Match 100.0%; Score 5599; DB 2; Length 1091;  
 Best local similarity 100.0%; Pred. No. 0;  
 Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAAGCLLATLTLFOSGLIGPSSEPPPSAVTIKSWDKMOEDVTLAKTASGVQALVDI 60
QY 61 YERYODLYVEPNNAQVLEIARDEIKLSNSKALVSLAEVYQAAHQWREDFASN 120

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DB 121 EYVYNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROISYQAAHAPTDIYEGSTYVL 180
QY 181 NEIWMTSALDEYKKNREEDPSILMOVFGSAGLARYPASPWVDSRTPNKIDLYDVR 240
DB 181 NEIWMTSALDEYKKNREEDPSILMOVFGSAGLARYPASPWVDSRTPNKIDLYDVR 240
QY 241 RPYIIGAASPKDMLILVYSGVSGTLTKLRTSVSEMLETISDDDFVNASFNSNAD 300
DB 241 RPYIIGAASPKDMLILVYSGVSGTLTKLRTSVSEMLETISDDDFVNASFNSNAD 300
QY 301 VSCFOHLVQANVANKKVLDAVNNITAKGITDYKKGSFAFOLLNYSRANCKITML 360
DB 301 VSCFOHLVQANVANKKVLDAVNNITAKGITDYKKGSFAFOLLNYSRANCKITML 360
QY 361 FTDGGERAOEIPNKYKKNKKVRFVSQHNHNGRPIQMACENKGYEIPSTIGAIR 420
DB 361 FTDGGERAOEIPNKYKKNKKVRFVSQHNHNGRPIQMACENKGYEIPSTIGAIR 420
QY 421 INTOEYLDVLAGRPVLAGDRAKQOVNTNYLDALDELGLVITGTLPENTTQGFENKTNLX 480
DB 421 INTOEYLDVLAGRPVLAGDRAKQOVNTNYLDALDELGLVITGTLPENTTQGFENKTNLX 480
QY 481 NQIILIGVMGVDSLEDIKLTPRTLCPNGYFAIDPNQYVLLHBNLOPKNKSQEPYTL 540
DB 481 NQIILIGVMGVDSLEDIKLTPRTLCPNGYFAIDPNQYVLLHBNLOPKNKSQEPYTL 540
QY 541 DELDALENDIVEIRNNKIDSESGKPTRTLYKSODEXYIDKGRRTYTWTPVNGTDSL 600
DB 541 DELDALENDIVEIRNNKIDSESGKPTRTLYKSODEXYIDKGRRTYTWTPVNGTDSL 600
QY 601 ALVLPYSEFYITAKLEETITQARSKKGMKDETLKPDNEESGYTFIAPRDYCNDLKI 660
DB 601 ALVLPYSEFYITAKLEETITQARSKKGMKDETLKPDNEESGYTFIAPRDYCNDLKI 660
QY 661 SUNNTEFLNENEFIDRTKTPNPNPCNADLINRVLLDAGFTNELVONYSKONIKGVAR 720
DB 661 SUNNTEFLNENEFIDRTKTPNPNPCNADLINRVLLDAGFTNELVONYSKONIKGVAR 720
QY 721 FVVTGCGITRVYPRKAGENMOENPETYEDSPYKRSLDNDNVETAPRYNKGSPAYESGI 780
DB 721 FVVTGCGITRVYPRKAGENMOENPETYEDSPYKRSLDNDNVETAPRYNKGSPAYESGI 780
QY 781 MYSKAVEIYIOGKLLKPAVVGIKIDVNSMIENFTKTSIRDPACAGVCDCKRNSDVMCVI 840
DB 781 MYSKAVEIYIOGKLLKPAVVGIKIDVNSMIENFTKTSIRDPACAGVCDCKRNSDVMCVI 840
QY 841 LDDGFEILMANDDYTNIGRFGFIDSLMRHLVNIYVAFNKSYSYDQVCEGGAAPKQ 900
DB 841 LDDGFEILMANDDYTNIGRFGFIDSLMRHLVNIYVAFNKSYSYDQVCEGGAAPKQ 900
QY 901 GAGHSASVPSVADILQIGMWATAAAMSILQOFLSLTFPRLLEAVEHEDEDDFTASLSKO 960
DB 901 GAGHSASVPSVADILQIGMWATAAAMSILQOFLSLTFPRLLEAVEHEDEDDFTASLSKO 960
QY 961 SCITEQOTYFFDNDNSKSSGVLDGNCRSRIFHGEKLMNTNLIIFTMVESKGTCPDTRLI 1020
DB 961 SCITEQOTYFFDNDNSKSSGVLDGNCRSRIFHGEKLMNTNLIIFTMVESKGTCPDTRLI 1020
QY 1021 QAEQTSDDGPNPCDMVKOPRYRKGPVCFDNNVLEDYTDGCGVS 1063
DB 1021 QAEQTSDDGPNPCDMVKOPRYRKGPVCFDNNVLEDYTDGCGVS 1063

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RESULT 2  
 US-08-455-543A-52  
 : Sequence 52, Application US/08455543A  
 : Patent No. 5792846

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GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESS: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
FILING DATE: May 31, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/866,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-455-543A-52

Query Match 100.0%; Score 5599; DB 1; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAGCLLALTLTLFOSILIGPSSSEPPPSAVITIKSVNDRKQEDLVTLAKTAGVNOVDI 60
DB 1 MAAGCLLALTLTLFOSILIGPSSSEPPPSAVITIKSVNDRKQEDLVTLAKTAGVNOVDI 60

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GenCore version 5.1.3  
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## OM protein - protein search, using sw model

Run on: February 10, 2003, 14:13:55 ; Search time 11.7901 Seconds  
(Without alignments)  
2652.785 Million cell updates/sec

Title: US-10-090-827-15

Perfect score: 5599

Sequence: 1 MAAGCLLALTLTLPQSLLIG.....PDVCFDNNVLEDTDCGVS 1063

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database :

Issued\_Patents\_AA.\*  
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2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PTCUTS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5599	100.0	1091	1	US-07-745-206A-25 Sequence 25, Appl
2	5599	100.0	1091	1	US-08-455-543A-52 Sequence 52, Appl
3	5599	100.0	1091	2	US-08-223-305C-52 Sequence 52, Appl
4	5599	100.0	1091	2	US-08-313-118-25 Sequence 25, Appl
5	5595	99.9	1091	3	US-08-713-118-4 Sequence 4, Appl
6	5595	99.9	1091	4	US-09-452-007-4 Sequence 4, Appl
7	5559.5	99.3	1086	1	US-08-455-543A-54 Sequence 54, Appl
8	5559.5	99.3	1086	2	US-08-223-305C-54 Sequence 54, Appl
9	5542.5	99.0	1084	1	US-08-455-543A-56 Sequence 56, Appl
10	5542.5	99.0	1084	2	US-08-223-305C-56 Sequence 56, Appl
11	5523	98.6	1103	1	US-08-455-543A-53 Sequence 53, Appl
12	5523	98.6	1103	2	US-08-223-305C-53 Sequence 53, Appl
13	5503	98.3	1079	1	US-08-455-543A-55 Sequence 55, Appl
14	5503	98.3	1079	2	US-08-223-305C-55 Sequence 55, Appl
15	5385.5	96.2	1106	1	US-08-435-675B-5 Sequence 5, Appl
16	5385.5	96.2	1106	2	US-08-435-675B-5 Sequence 5, Appl
17	5134.5	91.7	1086	6	US-08-336-257A-8 Patent No. 5386025
18	3004.5	53.7	1145	4	US-09-470-443-2 Sequence 2, Appl
19	3004.5	53.7	1145	4	US-09-470-443-4 Sequence 4, Appl
20	2983.5	53.3	1076	4	US-09-470-443-6 Sequence 6, Appl
21	2581.5	46.1	508	1	US-08-435-675B-6 Sequence 6, Appl
22	182	3.3	885	3	US-09-074-579-5 Sequence 5, Appl
23	182	3.3	885	3	US-09-388-774-5 Sequence 5, Appl
24	159.5	2.8	946	3	US-09-074-579-3 Sequence 3, Appl
25	159.5	2.8	946	4	US-09-388-774-3 Sequence 3, Appl
26	158.5	2.8	894	4	US-09-071-035-248 Sequence 248, App
27	158.5	2.8	962	4	US-09-071-035-246 Sequence 246, App

28	158.5	2.8	962	4	US-09-071-035-250 Sequence 250, App
29	158.5	2.8	962	4	US-09-071-035-254 Sequence 254, App
30	158.5	2.8	962	4	US-09-071-035-470 Sequence 470, App
31	158.5	2.8	962	4	US-09-071-035-474 Sequence 474, App
32	158.5	2.8	962	4	US-09-071-035-478 Sequence 478, App
33	154.5	2.8	946	4	US-09-546-153-1 Sequence 1, Appl
34	154	2.8	903	1	US-08-021-601-12 Sequence 12, Appl
35	154	2.8	903	1	US-08-082-849B-12 Sequence 12, Appl
36	154	2.8	903	5	PCR-US94-01624-12 Sequence 12, Appl
37	152.5	2.7	789	1	US-08-471-033-32 Sequence 32, Appl
38	152.5	2.7	789	2	US-08-471-044-32 Sequence 32, Appl
39	152.5	2.7	789	2	US-08-463-483A-32 Sequence 32, Appl
40	152.5	2.7	789	2	US-08-471-046A-32 Sequence 32, Appl
41	152.5	2.7	789	2	US-08-470-566B-32 Sequence 32, Appl
42	152.5	2.7	789	2	US-08-838-219B-4 Sequence 4, Appl
43	152.5	2.7	789	2	US-08-469-334-32 Sequence 32, Appl
44	152.5	2.7	789	3	US-09-300-529-32 Sequence 32, Appl
45	152.5	2.7	789	3	US-09-233-336A-4 Sequence 4, Appl

## ALIGNMENTS

RESULT 1  
US-07-745-206A-25  
Sequence 25, Application US/07745206A  
Patent No. 5429921  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: McCue, Ann  
APPLICANT: Feldman, Daniel  
TITLE OF INVENTION: Human Calcium Channel Compositions and  
TITLE OF INVENTION: Methods  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fitch, Even, Tabin & Flannery  
STREET: 135 S. LaSalle  
CITY: Chicago  
STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/745,206A  
FILING DATE: 19910815  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Feder, Scott B  
REFERENCE/DOCKET NUMBER: 51504  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-372-7842  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1091 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-745-206A-25

Query Match 100.0%; Score 5599; DB 1; Length 1091;  
Best local similarity 100.0%; Pred. No. 0;  
Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 MAAGCLLALTLTLPQSLLIGSPSEPPSAVTIRKSWDKMOEDLVTLAKTASGVNQLVDI 60  
DB 1 MAAGCLLALTLTLPQSLLIGSPSEPPSAVTIRKSWDKMOEDLVTLAKTASGVNQLVDI 60



Query Match 97.8%; Score 5526; DB 14; Length 1091;  
 Best Local Similarity 98.6%; Pred. No. 0;  
 Matches 1048; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

```

QY 1 MAACCLATLTLLFOSLIPSSOEPPSAVTIKSWDKMOEDLVTLAKASGVNOLVDI 60
DB 1 MAACCLATLTLLFOSLIPSSOEPPSAVTIKSWDKMOEDLVTLAKASGVNOLVDI 60
QY 61 YEKYODLYTEPNNAQOLVEIAARDIEKLLSNKALVRLALEAKYQAAHOMREDFASN 120
DB 61 YEKYODLYTEPNNAQOLVEIAARDIEKLLSNKALVSLAMEAEKYQAAHOMREDFASN 120
QY 121 EYVYTNNAKDDLDPEKNDSEPGSORIKPVTIDANFGHOISYQAAVAHIPTDIYEGSTIVL 180
DB 121 EYVYTNNAKDDLDPEKNDSEPGSORIKPVTIEDANFGHOISYQAAVAHIPTDIYEGSTIVL 180
QY 181 NELMWTSLDVEFPKKNEEDPSLLMOYFSGATGLARYYPASPMWDNSRTPNKIDLYDVR 240
DB 181 NELMWTSLDVEFPKKNEEDPSLLMOYFSGATGLARYYPASPMWDNSRTPNKIDLYDVR 240
QY 241 RPWTIOGAASPKDMLILVDVSGSVSGTLTKLIRTSVSEMLETISDDDFVNAVASFNSNAOD 300
DB 241 RPWTIOGAASPKDMLILVDVSGSVSGTLTKLIRTSVSEMLETISDDDFVNAVASFNSNAOD 300
QY 301 VSCFOHLVQANVRNKKVLAQAVNNITAKGTDYKGFSAFEOLLNVNSTRANCKIIML 360
DB 301 VSCFOHLVQANVRNKKVLAQAVNNITAKGTDYKGFSAFEOLLNVNSTRANCKIIML 360
QY 361 FTDGEERAQEIFAKYKDKKVRFPFSGOHVNDRGIOMMACENKGYEETPSIGAIR 420
DB 361 FTDGEERAQEIFAKYKDKKVRFPFSGOHVNDRGIOMMACENKGYEETPSIGAIR 420
QY 421 INTOEYLDVLGRPWVLAGDKAKOVMTNVLDALEGLVITGTLPVENITGONENKTNLK 480
DB 421 INTOEYLDVLGRPWVLAGDKAKOVMTNVLDALEGLVITGTLPVENITGONENKTNLK 480
QY 481 NQULIGWGVDSLEDIKRLTPRTLCPCNGYRAIDPBGVYLHPNLQPKNPKSOEPPVL 540
DB 481 NQULIGWGVDSLEDIKRLTPRTLCPCNGYRAIDPBGVYLHPNLQPKNPKSOEPPVL 540
QY 541 DFLDAELENDIKVEIRKMKIDGSEGEKTFRTLVKSODERYIDKGNRTYTWTVPNGTDYSL 600
DB 541 DFLDAELENDIKVEIRKMKIDGSEGEKTFRTLVKSODERYIDKGNRTYTWTVPNGTDYSL 600
QY 601 ALVLPYTSFYIIRAKIETITQARSKKGMKDETLKPDNEESGYTFIAPRDYCNLDKI 660
DB 601 ALVLPYTSFYIIRAKIETITQARSKKGMKDETLKPDNEESGYTFIAPRDYCNLDKI 660
QY 661 SDNNTFELNPFNEIDKTPNNSCNTDLINRYLLDAGFTNELVONYWSKOKNIKGVKAR 720
DB 661 SDNNTFELNPFNEIDKTPNNSCNTDLINRYLLDAGFTNELVONYWSKOKNIKGVKAR 720
QY 721 FVYTDGITRVYPREAGENOEPEDESFYRSLDNDNVFTAPYFNKSGPAGESGT 780
DB 721 FVYTDGITRVYPREAGENOEPEDESFYRSLDNDNVFTAPYFNKSGPAGESGT 780
QY 781 MVSRAVEIYIOGKLLPAAVVGIRKIDVNSWLENFTKTSIRDPGAGPYDCCKRNSDVMDCVY 840
DB 781 MVSRAVEIYIOGKLLPAAVVGIRKIDVNSWLENFTKTSIRDPGAGPYDCCKRNSDVMDCVY 840
QY 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVAYFNKSYDYOSVCEPGAAPKQ 900
DB 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVAYFNKSYDYOSVCEPGAAPKQ 900
QY 901 GAGHRSAYVPSIADILHIGWATAAAMSLIOQFLSLTPRLLAEVEMEDDDFTASLSKQ 960
DB 901 GAGHRSAYVPSIADILHIGWATAAAMSLIOQFLSLTPRLLAEVEMEDDDFTASLSKQ 960
QY 961 SCITEQTOYFFDNDKSFSGVLDGNCSTRIFHEKILMNTNLIIFINVESKGTCPDTRLLI 1020
DB 961 SCITEQTOYFFDNDKSFSGVLDGNCSTRIFHEKILMNTNLIIFINVESKGTCPDTRLLI 1020
QY 1021 QAEQTSDBGPDPCDMVKOPRYRKGPDYVCFDNNVLEDTDCGVS 1063
  
```

DB 1021 QAEQTSDBGPDPCDMVKOPRYRKGPDYVCFDNNVLEDTDCGVS 1063  
 Search completed: February 10, 2003, 14:18:14  
 Job time : 38.6916 secs



CC and omega-conotoxin GVIA toxin sensitive potassium-stimulated  
CC calcium uptake, indicating that the proteins expressed by the  
CC clones are capable of forming a functioning calcium channel.  
CC Nucleic acids encoding the 3 subunits, as well as vectors, host  
CC cells and methods of isolating nucleic acids encoding related  
CC calcium channels are disclosed. Fusion proteins incorporating the  
CC subunit proteins, antibodies, and assays for identifying agents  
CC that modulate calcium channel activity are also provided. Such  
CC agents can be used to treat certain central nervous system  
CC disorders by altering calcium channel activity. Methods of  
CC diagnosing diseases associated with particular calcium channels,  
CC such as Lambert-Eaton syndrome, are disclosed.

Sequence 1091 AA:

Query Match 97.8%; Score 5528; DB 19; Length 1091;  
Best Local Similarity 98.6%; Pred. No. 0;  
Matches 1048; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

```

OY 1 MAAGCLALTLTLFQSLILGSPSSQEPFSAVTIKSWDKMOEDLTAKTASGVNQVLDI 60
DB 1 MAAGCLALTLTLFQSLILGSPSSQEPFSAVTIKSWDKMOEDLTAKTASGVNQVLDI 60
OY 61 YEKYODLYTVEPNNAQOLVETIARDIEKLNSRKALVRLALEAKVOAAHQWREDFASN 120
DB 61 YEKYODLYTVEPNNAQOLVETIARDIEKLNSRKALVRLALEAKVOAAHQWREDFASN 120
OY 121 EYVYNNADDDLPKENDSEPSQRIKPVFIDANFGROISTOHAHVHPTDIYEGSTIVL 180
DB 121 EYVYNNADDDLPKENDSEPSQRIKPVFIDANFGROISTOHAHVHPTDIYEGSTIVL 180
OY 181 NELNMTSALDEVFKKREDEPSLLMQVGSATGLARVYPAPWVNDSTPKIDLYDVR 240
DB 181 NELNMTSALDEVFKKREDEPSLLMQVGSATGLARVYPAPWVNDSTPKIDLYDVR 240
OY 241 RPWTYOGAASPKDMLILDVSGSVGLTKLIRTSVSEMLETSDDDPVNVAENSNAD 300
DB 241 RPWTYOGAASPKDMLILDVSGSVGLTKLIRTSVSEMLETSDDDPVNVAENSNAD 300
OY 301 VSCFQHLVQAVNRKKVYLKDAVNNTAKGIDYKGSFAEFQDLNNTVSRANCKIIML 360
DB 301 VSCFQHLVQAVNRKKVYLKDAVNNTAKGIDYKGSFAEFQDLNNTVSRANCKIIML 360
OY 361 FTDGEERAQELIFAKYNDKRYVETFSVGOHNDROGLOMACENGGYIEISIGAIR 420
DB 361 FTDGEERAQELIFAKYNDKRYVETFSVGOHNDROGLOMACENGGYIEISIGAIR 420
OY 421 INTQETLDVIGRPVYLAGDKAKOVQWNTVYDALELGLVITGLPVFNITGQFENKTNLK 480
DB 421 INTQETLDVIGRPVYLAGDKAKOVQWNTVYDALELGLVITGLPVFNITGQFENKTNLK 480
OY 481 NOLITGVNGVSVLEDIRKLTLPRTLCNNGYFFAIDPNGVYLHPNIQPKPKSQEPVTL 540
DB 481 NOLITGVNGVSVLEDIRKLTLPRTLCNNGYFFAIDPNGVYLHPNIQPKPKSQEPVTL 540
OY 541 DELDALENDJKVEIRNKIDGSEGEKTFRTLVKSODERYIDKGNRYTWTWVPVGTYSL 600
DB 541 DELDALENDJKVEIRNKIDGSEGEKTFRTLVKSODERYIDKGNRYTWTWVPVGTYSL 600
OY 601 ALVLPYTSFYIKAKIEETITQARSKKGMKDSSETLPKDNFEESGYFIAPRDQNDLKI 660
DB 601 ALVLPYTSFYIKAKIEETITQARSKKGMKDSSETLPKDNFEESGYFIAPRDQNDLKI 660
OY 661 SDNTEFLANNEFIDRTKTPNPNPCNDLNRVLLDAGFNLVQNTWWSKOKNKGAKAR 720
DB 661 SDNTEFLANNEFIDRTKTPNPNPCNDLNRVLLDAGFNLVQNTWWSKOKNKGAKAR 720
OY 721 FVVTDGGITRYYPKAGEENMOENPETEYEDSFYKRSNDNDNVETAPYFNKSGPEATSGI 780
DB 721 FVVTDGGITRYYPKAGEENMOENPETEYEDSFYKRSNDNDNVETAPYFNKSGPEATSGI 780
OY 781 MYSKAVEIYIOGKLKPAVVGIKIDVNSWIENFTKISRDCAGPVCDCKRNSDVMDCVI 840
DB 781 MYSKAVEIYIOGKLKPAVVGIKIDVNSWIENFTKISRDCAGPVCDCKRNSDVMDCVI 840

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DB 781 MYSKAVEIYIOGKLKPAVVGIKIDVNSWIENFTKISRDCAGPVCDCKRNSDVMDCVI 840
OY 841 LDDGFFLLMANHDDYTNQIGRFEIDPSIMRHLVNISVYAFNKSXYQSVCEPAAAPK 900
DB 841 LDDGFFLLMANHDDYTNQIGRFEIDPSIMRHLVNISVYAFNKSXYQSVCEPAAAPK 900
OY 901 GAGRSATVPSIADITLHGMMATRAANSIIQOFLSLTFPRLLEAVEMEDDFTASISK 960
DB 901 GAGRSATVPSIADITLHGMMATRAANSIIQOFLSLTFPRLLEAVEMEDDFTASISK 960
OY 961 SCITEQOYFPDNDKSGFSGVLDGNCRIPIHVEKILMNTLITFMWESKGTCCDTRLI 1020
DB 961 SCITEQOYFPDNDKSGFSGVLDGNCRIPIHVEKILMNTLITFMWESKGTCCDTRLI 1020
OY 1021 QAFQTSQGPNDQVWKQPRYRKGPVCFDNNALEDYTCGVS 1063
DB 1021 QAFQTSQGPNDQVWKQPRYRKGPVCFDNNALEDYTCGVS 1063

```

RESULT 15

AAR33553 standard; Protein; 1091 AA.

AAR33553;

30-JUN-1993 (first entry)

Sequence of the alpha 2 human calcium channel subunit.

Human calcium channel subunit; diagnosis; agonist; antagonist;  
Lambert Eaton syndrome.

Homo sapiens.

MO304083-A.

04-MAR-1993.

14-AUG-1992; 92WO-0506903.

15-AUG-1991; 91US-0745206.

10-APR-1992; 92US-0868354.

(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.

Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;  
Williams ME;

WPT: 1993-093936/11.

N-PSDB; AAQ37821.

DNA encoding specific human calcium channel sub-units - used for  
identifying calcium channel agonists and antagonists and  
diagnosing Lambert Eaton syndrome

Disclosure; Page 134-138; 150pp; English.

DNA encoding a human neuronal calcium channel alpha 2 subunit was  
isolated from a human genomic DNA library probed under low and high  
stringency conditions with a fragment of DNA encoding the rabbit  
skeletal muscle calcium channel alpha 2 subunit. The fragment  
included nucleotides having a sequence corresponding to the  
nucleotide sequence between nucleotides 43 and 272 inclusive of  
rabbit back skeletal muscle calcium channel alpha 2 subunit cDNA.  
PCR analysis identified splice variants of the human calcium alpha  
2 subunit transcript. In particularly preferred embodiments, the  
DNA encoding the alpha 2 subunit is produced by alternative  
processing of a primary transcript that includes DNA encoding the  
amino acids set forth in AAR33553 and the DNA of AAQ37823 inserted  
between nucleotides 1624 and 1625 of AAQ37821.

Sequence 1091 AA:

XX MPI: 2001-257902/26.  
 DR N-PSDB; AAF57563.  
 XX  
 PT Competitive binding assay for screening ligands which bind a cerebral  
 PT cortical voltage-dependent calcium channel alpha2-delta-1 subunit,  
 PT where the ligands identified are useful for treating disorders of the  
 PT nervous system, including pain -  
 XX  
 XX Claim 7: Page 139-142; 158pp; English.  
 CC The invention relates to a new method for screening ligands which bind a  
 CC cerebral cortical voltage-dependent calcium channel alpha2delta subunit,  
 CC preferably alpha2delta-1 subunit. The method comprises contacting a  
 CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of  
 CC interest and a labelled compound which binds the subunit, followed by  
 CC measuring the level of binding of the labelled compound to alpha2delta-1  
 CC subunit. The method is useful for screening ligands, preferably  
 CC biologically active products that modulate a nervous system function,  
 CC which bind a cerebral cortical voltage-dependent calcium channel  
 CC alpha2delta-1 subunit. The ligands identified by the method are useful  
 CC for treating disorders of the nervous system, including pain, epilepsy  
 CC and anxiety. The present sequence represents a porcine calcium channel  
 CC alpha2delta subunit.  
 XX  
 XX Sequence 1091 AA:  
 Query Match 97.9%; Score 5532; DB 22; Length 1091;  
 Best local Similarity 98.7%; Pred. No. 0;  
 Matches 1049; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLTFLGSLIGSSQEPFSAVITIKSWDKQEDLVTLAKTASGVNOLVDI 60  
 DB 1 MAAGCLLALTLTFLGSLIGSSQEPFSAVITIKSWDKQEDLVTLAKTASGVNOLVDI 60  
 QY 61 YEKYQOLTYEPNNAQOLVEIARQIEKLNSKALVRLALEKVQAHOHREDFASN 120  
 DB 61 YEKYQOLTYEPNNAQOLVEIARQIEKLNSKALVRLALEKVQAHOHREDFASN 120  
 QY 121 EYVYNAKDDLDPEKNDSEPSQRIKPFVLTIDANFGRLSYQHAHIFPDIEGSIYL 180  
 DB 121 EYVYNAKDDLDPEKNDSEPSQRIKPFVLTIDANFGRLSYQHAHIFPDIEGSIYL 180  
 QY 181 NEIENMTSALDEVYKKRREDDPSLLMOVFGSAGLARVYSPASWDNSRTPNKIDLYVRR 240  
 DB 181 NEIENMTSALDEVYKKRREDDPSLLMOVFGSAGLARVYSPASWDNSRTPNKIDLYVRR 240  
 QY 241 RPYVIGGAASPKDMLITLVNVSGLTLKLRISVSEMLETISDDDFYNVASFNSNAD 300  
 DB 241 RPYVIGGAASPKDMLITLVNVSGLTLKLRISVSEMLETISDDDFYNVASFNSNAD 300  
 QY 301 VSCFOHLYOANVRNKKVLDVANNITAKGITDYKKGSPAFEDLLNYSRANCKNTIML 360  
 DB 301 VSCFOHLYOANVRNKKVLDVANNITAKGITDYKKGSPAFEDLLNYSRANCKNTIML 360  
 QY 361 FIDGGERAOETFAKYNCKKRVFTFSVGHNYDRGPIQWMAKCNKGYEIPISGAIR 420  
 DB 361 FIDGGERAOETFAKYNCKKRVFTFSVGHNYDRGPIQWMAKCNKGYEIPISGAIR 420  
 QY 421 INTQETLVLDGRPMVLASGAKOVONTNYLDALDELGLVITGLTPFNTTGNENKNTNK 480  
 DB 421 INTQETLVLDGRPMVLASGAKOVONTNYLDALDELGLVITGLTPFNTTGNENKNTNK 480  
 QY 481 NQILIGVMGVDSLEDIKRLTPEFTLCPNGYFAIDPNQVYLHPVLQPKNKSOEPVYL 540  
 DB 481 NQILIGVMGVDSLEDIKRLTPEFTLCPNGYFAIDPNQVYLHPVLQPKNKSOEPVYL 540  
 QY 541 DFLDAELNDIKVEIKNNKIDGESGKTRTLVKSODERYIDKGNFTYTWTPVNGTDSL 600  
 DB 541 DFLDAELNDIKVEIKNNKIDGESGKTRTLVKSODERYIDKGNFTYTWTPVNGTDSL 600  
 QY 601 ALVLPYISFYIKAKIEETITQARSKKGMKDSSETLKPNFEESGTYFIAPRDYCNDLKI 660  
 DB 601 ALVLPYISFYIKAKIEETITQARSKKGMKDSSETLKPNFEESGTYFIAPRDYCNDLKI 660

DB 601 ALVLPYISFYIKAKIEETITQARSKKGMKDSSETLKPNFEESGTYFIAPRDYCNDLKI 660  
 QY 661 SPNTEPFLNFEETDRKTPNNPSCNTDLINRVLIDAGETNEIYONWWSKOKNIKGYKAR 720  
 DB 661 SPNTEPFLNFEETDRKTPNNPSCNTDLINRVLIDAGETNEIYONWWSKOKNIKGYKAR 720  
 QY 721 FVYTDGGITRYVPKKEAGNMOENPETYEDSFYKSLDNDVYFTAPYFNKSGPAGYESGI 780  
 DB 721 FVYTDGGITRYVPKKEAGNMOENPETYEDSFYKSLDNDVYFTAPYFNKSGPAGYESGI 780  
 QY 781 MYSKAVEIYIOGKLKPAVVGKIDVNSWIENTFTKTSIRDCAAPVDCCKRNSVMOCVI 840  
 DB 781 MYSKAVEIYIOGKLKPAVVGKIDVNSWIENTFTKTSIRDCAAPVDCCKRNSVMOCVI 840  
 QY 841 LDDGFFLLMANHDVYTNQIGRPFGEIDSLMRHLVNISVAFNKSVDYQSCFEGGAAPKQ 900  
 DB 841 LDDGFFLLMANHDVYTNQIGRPFGEIDSLMRHLVNISVAFNKSVDYQSCFEGGAAPKQ 900  
 QY 901 GAGHSAYVPSIADILHIGMWATAAASIILOFLLSLTFPRLLEAVEMEDDFTASLSKQ 960  
 DB 901 GAGHSAYVPSIADILHIGMWATAAASIILOFLLSLTFPRLLEAVEMEDDFTASLSKQ 960  
 QY 961 SCITPOTQYFPDNDKSRFVLDGNCNRIFHVEKIMNTNLIPTMBSKGTCPDTRLI 1020  
 DB 961 SCITPOTQYFPDNDKSRFVLDGNCNRIFHVEKIMNTNLIPTMBSKGTCPDTRLI 1020  
 QY 1021 QAEQTSQDGPDDPCDMVKOPRRKGPVPCFNNALBEDYTCGGVS 1063  
 DB 1021 QAEQTSQDGPDDPCDMVKOPRRKGPVPCFNNALBEDYTCGGVS 1063

RESULT 14  
 ID AAM37879  
 ID AAM37879 standard; Protein: 1091 AA.  
 XX  
 AC AAM37879;  
 XX  
 DT 28-AUG-1998 (first entry)  
 XX  
 DE Human calcium channel a2d subunit.  
 XX  
 KW Calcium channel; human; central nervous system disorder;  
 KW Lambert-Eaton syndrome; diagnosis; therapy.  
 OS Homo sapiens.  
 XX  
 PN MO9811131-A2.  
 XX  
 PD 19-MAR-1998.  
 XX  
 PF 11-SEP-1997; 97WO-US16146.  
 XX  
 PR 16-SEP-1996; 96US-0713118.  
 XX  
 PA (AMHP ) AMERICAN HOME PROD CORP.  
 PA  
 PI Chen ARS, Franco R, Shuey DJ;  
 PI  
 DR MPI: 1998-207325/18.  
 DR N-PSDB; AAV29060.  
 XX  
 PT DNA encoding human neuronal calcium channel subunit(s) - useful for  
 PT diagnosis of and treatment of central nervous system disorders, e.g.  
 PT Lambert-Eaton syndrome  
 PS Disclosure; Fig 2; 89pp; English.  
 CC This polypeptide comprises the a2d subunit of the human neuronal  
 CC calcium channel. cDNA clones (see AAV29059-61) encoding the a1b  
 CC subunit (see AAM37878), the a2d subunit and a b3 subunit (see AAM37880)  
 CC have been isolated. These have been inserted into expression  
 CC vectors and are stably expressed in transformed cell lines. The  
 CC transformed cells show omega-conotoxin GVIA binding activity,

PN W0200119870-A2.  
 XX  
 PD 22-MAR-2001.  
 XX  
 PF 18-SEP-2000; 2000WO-EP09137.  
 XX  
 PR 16-SEP-1999; 99US-0397550.  
 XX  
 PA (WARN ) WARNER LAMBERT CO.  
 XX  
 PI Brown JP, Bertelli F;  
 XX  
 DR WPI: 2001-235262/24.  
 DR N-PSDB; AAS01426.  
 XX  
 PT Calcium channel alpha2delta subunits, useful in e.g. SPA assays,  
 PT Flashplate assays, Nickel Flashplate assays, Filter binding assays or  
 PT Wheat Germ Lectin Flashplate assays -  
 XX  
 PS  
 XX  
 CC Claim 30; Page 141-144; 160pp; English.  
 CC  
 CC The present sequence represents human secreted calcium channel  
 CC alpha2delta subunit #15 which is soluble and retains the functional  
 CC characteristics of the full length or wild type alpha2delta subunit  
 CC (AAU01025) from which it is derived. The invention relates to truncated  
 CC alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins  
 CC which retain their affinity for radioactively labeled gabapentin. The  
 CC alpha2delta subunit is 1 of the components of the heteromultimeric  
 CC voltage-dependent calcium channel (VDCC) complexes present in neuronal  
 CC and non-neuronal tissues including heart and skeletal muscle. Numerous  
 CC soluble forms of the human calcium channel alpha2delta subunits  
 CC (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the  
 CC porcine calcium channel alpha2delta subunits (AAU01027-AAU01031) are  
 CC described. The secreted soluble alpha2delta subunit may be used in assays  
 CC e.g. scintillation proximity assay (SPA), flashplate, nickel flashplate,  
 CC filter binding or wheat germ lectin flashplate assays to detect or  
 CC measure the binding or interaction of a ligand (e.g. gabapentin,  
 CC L-Norleucine, L-Allo-Isoleucine, L-methionine, L-leucine, L-Isoleucine,  
 CC L-Valine, Spermine and/or L-Phenylalanine) of a calcium channel  
 CC alpha2delta subunit.  
 CC  
 XX  
 XX Sequence 1091 AA;  
 Query Match 97.9%; Score 5532; DB 22; Length 1091;  
 Best Local Similarity 98.7%; Pred. No. 0;  
 Matches 1049; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

DB 361 FTDCGEERAQIEFNKKYKDKKVRVFTSVGOHNTERGPIOMMACENKGYEYIPISIGAIR 420  
 QY 421 INTQEYLDVIGRPVAVLAGDAKQVOAMTNVYLDALDELGLVITGTLVPENITGONENKTNLK 480  
 DB 421 INTQEYLDVIGRPVAVLAGDAKQVOAMTNVYLDALDELGLVITGTLVPENITGONENKTNLK 480  
 QY 481 NQILIGWGVDSVLEDIKRLTPFTLCPNGYYFAIDPNGVYLLHPNLQPNRKSQEPVTL 540  
 DB 481 NQILIGWGVDSVLEDIKRLTPFTLCPNGYYFAIDPNGVYLLHPNLQPNRKSQEPVTL 540  
 QY 541 DELDAELENIDIKVEIRKMKMIDGESGEKTERFVKSQDERYIDGNRTYTPVNGIDYSL 600  
 DB 541 DELDAELENIDIKVEIRKMKMIDGESGEKTERFVKSQDERYIDGNRTYTPVNGIDYSL 600  
 QY 601 ALVLPYTSFYVYIKAKIEETITQARSKKGMKDSSETLKPDPFEESGYFLIAPROYCDLKI 660  
 DB 601 ALVLPYTSFYVYIKAKIEETITQARSKKGMKDSSETLKPDPFEESGYFLIAPROYCDLKI 660  
 QY 661 SDNTEFLNFEFIDKRTPNPNSCNTDLINRVLLDAGFTNELVQNYMSKOKNIKGVKAR 720  
 DB 661 SDNTEFLNFEFIDKRTPNPNSCNTDLINRVLLDAGFTNELVQNYMSKOKNIKGVKAR 720  
 QY 721 FVVTDDGITTTPYPRKAEENMOENPEYEDSFYKRSJLNDNYVFTAPYFNKSGPAGESGI 780  
 DB 721 FVVTDDGITTTPYPRKAEENMOENPEYEDSFYKRSJLNDNYVFTAPYFNKSGPAGESGI 780  
 QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRPCCAGPYCDDCKRNSDVMDCYI 840  
 DB 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRPCCAGPYCDDCKRNSDVMDCYI 840  
 QY 841 LDGSGFLMANHDDYTNQIRFEGEIDPSIMRHLVNISYVAFKSYDYOSVCEBGAAPQ 900  
 DB 841 LDGSGFLMANHDDYTNQIRFEGEIDPSIMRHLVNISYVAFKSYDYOSVCEBGAAPQ 900  
 QY 901 GAGHRSAYVSIADIIHIGMMATAAWSIIQOFLSLTTPRILEAVEMEDDDPTASLSQ 960  
 DB 901 GAGHRSAYVSIADIIHIGMMATAAWSIIQOFLSLTTPRILEAVEMEDDDPTASLSQ 960  
 QY 961 SCITEGTQYFFPDNDKSKFSFSGVLDCGNCSTRIFHEKIMLNTLIFIMVESKGTQCPDRLLI 1020  
 DB 961 SCITEGTQYFFPDNDKSKFSFSGVLDCGNCSTRIFHEKIMLNTLIFIMVESKGTQCPDRLLI 1020  
 QY 1021 QAEOTSGRPDPCDMYKOPRTKRGPDVCFNNALIEDYTDGCVS 1063  
 DB 1021 QAEOTSGRPDPCDMYKOPRTKRGPDVCFNNALIEDYTDGCVS 1063

RESULT 13  
 AAB62259  
 ID AAB62259 standard; Protein; 1091 AA.  
 XX  
 AC AAB62259;  
 AC  
 DT 11-JUN-2001. (first entry)  
 XX  
 DE Porcine calcium channel alpha2delta subunit.  
 XX  
 KW Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;  
 OS nervous system disorder; pain; epilepsy; anxiety; pig.  
 OS  
 XX Sus scrofa.  
 PN W0200120336-A2.  
 XX  
 PD 22-MAR-2001.  
 XX  
 PF 18-SEP-2000; 2000WO-EP09136.  
 PF  
 PR 16-SEP-1999; 99US-0397549.  
 PR  
 XX (WARN ) WARNER LAMBERT CO.  
 PA  
 PI Bertelli F, Brown JP, Dissanayake V, Suman-Chaunhan N, Gee NS;

XX US0696514-A.  
 XX 01-AUG-2000.  
 PD 25-MAY-1995: 9505-0450562.  
 XX 04-APR-1988: 8805-0176689.  
 PR 02-FEB-1990: 9005-0482384.  
 PR 08-NOV-1990: 9005-0603751.  
 PR 30-NOV-1990: 9005-0620250.  
 PR 15-AUG-1991: 9105-0745206.  
 PR 10-APR-1992: 9205-0868354.  
 PR 13-JUL-1992: 9205-0914231.  
 PR 11-AUG-1993: 9305-0105536.  
 PR 05-NOV-1993: 9305-0149097.  
 PR 07-FEB-1994: 9405-0193078.  
 PR 04-APR-1994: 9405-0223305.  
 PR 11-AUG-1994: 9405-0290012.  
 PR 23-SEP-1994: 9405-0311363.  
 PR 28-SEP-1994: 9405-0314083.  
 PR 07-NOV-1994: 9405-0336257.  
 PR 13-MAR-1995: 9505-0404950.  
 XX (SIBI-) SIBIA NEUROSCIENCES INC.  
 PA Ellis SB, Williams ME, McCue AF, Harpold MM;  
 XX WPI; 2000-548230/50.  
 DR N-PSDB; AAAA1707.  
 XX Human calcium channel beta subunit polynucleotides, useful for  
 PT producing recombinant eukaryotic cells and for diagnosing Lambert Eaton  
 PT Syndrome -  
 XX Example IV; Column 135-144; 153pp; English.  
 XX This invention describes a novel isolated DNA molecule (I) comprising a  
 CC sequence encoding a beta3-1 subunit of a human calcium channel.  
 CC Nucleic acid probes comprising 14-30 contiguous nucleotides of  
 CC beta3 subunit encoding DNA are useful for isolation and cloning of  
 CC calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that  
 CC express heterologous calcium channel are useful for identifying compounds  
 CC that modulate calcium channel activity and in assays for identifying  
 CC agonists and antagonists of calcium channel activity in humans. Human  
 CC calcium channel subunit or eukaryotic cells expressing the channel are  
 CC useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This  
 CC sequence represents the human calcium channel alpha-2 subunit which is  
 CC described in the method of the invention.  
 CC  
 XX Sequence 1091 AA:  
 SQ  
 Query Match 97.9%; Score 5532; DB 21; Length 1091;  
 Best Local Similarity 98.7%; Pred. No. 0;  
 Matches 1049; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Db 241 RPWYIOGAASPDKMDLILVDVSGSVGLTLKILRTSVSEMLETLSDDEEVNVAFSNSMAD 300  
 QY 301 VSCFOHLVQANRNKKVYLKDAVNNITANGIDYKKGSEFAFEPOLLNVVSAANCKITML 360  
 Db 301 VSCFOHLVQANRNKKVYLKDAVNNITANGIDYKKGSEFAFEPOLLNVVSAANCKITML 360  
 QY 361 FPDGGEERAOEIFAKYKNDKRVFTFVGHNDRGFIOMMACENKGYEIPISGAIR 420  
 Db 361 FPDGGEERAOEIFAKYKNDKRVFTFVGHNDRGFIOMMACENKGYEIPISGAIR 420  
 QY 421 INTQEVLDVLAGRPVYLAGDKAKOVOMTVNYLDALDELGLVITGTLPEVNTIQONEKNTLK 480  
 Db 421 INTQEVLDVLAGRPVYLAGDKAKOVOMTVNYLDALDELGLVITGTLPEVNTIQONEKNTLK 480  
 QY 481 NOLLIGVMGVDSLEDIKRLPRFTLCNGVYFAIDPBGVYLHNLOPKPKSQEPVTL 540  
 Db 481 NOLLIGVMGVDSLEDIKRLPRFTLCNGVYFAIDPBGVYLHNLOPKPKSQEPVTL 540  
 QY 541 DFLDAELENDDIKVEIRNKKIDSEGEKTRTLVKSODERYIDKGRITWTTPVNGDYSL 600  
 Db 541 DFLDAELENDDIKVEIRNKKIDSEGEKTRTLVKSODERYIDKGRITWTTPVNGDYSL 600  
 QY 601 ALVLPYSFYIKAKIETITQARSKKGMKDETLKPDNFEESGYTPIADRYCNDIKI 660  
 Db 601 ALVLPYSFYIKAKIETITQARSKKGMKDETLKPDNFEESGYTPIADRYCNDIKI 660  
 QY 661 SDNTEFFLNFEFLDRKTPNNPSCNADLINVLDAFTFELVONVSKOKNIKGVAR 720  
 Db 661 SDNTEFFLNFEFLDRKTPNNPSCNADLINVLDAFTFELVONVSKOKNIKGVAR 720  
 QY 721 FVVTGGITRVYKPKAGEWMOENPETYEDSFYKRSILDNDNVYFTAPYFNKSGPAYESGI 780  
 Db 721 FVVTGGITRVYKPKAGEWMOENPETYEDSFYKRSILDNDNVYFTAPYFNKSGPAYESGI 780  
 QY 781 MYSKAVEITIQKLLKPAVVGIKIDVNSKIENFTTSIRDPACAGVCCCKNSDMDCVI 840  
 Db 781 MYSKAVEITIQKLLKPAVVGIKIDVNSKIENFTTSIRDPACAGVCCCKNSDMDCVI 840  
 QY 841 LDDGGFLMANHDDVTNOIGRFGELDPSIMHILNISVYAFNKSYDQSCPEGAARQ 900  
 Db 841 LDDGGFLMANHDDVTNOIGRFGELDPSIMHILNISVYAFNKSYDQSCPEGAARQ 900  
 QY 901 GAGHSAYVPSVADILQIGWMTAAWMSILQGFLLSLFPRLLAEVEMEDDFTASLSKQ 960  
 Db 901 GAGHSAYVPSVADILQIGWMTAAWMSILQGFLLSLFPRLLAEVEMEDDFTASLSKQ 960  
 QY 961 SCITEGTOYFENDSKSFSGVLDGCGNSRIFVEKLTMTNLIFFINVESKGTCPDTRLII 1020  
 Db 961 SCITEGTOYFENDSKSFSGVLDGCGNSRIFVEKLTMTNLIFFINVESKGTCPDTRLII 1020  
 QY 1021 QABOTSDEGPNPCDMYKOPRYRKGPDVPCPDNNALLETTCGGVS 1063  
 Db 1021 QABOTSDEGPNPCDMYKOPRYRKGPDVPCPDNNALLETTCGGVS 1063  
 RESULT 12  
 AAU01035  
 ID AAU01035 standard; Protein; 1091 AA.  
 XX AAU01035:  
 AC 04-JUL-2001 (first entry)  
 DT  
 DE Human secreted soluble alpha2delta calcium channel subunit #15 protein.  
 XX Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;  
 KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;  
 KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;  
 XX filter binding assay; wheat germ lectin flashplate assay.  
 OS Homo sapiens.  
 XX

AC AAM63145;  
 XX  
 DT 12-OCT-1998 (first entry)  
 XX  
 DE Human calcium channel alpha-2 subunit.  
 XX  
 KW Alpha-2 subunit; human; calcium channel; assay; detection;  
 XX characterisation; Lambert Eaton Syndrome; LES; diagnosis.  
 OS Homo sapiens.  
 XX  
 PN US5792846-A.  
 XX  
 PD 11-AUG-1998.  
 XX  
 PF 31-MAY-1995; 9505-0455543.  
 XX  
 PR 04-APR-1994; 9405-0223305.  
 PR 04-APR-1988; 8805-0176899.  
 PR 04-APR-1989; 8905-0603751.  
 PR 04-APR-1989; 8905-0603751.  
 PR 20-FEB-1990; 9005-0482384.  
 PR 30-NOV-1990; 9005-0620250.  
 PR 15-AUG-1991; 9105-0745206.  
 PR 31-MAY-1995; 9505-0455543.  
 XX  
 PA (SIBI-) SIBIA NEUROSCIENCES INC.  
 XX  
 PI Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;  
 PI Williams ME;  
 XX  
 DR WPI: 1998-456192/39.  
 DR N-PSDB: AAV42689.  
 XX  
 PT DNA encoding human calcium channel alpha 1b sub:unit protein -  
 PT useful for recombinant production of the channel for screening of  
 PT its modulators, and diagnosis of Lambert Eaton Syndrome  
 XX  
 PS Claim 4: Columns 283-288; 16pp; English.  
 XX  
 CC The present sequence represents the alpha-2 subunit of a human calcium  
 CC channel. Calcium channels are membrane-spanning, multi-subunit proteins  
 CC that allow controlled entry of calcium ions into cells. This leads  
 CC to depolarisation events required for muscle contraction. The recombinant  
 CC subunit, when expressed with nucleic acids encoding the complete calcium  
 CC channel, can be used in assays for the detection and characterisation of  
 CC compounds that modulate the channel. The DNA encoding the subunits can  
 CC be alternatively spliced when transcribed, giving more than one form of  
 CC the protein from the same transcript, each having slightly different  
 CC properties. In addition, the reactivity of the alpha 1 subunit with IgG  
 CC molecules from the serum of an individual with Lambert Eaton Syndrome  
 CC (LES) can be used as a diagnostic for the disease.  
 XX  
 SQ Sequence 1091 AA;  
 Query Match 97.9%; Score 5532; DB 19; Length 1091;  
 Best Local Similarity 98.7%; Pred. No. 0;  
 Matches 1049; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

DB 181 NELNMTSALDEVFKKNNREEDPSLMQVFGSATGLARITYPASPMWDSNTPKIDLYDVR 240  
 QY 241 RPYIYOGAASPMDLILVDVSGVSGLTITLKLRTSVSEMLETISDDDPVNVASFNNAOD 300  
 DB 241 RPYIYOGAASPMDLILVDVSGVSGLTITLKLRTSVSEMLETISDDDPVNVASFNNAOD 300  
 QY 301 VSCFOHLVQANRNKKVLLKDAVNNITANGITDYKKGFSFAEQLLNVSRANCKITML 360  
 DB 301 VSCFOHLVQANRNKKVLLKDAVNNITANGITDYKKGFSFAEQLLNVSRANCKITML 360  
 QY 361 FTDGGEERAOEIEFAKYNKDKVRFVFEVSGOHNDRGIQMACENKGYIEISGAIR 420  
 DB 361 FTDGGEERAOEIEFAKYNKDKVRFVFEVSGOHNDRGIQMACENKGYIEISGAIR 420  
 QY 421 INFOEYLDVLGRPMVLAADKAKQVQMTNVYLDALDELGLVITGTLPVENITGONNKTNLK 480  
 DB 421 INFOEYLDVLGRPMVLAADKAKQVQMTNVYLDALDELGLVITGTLPVENITGONNKTNLK 480  
 QY 481 NOLILGVKGVDSLEDIRLRLPRTLCPNGYYPALIDPNGYVLLHPNLOPKNPKSOEPTVL 540  
 DB 481 NOLILGVKGVDSLEDIRLRLPRTLCPNGYYPALIDPNGYVLLHPNLOPKNPKSOEPTVL 540  
 QY 541 DFLDAELENDIKVEIRNKKIDGEGSEKTEFTLVKSQDERYIDKGNRTYTWTPVNGTYSL 600  
 DB 541 DFLDAELENDIKVEIRNKKIDGEGSEKTEFTLVKSQDERYIDKGNRTYTWTPVNGTYSL 600  
 QY 601 ALVLPYSPYYIKAKIEETITQANSKKGKMKDSEITLKPNEEESGYTFIAPRODCNDLKI 660  
 DB 601 ALVLPYSPYYIKAKIEETITQANSKKGKMKDSEITLKPNEEESGYTFIAPRODCNDLKI 660  
 QY 661 SDNTEFLNNEFLDKRTPNNPSCNTDLIRVLLDAGFTNELVQNTWSKOKNIKVKAR 720  
 DB 661 SDNTEFLNNEFLDKRTPNNPSCNTDLIRVLLDAGFTNELVQNTWSKOKNIKVKAR 720  
 QY 721 FVYTDGGITRYYPKAGNMENPEYEDSFYKSLINDNVYFAFVFNKSGCAVYSGI 780  
 DB 721 FVYTDGGITRYYPKAGNMENPEYEDSFYKSLINDNVYFAFVFNKSGCAVYSGI 780  
 QY 781 MYSKAVEIYIGKLLKPAVVGIKIDVNSWLENFTKTSIRPCAGPVCDCRNSDVMCVI 840  
 DB 781 MYSKAVEIYIGKLLKPAVVGIKIDVNSWLENFTKTSIRPCAGPVCDCRNSDVMCVI 840  
 QY 841 LDDGFFLMAHDDYTNOIGFSEIDPSLMRLHVNISVYAFNKSXYQSVCEPAAKQ 900  
 DB 841 LDDGFFLMAHDDYTNOIGFSEIDPSLMRLHVNISVYAFNKSXYQSVCEPAAKQ 900  
 QY 901 GAGRSAYVPSIADILHGMWATAAMSIIQOFLSLTPPRLLEAVYMEDDDFTASLSQ 960  
 DB 901 GAGRSAYVPSIADILHGMWATAAMSIIQOFLSLTPPRLLEAVYMEDDDFTASLSQ 960  
 QY 961 SCITEQYQYFFDNDKSKFSGLDCGNSRIFHVEKLMNTNLIIFIMBSKGTCPDTRLLI 1020  
 DB 961 SCITEQYQYFFDNDKSKFSGLDCGNSRIFHVEKLMNTNLIIFIMBSKGTCPDTRLLI 1020  
 QY 1021 QAEQTSQSPDPCDMVKOPRYKKGPDVCFDNNALLEDYIDCGVS 1063  
 DB 1021 QAEQTSQSPDPCDMVKOPRYKKGPDVCFDNNALLEDYIDCGVS 1063  
 RESULT 11  
 AAB10576  
 ID AAB10576 standard; Protein: 1091 AA.  
 AC AAB10576;  
 XX  
 DT 22-DEC-2000 (first entry)  
 XX  
 DE Human calcium channel alpha-2 subunit protein.  
 XX  
 KW Human; calcium channel; calcium channel subunit; diagnosis;  
 KW Lambert Eaton Syndrome; calcium channel subunit alpha-2.  
 OS Homo sapiens.

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Db 961 SCITEGTOYFFDNDKSSKSGVLDCGNCSTRIFHGEKLMNTNLIIFIMVESKGTCPDTRLLI 1020
OY 1021 QAEOTSDGPDPCDMVKOPRYRKGPVCFDNNALLEDYDCCGVS 1063
Db 1021 QAEOTSDGPNPCDMVKOPRYRKGPVCFDNNALLEDYDCCGVS 1063

RESULT 9
AAR71011
ID AAR71011 standard; Protein; 1091 AA.
XX
AC AAR71011;
DT 01-DEC-1995 (first entry)
XX
DE Human neuronal calcium channel subunit alpha 2b.
XX
KW Calcium channel subunit; antagonist; agonist; diagnosis;
KW Lambert Eaton Syndrome.
XX
OS Homo sapiens.
XX
PN W09504822-A.
PD 16-FEB-1995.
XX
PE 11-AUG-1994; 94WO-US09230.
XX
PR 11-AUG-1993; 93US-0105536.
PR 05-NOV-1993; 93US-0149097.
XX
PA (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
XX
PI Ellis SB, Gillespie A, Harpold MM, McCue AF, Williams ME;
DR WPI: 1995-090900/12.
DR N-PSDB: AA084664.
XX
PT DNA encoding human calcium channel sub-unit(s) - used for
PT developing prods. for studying calcium channels, e.g. for
PT obtaining agonists and antagonists
XX
PS Disclosure: Page 166-171; 285pp; English.
XX
CC Human neuronal alpha 2 coding sequence (AA084664) transcript is
CC differentially processed in skeletal muscle, aorta, and CNS in
CC the region corresp. to nt 1595-1942 of AA084664 in each of the
CC tissues. Five alternatively spliced variant transcripts that differ
CC in the presence or absence of one to three different portions of
CC this region. There are three sequences involved (see AA084664 FT
CC and AA084665 FT), sequence 1, sequence 2 and sequence 3. The five
CC alpha 2 encoding transcripts from the different tissues include
CC different combinations of the three sequences, except for one of
CC the alpha 2 transcripts expressed in aorta which lacks all three
CC sequences. The five alpha 2 forms identified are (1) a form that
CC lacks sequence 3 called alpha 2a, expressed in skeletal muscle
CC (2) one that lacks sequence 1 called alpha 2b, expressed in CNS
CC (3) one that lacks sequences 1 and 2 called alpha 2c, expressed in
CC aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,
CC expressed in aorta and (5) one that lacks sequences 1 and 3
CC called alpha 2e.
XX
CC
XX
SQ Sequence 1091 AA;
Query Match 97.9%; Score 5532; DB 16; Length 1091;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 1049; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 1 MAAGCLALTLTLFOSLLIGSPSPSAVTIKSWDKMOEDLVTLAKTASGVNOLVDI 60
Db 1 MAAGCLALTLTLFOSLLIGSPSPSAVTIKSWDKMOEDLVTLAKTASGVNOLVDI 60

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OY 61 YEKYODLYVEPNNAQVLEIAARDIEKLLSNRSKALVLEAEKVAQAHHQREDPASN 120
Db 61 YEKYODLYVEPNNAQVLEIAARDIEKLLSNRSKALVLEAEKVAQAHHQREDPASN 120
OY 121 EYVYNAKDLDPEKNDSEPGSQRIRKPVETIDANGROISTYQAAVHPTDIEBSTYVL 180
Db 121 EYVYNAKDLDPEKNDSEPGSQRIRKPVETIDANGROISTYQAAVHPTDIEBSTYVL 180
OY 121 EYVYNAKDLDPEKNDSEPGSQRIRKPVETIDANGROISTYQAAVHPTDIEBSTYVL 180
Db 121 EYVYNAKDLDPEKNDSEPGSQRIRKPVETIDANGROISTYQAAVHPTDIEBSTYVL 180
OY 181 NELNMTSALDEYFKKREEDPSLLMQVFGSATGLARYPASPMVDNSPTPKIDLYDPR 240
Db 181 NELNMTSALDEYFKKREEDPSLLMQVFGSATGLARYPASPMVDNSPTPKIDLYDPR 240
OY 241 RPYWIGGAASPKDMLILVYSGSVGLTKLIRTSYSEMLETLSDDEPVNVAFSNSMAD 300
Db 241 RPYWIGGAASPKDMLILVYSGSVGLTKLIRTSYSEMLETLSDDEPVNVAFSNSMAD 300
OY 301 VSCFOHLVQANVANKKVLDAVNNITAKGITDYKKGSFAEQLLNYSRANCKIIML 360
Db 301 VSCFOHLVQANVANKKVLDAVNNITAKGITDYKKGSFAEQLLNYSRANCKIIML 360
OY 361 FTDGEERAQELPAKYNKKKVVFTFSVGOHNYDRGPLOMMACENKGYEIPSIGAIR 420
Db 361 FTDGEERAQELPAKYNKKKVVFTFSVGOHNYDRGPLOMMACENKGYEIPSIGAIR 420
OY 421 INTQEXLDVLGRPMVLADGAKAKOVNTNVLDALEGLVITGLPVFNITGONENKTNLK 480
Db 421 INTQEXLDVLGRPMVLADGAKAKOVNTNVLDALEGLVITGLPVFNITGONENKTNLK 480
OY 481 NQILIGVMGVDSLEDIKRLTPRETLCPNGYFPAIDPNQVYLLHPLOKPKNSQEPVTL 540
Db 481 NQILIGVMGVDSLEDIKRLTPRETLCPNGYFPAIDPNQVYLLHPLOKPKNSQEPVTL 540
OY 541 DFLDAELENDIKKEIRNKKMIDGSGEKTFTLVKSDQEIYIKGNRTYWTPTVNGTDSL 600
Db 541 DFLDAELENDIKKEIRNKKMIDGSGEKTFTLVKSDQEIYIKGNRTYWTPTVNGTDSL 600
OY 601 ALVLPYISFYIYAKIEETITQARSKKGMKDSITLKPNEBEGYTIAPDQYCNLKI 660
Db 601 ALVLPYISFYIYAKIEETITQARSKKGMKDSITLKPNEBEGYTIAPDQYCNLKI 660
OY 661 SDNTEFLNFEIDIRKPPNPNSCNTDLINRVLADGFTNELVQVYMSKONINGVKAR 720
Db 661 SDNTEFLNFEIDIRKPPNPNSCNTDLINRVLADGFTNELVQVYMSKONINGVKAR 720
OY 721 FVYTDGITRVYPRKEAGENQENPETTEDSFYKRSIDNDNYVFTAFYFNKSGPAYESGI 780
Db 721 FVYTDGITRVYPRKEAGENQENPETTEDSFYKRSIDNDNYVFTAFYFNKSGPAYESGI 780
OY 781 MYSKAVEIYIYOGKLLRPAYVGIKIDVNSIENFTKTSIDPCAGPYCDCKRNSDVWDYI 840
Db 781 MYSKAVEIYIYOGKLLRPAYVGIKIDVNSIENFTKTSIDPCAGPYCDCKRNSDVWDYI 840
OY 841 LDDGGFLMANHNDYINQIGRFGELIDPSLMRLVINSYAFKSKVDYOSVCEPGAAPQ 900
Db 841 LDDGGFLMANHNDYINQIGRFGELIDPSLMRLVINSYAFKSKVDYOSVCEPGAAPQ 900
OY 901 GACHRSAYVSIADLIHIGMATTAAMSILQOPLSLTPRRLLEAVEMEDDFTASLSKQ 960
Db 901 GACHRSAYVSIADLIHIGMATTAAMSILQOPLSLTPRRLLEAVEMEDDFTASLSKQ 960
OY 961 SCITEGTOYFFDNDKSSKSGVLDCGNCSTRIFHGEKLMNTNLIIFIMVESKGTCPDTRLLI 1020
Db 961 SCITEGTOYFFDNDKSSKSGVLDCGNCSTRIFHGEKLMNTNLIIFIMVESKGTCPDTRLLI 1020
OY 1021 QAEOTSDGPDPCDMVKOPRYRKGPVCFDNNALLEDYDCCGVS 1063
Db 1021 QAEOTSDGPNPCDMVKOPRYRKGPVCFDNNALLEDYDCCGVS 1063

RESULT 10
AAM63145
ID AAM63145 standard; Protein; 1091 AA.
XX

```

Db 721 FVTDGGITRVPKAGEMWQENPEYEDSFYKRSLDNNYVFTAPYFNKSGPAGESGI 780  
 QY 781 MYSKAVEITYIOGKLLKPAVVGIKIDVNSWIEFNTKTSIDPCAGPCVDCCKRNSDVMDCVI 840  
 Db 781 MYSKAVEITYIOGKLLKPAVVGIKIDVNSWIEFNTKTSIDPCAGPCVDCCKRNSDVMDCVI 840  
 QY 841 LDDGGFLMAHNDYTNIGRFFGEIDPSLMRLHVNISYAFNKSXYQSCVCEGAPKQ 900  
 Db 841 LDDGGFLMAHNDYTNIGRFFGEIDPSLMRLHVNISYAFNKSXYQSCVCEGAPKQ 900  
 QY 901 GAGHRSAYVPSADILHIGMWATAAAMSILOQFLSLTFPRLLEAVEMDDFTASLSKQ 960  
 Db 901 GAGHRSAYVPSADILHIGMWATAAAMSILOQFLSLTFPRLLEAVEMDDFTASLSKQ 960  
 QY 961 SCITEGTYFFNDKSFSGVLDGCGNSRIFFHEKLMNTLFIIMVESKGTCPDTRLLI 1020  
 Db 961 SCITEGTYFFNDKSFSGVLDGCGNSRIFFHEKLMNTLFIIMVESKGTCPDTRLLI 1020  
 QY 1021 QAEQTSDFPCDMVKOPRYRRKGPVYCFDNNALLEDYTCGGSV 1063  
 Db 1021 QAEQTSDFPCDMVKOPRYRRKGPVYCFDNNALLEDYTCGGSV 1063

RESULT 8  
AAB62258

ID AAB62258 standard; Protein; 1063 AA.

XX AAB62258;

XX 11-JUN-2001 (first entry)

XX Porcine calcium channel alpha2delta subunit.

XX Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;

XX nervous system disorder; pain; epilepsy; anxiety; pig.

XX Sus scrofa.

XX WO200120336-A2.

XX 22-MAR-2001.

XX 18-SEP-2000; 2000WO-EP09136.

XX 16-SEP-1999; 99US-0397549.

XX (WARN) WARNER LAMBERT CO.

XX Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;

XX WPI; 2001-257902/26.

XX N-PSDB; AAF57562.

XX Competitive binding assay for screening ligands which bind a cerebral

XX cortical voltage-dependent calcium channel alpha2-delta-1 subunit,

XX where the ligands identified are useful for treating disorders of the

XX nervous system, including pain -

XX Claim 8; Page 135-139; 158pp; English.

XX The invention relates to a new method for screening ligands which bind a

XX cerebral cortical voltage-dependent calcium channel alpha2delta subunit,

XX preferably alpha2delta-1 subunit. The method comprises contacting a

XX secreted soluble recombinant alpha2delta-1 subunit with a ligand of

XX interest and a labelled compound which binds the subunit, followed by

XX measuring the level of binding of the labelled compound to alpha2delta-1

XX subunit. The method is useful for screening ligands, preferably

XX biologically active products that modulate a nervous system function,

XX which bind a cerebral cortical voltage-dependent calcium channel

XX alpha2delta-1 subunit. The ligands identified by the method are useful

XX for treating disorders of the nervous system, including pain, epilepsy

XX and anxiety. The present sequence represents a porcine calcium channel

CC alpha2delta subunit.

XX Sequence 1063 AA;

Query Match 97.9%; Score 5532; DB 22; Length 1063;

Best Local Similarity 98.7%; Pred. No. 0;

Matches 1049; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLTQSLIGSSQEPFSAVTIKSWDKMOEDVLTAKTASGVNQLVDI 60  
 Db 1 MAAGCLLALTLTQSLIGSSQEPFSAVTIKSWDKMOEDVLTAKTASGVNQLVDI 60  
 QY 61 YEKYODLYTVBPNNARQIVETIARDIEKLSNRSKALVRLAEKVAQAHHQWEDFASN 120  
 Db 61 YEKYODLYTVBPNNARQIVETIARDIEKLSNRSKALVRLAEKVAQAHHQWEDFASN 120  
 QY 121 EYVYNAKDLDLDPKKNSEPSQRIKPFEDANFGQISYQAAVHPIDYEGSTIVL 180  
 Db 121 EYVYNAKDLDLDPKKNSEPSQRIKPFEDANFGQISYQAAVHPIDYEGSTIVL 180  
 QY 181 NELNMTSALDEVFKKNREDEPSLLMOVFGSATGLARYYPASPWVNSRTFNKIDLYDVR 240  
 Db 181 NELNMTSALDEVFKKNREDEPSLLMOVFGSATGLARYYPASPWVNSRTFNKIDLYDVR 240  
 QY 241 RPWYIOGAASPKDMLILVDVSGSVGLTLKLI RTSVSEMLETSDDDFVAVASFNSAOD 300  
 Db 241 RPWYIOGAASPKDMLILVDVSGSVGLTLKLI RTSVSEMLETSDDDFVAVASFNSAOD 300  
 QY 301 VSCFOHLVQAVNRKVKYLKDAVNNTAKGITDYKKGFSFAEQLLNTVSRANCKITML 360  
 Db 301 VSCFOHLVQAVNRKVKYLKDAVNNTAKGITDYKKGFSFAEQLLNTVSRANCKITML 360  
 QY 361 FTDGGEERAOEIFAKYNNKDKRVRFVTSVGOHNDRPIQMMACENGGYYEIPISGAI 420  
 Db 361 FTDGGEERAOEIFAKYNNKDKRVRFVTSVGOHNDRPIQMMACENGGYYEIPISGAI 420  
 QY 421 INTQFYLDVLCRPVYLADKAKOVQWTVNYLDALIELGLVITGTLVPVNTIGQNEKTNL 480  
 Db 421 INTQFYLDVLCRPVYLADKAKOVQWTVNYLDALIELGLVITGTLVPVNTIGQNEKTNL 480  
 QY 481 NOLITGVKGVSVLEDIKRLTPRFLCPNGYFALIDNGVYLLHPNLQPNKPSQSEVTL 540  
 Db 481 NOLITGVKGVSVLEDIKRLTPRFLCPNGYFALIDNGVYLLHPNLQPNKPSQSEVTL 540  
 QY 541 DFLDAELENDIKVEIRNMKIDGSEGEKTFRTLVASQDERYIDKNGRTYTTPVNGTDSL 600  
 Db 541 DFLDAELENDIKVEIRNMKIDGSEGEKTFRTLVASQDERYIDKNGRTYTTPVNGTDSL 600  
 QY 601 ALVLPYTSFYIYAKIEETITQANSKKGKMDSETLKPDNFEESGYTFIAPRDYCNLKI 660  
 Db 601 ALVLPYTSFYIYAKIEETITQANSKKGKMDSETLKPDNFEESGYTFIAPRDYCNLKI 660  
 QY 661 SDNNTPEFLNFEIDRTPNNPSCNDLIRVYLLDGFNTLQVONWSOKNKGKAR 720  
 Db 661 SDNNTPEFLNFEIDRTPNNPSCNDLIRVYLLDGFNTLQVONWSOKNKGKAR 720  
 QY 721 FVYTDGGITRVPKAGEMWQENPEYEDSFYKRSLDNNYVFTAPYFNKSGPAGESGI 780  
 Db 721 FVYTDGGITRVPKAGEMWQENPEYEDSFYKRSLDNNYVFTAPYFNKSGPAGESGI 780  
 QY 781 MYSKAVEITYIOGKLLKPAVVGIKIDVNSWIEFNTKTSIDPCAGPCVDCCKRNSDVMDCVI 840  
 Db 781 MYSKAVEITYIOGKLLKPAVVGIKIDVNSWIEFNTKTSIDPCAGPCVDCCKRNSDVMDCVI 840  
 QY 841 LDDGGFLMAHNDYTNIGRFFGEIDPSLMRLHVNISYAFNKSXYQSCVCEGAPKQ 900  
 Db 841 LDDGGFLMAHNDYTNIGRFFGEIDPSLMRLHVNISYAFNKSXYQSCVCEGAPKQ 900  
 QY 901 GAGHRSAYVPSADILHIGMWATAAAMSILOQFLSLTFPRLLEAVEMDDFTASLSKQ 960  
 Db 901 GAGHRSAYVPSADILHIGMWATAAAMSILOQFLSLTFPRLLEAVEMDDFTASLSKQ 960  
 QY 961 SCITEGTYFFNDKSFSGVLDGCGNSRIFFHEKLMNTLFIIMVESKGTCPDTRLLI 1020





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QY 361 FTDGEERAQEIFAKYKNDKAVRTFVSQGHNDRCPIQWMAKCNKGYEIPISGAIR 420
DB 361 FTDGEERAQEIFAKYKNDKAVRTFVSQGHNDRCPIQWMAKCNKGYEIPISGAIR 420
QY 421 INTQEVLDVIGRPVLAGDAKAKOVMTNYLDALDELGLVITGTLVPFNITQONENKTNLK 480
DB 421 INTQEVLDVIGRPVLAGDAKAKOVMTNYLDALDELGLVITGTLVPFNITQONENKTNLK 480
QY 481 NQILIGVGVDSLEDDIKRLTPRFTLCPNGYFAIDPNQYVLLHPNLOPKNKSOEPTYL 540
DB 481 NQILIGVGVDSLEDDIKRLTPRFTLCPNGYFAIDPNQYVLLHPNLOPKNKSOEPTYL 540
QY 541 DFLDAELENDIKVEIKRNMKIDGSEKFTFRLVKSQDERYIDKGNRTYTWPNVGTDSL 600
DB 541 DFLDAELENDIKVEIKRNMKIDGSEKFTFRLVKSQDERYIDKGNRTYTWPNVGTDSL 600
QY 601 ALVLPYTSFYTKAKIETITQARSKKGMDSFTLKDPNFEESGYTFLAPDVCNDLKI 660
DB 601 ALVLPYTSFYTKAKIETITQARSKKGMDSFTLKDPNFEESGYTFLAPDVCNDLKI 660
QY 661 SDNTEFTLNFETIDKRTPNNSCNTDLINRVLIDAGFTNELVONYMSKONIKGVKAR 720
DB 661 SDNTEFTLNFETIDKRTPNNSCNTDLINRVLIDAGFTNELVONYMSKONIKGVKAR 720
QY 721 FVYTDGGITRYPKRAGENMQENPETEDSTYKRSLDNDNTVFTAPRYNKGSPAYESGI 780
DB 721 FVYTDGGITRYPKRAGENMQENPETEDSTYKRSLDNDNTVFTAPRYNKGSPAYESGI 780
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSMIFNTKTSIRDCACAPVCCKRNSDVMDCVI 840
DB 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSMIFNTKTSIRDCACAPVCCKRNSDVMDCVI 840
QY 841 LDDGFFLLMANHDDYTNOIGRFFGIDPSLMRHLVNISVYAFNKSXYDQSVCEBGAAPKQ 900
DB 841 LDDGFFLLMANHDDYTNOIGRFFGIDPSLMRHLVNISVYAFNKSXYDQSVCEBGAAPKQ 900
QY 901 GAGHSASVPSIADILHIGMWATAAASIILOFLLSTLFFPRLLEAVEHEDDDFTASLSKQ 960
DB 901 GAGHSASVPSIADILHIGMWATAAASIILOFLLSTLFFPRLLEAVEHEDDDFTASLSKQ 960
QY 961 SCITEQOTYFFPDNDKSKFSVGLDCGNCRIPIHVEKLMNTNLIETLWESKGTGCPDTRLII 1020
DB 961 SCITEQOTYFFPDNDKSKFSVGLDCGNCRIPIHVEKLMNTNLIETLWESKGTGCPDTRLII 1020
QY 1021 QAEQTSDEPDPDCMVKQPRYRKGPVCHDNALDELDTDCGCVS 1063
DB 1021 QAEQTSDEPDPDCMVKQPRYRKGPVCHDNALDELDTDCGCVS 1063

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RESULT 6  
AAB62251  
ID AAB62251 standard; Protein; 1091 AA.

AAB62251:  
11-JUN-2001 (first entry)  
Porcine calcium channel subunit alpha2delta-1.  
Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;  
nervous system disorder; pain; epilepsy; anxiety; pig.  
Sus scrofa.  
WO200120336-A2.  
22-MAR-2001.  
18-SEP-2000; 2000WO-EP09136.  
16-SEP-1999; 99US-0397549.  
(WARN) WARNER LAMBERT CO.

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XX Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;
PI WPL: 2001-257902/26.
DR N-PSDB: AAF57536.
XX Competitive binding assay for screening ligands which bind a cerebral
PT cortical voltage-dependent calcium channel alpha2delta-1 subunit,
PT where the ligands identified are useful for treating disorders of the
PT nervous system, including pain.
XX Claim 7; Page 109-112; 158pp; English.
PS
XX The invention relates to a new method for screening ligands which bind a
CC cerebral cortical voltage-dependent calcium channel alpha2delta subunit,
CC preferably alpha2delta-1 subunit. The method comprises contacting a
CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of
CC interest and a labelled compound which binds the subunit, followed by
CC measuring the level of binding of the labelled compound to alpha2delta-1
CC subunit. The method is useful for screening ligands, preferably
CC biologically active products that modulate a nervous system function,
CC which bind a cerebral cortical voltage-dependent calcium channel
CC alpha2delta-1 subunit. The ligands identified by the method are useful
CC for treating disorders of the nervous system, including pain, epilepsy
CC and anxiety. The present sequence represents a porcine calcium channel
CC subunit alpha2delta-1.
SQ Sequence 1091 AA:
Query Match 99.28; Score 5602; DB 22; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAGCLALTLTLFQSLILGSPSOEPPSAVTIKSWDKQEDLYLATASGVNOLVI 60
DB 1 MAAGCLALTLTLFQSLILGSPSOEPPSAVTIKSWDKQEDLYLATASGVNOLVI 60
QY 61 YEKYQDLTYEPNNAAROLVEIARDEIKLSNRSKALVRLALEAEKVQAHOHREDFASN 120
DB 61 YEKYQDLTYEPNNAAROLVEIARDEIKLSNRSKALVRLALEAEKVQAHOHREDFASN 120
QY 121 EYVYNNAKDDLDEPKNDSESGSORIKPVFIDDAFNGROISYQHAHVHPTDIYEGSTIVL 180
DB 121 EYVYNNAKDDLDEPKNDSESGSORIKPVFIDDAFNGROISYQHAHVHPTDIYEGSTIVL 180
QY 181 NEIWNTSALDEVEFKKNEEDPSILMOVFGSATGLARYYPASPVNDSRPNTKIDLYDVR 240
DB 181 NEIWNTSALDEVEFKKNEEDPSILMOVFGSATGLARYYPASPVNDSRPNTKIDLYDVR 240
QY 241 RPYWIOGAASPKDMLILVDVSGVSGLTJLKLRTSVSEMLETISDDDFYNVASFNSAOD 300
DB 241 RPYWIOGAASPKDMLILVDVSGVSGLTJLKLRTSVSEMLETISDDDFYNVASFNSAOD 300
QY 301 VSCFOHLVQANVRNKKVLDVANNITAKGTDYKKGFSAFEDOLNNTSRANCKIIML 360
DB 301 VSCFOHLVQANVRNKKVLDVANNITAKGTDYKKGFSAFEDOLNNTSRANCKIIML 360
QY 361 FTDGEERAQEIFAKYKNDKAVRTFVSQGHNDRCPIQWMAKCNKGYEIPISGAIR 420
DB 361 FTDGEERAQEIFAKYKNDKAVRTFVSQGHNDRCPIQWMAKCNKGYEIPISGAIR 420
QY 421 INTQEVLDVIGRPVLAGDAKAKOVMTNYLDALDELGLVITGTLVPFNITQONENKTNLK 480
DB 421 INTQEVLDVIGRPVLAGDAKAKOVMTNYLDALDELGLVITGTLVPFNITQONENKTNLK 480
QY 481 NQILIGVGVDSLEDDIKRLTPRFTLCPNGYFAIDPNQYVLLHPNLOPKNKSOEPTYL 540
DB 481 NQILIGVGVDSLEDDIKRLTPRFTLCPNGYFAIDPNQYVLLHPNLOPKNKSOEPTYL 540
QY 541 DFLDAELENDIKVEIKRNMKIDGSEKFTFRLVKSQDERYIDKGNRTYTWPNVGTDSL 600
DB 541 DFLDAELENDIKVEIKRNMKIDGSEKFTFRLVKSQDERYIDKGNRTYTWPNVGTDSL 600

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Db 181 NELNMTSALDEVEFKKREEDPSILMQVFGSATGLARYYPASPWVNSRTPNKIDLYDVR 240
QY 241 RFWYTOGAASPKDMLILVDSGVSGLTKLRTSVSEMLLETLSDDDPVNVAASFNMAOD 300
Db 241 RFWYTOGAASPKDMLILVDSGVSGLTKLRTSVSEMLLETLSDDDPVNVAASFNMAOD 300
QY 301 VSCFOHLVQANRNKKVYLKDAVNNITAKGIDYKKGFSAFEOQLLNNVSRANCKIIML 360
Db 301 VSCFOHLVQANRNKKVYLKDAVNNITAKGIDYKKGFSAFEOQLLNNVSRANCKIIML 360
QY 361 FPDGGERAOEITPAKYNKDKKVRVETPSVGOHNDRGPIOMACENKGYEIEPSIGAIR 420
Db 361 FPDGGERAOEITPAKYNKDKKVRVETPSVGOHNDRGPIOMACENKGYEIEPSIGAIR 420
QY 421 IMPOEYLVIGRPMVLACGAKOVOMTNYLDALDELGLVITLTPPENTTGNENKNTNK 480
Db 421 IMPOEYLVIGRPMVLACGAKOVOMTNYLDALDELGLVITLTPPENTTGNENKNTNK 480
QY 481 NOLLVGMGVDSLEDIKRLTFRFTLCPNGYFAIDPNGYVLLHPTLOPKRKSQEPVTL 540
Db 481 NOLLVGMGVDSLEDIKRLTFRFTLCPNGYFAIDPNGYVLLHPTLOPKRKSQEPVTL 540
QY 541 DELDALENDIKVEIRNKMIDGESGKERTTLVKSDERYIDKGNKTYTWTVNGTDSL 600
Db 541 DELDALENDIKVEIRNKMIDGESGKERTTLVKSDERYIDKGNKTYTWTVNGTDSL 600
QY 601 ALVLPYVSFYIKAKTEETITQARSKKGMKOSETLKPNEFSGTFTAPRDYCDMLKI 660
Db 601 ALVLPYVSFYIKAKTEETITQARSKKGMKOSETLKPNEFSGTFTAPRDYCDMLKI 660
QY 661 SDNTEFLNFEIDRKTNNPNSCTDLINRYLDAGFTNELVONYSKOKNIKGVKAR 720
Db 661 SDNTEFLNFEIDRKTNNPNSCTDLINRYLDAGFTNELVONYSKOKNIKGVKAR 720
QY 721 FVVTGCGITRVYKPEKAGEWMOENPEFYEDSFYKRSIDNDNYFTAPYFNKSGPAGESCI 780
Db 721 FVVTGCGITRVYKPEKAGEWMOENPEFYEDSFYKRSIDNDNYFTAPYFNKSGPAGESCI 780
QY 781 MYSKAEIYIOGKLPAYVGIKIDVNSMLENFTKTSIDPCAGPVCDCRNSDVMDCYI 840
Db 781 MYSKAEIYIOGKLPAYVGIKIDVNSMLENFTKTSIDPCAGPVCDCRNSDVMDCYI 840
QY 841 LDDGGLFLMANHDDYTNQIGRFEGLDPSIMRLVNIISYAFNKSXYDQSVCEPGAAPRO 900
Db 841 LDDGGLFLMANHDDYTNQIGRFEGLDPSIMRLVNIISYAFNKSXYDQSVCEPGAAPRO 900
QY 901 GAGHRARAYPSTDIHIGWMAAAMSTIQQFLSLTFPRILEAEMDDPTASLSKO 960
Db 901 GAGHRARAYPSTDIHIGWMAAAMSTIQQFLSLTFPRILEAEMDDPTASLSKO 960
QY 961 SCITEOTQVFFNDKSFSGVLDGNCNRIFFHEKILMNTNLIPIVNESKGTGCPDTRLLI 1020
Db 961 SCITEOTQVFFNDKSFSGVLDGNCNRIFFHEKILMNTNLIPIVNESKGTGCPDTRLLI 1020
QY 1021 QAEQTSDDGPPCDMKQPRTRKGPDYCFDNNALIEDYTDGCGYS 1063
Db 1021 QAEQTSDDGPPCDMKQPRTRKGPDYCFDNNALIEDYTDGCGYS 1063

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RESULT 5  
AAU01027  
ID AAU01027 standard; Protein: 1091 AA.

AC AAU01027;

DT 04-JUL-2001 (first entry)

XX pig secreted soluble alpha2delta calcium channel subunit #1 protein.

XX pig: secreted calcium channel alpha2delta subunit; alpha2delta-2;

KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;

KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;

KW filter binding assay; wheat germ lectin flashplate assay; porcine.

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XX OS Sus scrofa.
XX WO200119870-A2.
XX 22-MAR-2001.
XX 18-SEP-2000; 2000WO-EP09137.
XX 16-SEP-1999; 99US-0397550.
XX (WARN ) WARNER LAMBERT CO.
XX Brown JP, Bertella F;
XX WPI: 2001-235262/24.
XX N-PSDB: AAS01419.
XX Claim 30; Page 110-113; 160pp; English.

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The present sequence represents pig secreted calcium channel alpha2delta subunit #1 which is soluble and retains the functional characteristics of the full length or wild type alpha2delta subunit from which it is derived. The invention relates to truncated alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins which retain their affinity for radioactively labeled gabapentin. The alpha2delta subunit is 1 of the components of the heteromultimeric voltage-dependent calcium channel (VDCC) complexes present in neuronal and non-neuronal tissues including heart and skeletal muscle. Numerous soluble forms of the human calcium channel alpha2delta subunits (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the porcine calcium channel alpha2delta subunits (AAU01027-AAU01031) are described. The secreted soluble alpha2delta subunit may be used in assays e.g. scintillation proximity assay (SPA), flashplate, nickel flashplate, filter binding or wheat germ lectin flashplate assays to detect or measure the binding or interaction of a ligand (e.g. gabapentin, L-Norleucine, L-Allo-Isoleucine, L-methionine, L-leucine, L-Isoleucine, L-Valine, Spermine and/or L-phenylalanine) of a calcium channel alpha2delta subunit.

Sequence 1091 AA:

Query Match 99.2%; Score 5602; DB 22; Length 1091;  
Best local similarity 100.0%; Pred. No. 0;  
Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MAAGCLALTLTLEFQSLIGPSSQEPSPSAVTIKSWDKMOEDLVTLAKTAGVNOLVDI 60
Db 1 MAAGCLALTLTLEFQSLIGPSSQEPSPSAVTIKSWDKMOEDLVTLAKTAGVNOLVDI 60
QY 61 YEKYODLTVEPNNAROLVETIARDIEKLNSRSALVRLALEKVOAAHOMREDFASN 120
Db 61 YEKYODLTVEPNNAROLVETIARDIEKLNSRSALVRLALEKVOAAHOMREDFASN 120
QY 121 EYVYVYNAKDDLDPEKNDSEPSQRIKPFIDANRGROISYQHAANHPTDIYEGSTIVL 180
Db 121 EYVYVYNAKDDLDPEKNDSEPSQRIKPFIDANRGROISYQHAANHPTDIYEGSTIVL 180
QY 181 NELNMTSALDEVEFKKREEDPSILMQVFGSATGLARYYPASPWVNSRTPNKIDLYDVR 240
Db 181 NELNMTSALDEVEFKKREEDPSILMQVFGSATGLARYYPASPWVNSRTPNKIDLYDVR 240
QY 241 RFWYTOGAASPKDMLILVDSGVSGLTKLRTSVSEMLLETLSDDDPVNVAASFNMAOD 300
Db 241 RFWYTOGAASPKDMLILVDSGVSGLTKLRTSVSEMLLETLSDDDPVNVAASFNMAOD 300
QY 301 VSCFOHLVQANRNKKVYLKDAVNNITAKGIDYKKGFSAFEOQLLNNVSRANCKIIML 360
Db 301 VSCFOHLVQANRNKKVYLKDAVNNITAKGIDYKKGFSAFEOQLLNNVSRANCKIIML 360

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Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MAAGCLLALTLTLPFOSLLIGPSSQEPPEPSAVTIKSWDKMOEDVTLAKTASGVNOVDI 60
DB 1 MAAGCLLALTLTLPFOSLLIGPSSQEPPEPSAVTIKSWDKMOEDVTLAKTASGVNOVDI 60
QY 61 YEKYODLTYVEPNNAQOLVEIARDIEKLNSRKALVRLALEAKYQAHHOMREDFASN 120
DB 61 YEKYODLTYVEPNNAQOLVEIARDIEKLNSRKALVRLALEAKYQAHHOMREDFASN 120
QY 121 EYVYINAKDDLPEKNDSEPGSORIKPVFIDANFGROIStYQAAVHIPDIDYEGSTIVL 180
DB 121 EYVYINAKDDLPEKNDSEPGSORIKPVFIDANFGROIStYQAAVHIPDIDYEGSTIVL 180
QY 181 NEIANTSAIDVEYFKNRREDPSLLMOVFGSATGLARYYPASPWNSRTNPKIDLYVRR 240
DB 181 NEIANTSAIDVEYFKNRREDPSLLMOVFGSATGLARYYPASPWNSRTNPKIDLYVRR 240
QY 241 RPYVIGGAASPKMDLILVDVSGSVGLTLKILRTSVSEMLETISDDDEFVNASFNSNAD 300
DB 241 RPYVIGGAASPKMDLILVDVSGSVGLTLKILRTSVSEMLETISDDDEFVNASFNSNAD 300
QY 301 VSCFOHLVQANVRNKKVLDVANNITAKGITDYKKGFSFEQLLNYNSRANCKITML 360
DB 301 VSCFOHLVQANVRNKKVLDVANNITAKGITDYKKGFSFEQLLNYNSRANCKITML 360
QY 361 FTGGGERAOETPAKYNKOKKRVFTFSVGOHNYDRGPLOMACENKGYEYIPISIGAIR 420
DB 361 FTGGGERAOETPAKYNKOKKRVFTFSVGOHNYDRGPLOMACENKGYEYIPISIGAIR 420
QY 421 INTQELDVLGRPMVLADGKAKOVONTNYDALGLTGLTGLPENTIGNENKNTNK 480
DB 421 INTQELDVLGRPMVLADGKAKOVONTNYDALGLTGLTGLPENTIGNENKNTNK 480
QY 481 NQILIGMVDVSLIEDIKRLTPRTLCPNGYFAIDPNGVILLHPMLQPKNKSOEPTVL 540
DB 481 NQILIGMVDVSLIEDIKRLTPRTLCPNGYFAIDPNGVILLHPMLQPKNKSOEPTVL 540
QY 541 DFLDALDELNDIKVEIKNNKIDGESGKTRTLVKSODEYIDKGNFTYWTVPNGTDYSL 600
DB 541 DFLDALDELNDIKVEIKNNKIDGESGKTRTLVKSODEYIDKGNFTYWTVPNGTDYSL 600
QY 601 ALVLPYSEFYIKAEITITQARSKKGMKDETLKPNFEESGTYTAPRDYCDLXI 660
DB 601 ALVLPYSEFYIKAEITITQARSKKGMKDETLKPNFEESGTYTAPRDYCDLXI 660
QY 661 SDNTEFLLNFEIDRKTTPNNSCMTDLINRYLDAGFTNELVONYSKOKNIKGVKAR 720
DB 661 SDNTEFLLNFEIDRKTTPNNSCMTDLINRYLDAGFTNELVONYSKOKNIKGVKAR 720
QY 721 FYVTGDIRRVYKKEGEMWQENPETEYEFYKRSIDNNNYFTAFYKSGPAGESCI 780
DB 721 FYVTGDIRRVYKKEGEMWQENPETEYEFYKRSIDNNNYFTAFYKSGPAGESCI 780
QY 781 MYSKAVEIYIOGKLKPAVVGKIDVNSWLENFTKTSINDPACGPCCDKRSSDVMDCVI 840
DB 781 MYSKAVEIYIOGKLKPAVVGKIDVNSWLENFTKTSINDPACGPCCDKRSSDVMDCVI 840
QY 841 LDDGGFLMANHDDYTNQIGREFGEIDPSIMRHLVNI SYAFAKNSYDYOVCPEGAAPKO 900
DB 841 LDDGGFLMANHDDYTNQIGREFGEIDPSIMRHLVNI SYAFAKNSYDYOVCPEGAAPKO 900
QY 901 GAGHRAAYPSTADILHITGMATTAAMSLIOQFLSLTPRLLEAVEMDDDFITASLSKO 960
DB 901 GAGHRAAYPSTADILHITGMATTAAMSLIOQFLSLTPRLLEAVEMDDDFITASLSKO 960
QY 961 SCITEBOTYFFPNDKSPFSGVLDGNCSSRIPIHEKLMNTNLIPIWESGCTGPCDRLI 1020
DB 961 SCITEBOTYFFPNDKSPFSGVLDGNCSSRIPIHEKLMNTNLIPIWESGCTGPCDRLI 1020
QY 1021 QABQTSIDGPPCDMKOPRYRKGPDYCEDNNALLEDYTDGCGVVS 1063
DB 1021 QABQTSIDGPPCDMKOPRYRKGPDYCEDNNALLEDYTDGCGVVS 1063

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RESULT 4  
AAB62254  
ID AAB62254 standard; Protein: 1063 AA.

AAB62254;

11-JUN-2001 (first entry)

Porcine calcium channel subunit alpha2delta-4.

Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex; nervous system disorder; pain; epilepsy; anxiety; pig.

Sus scrofa.

MO200120336-A2.

22-MAR-2001.

18-SEP-2000; 2000WO-EP09136.

16-SEP-1999; 99US-0397549.

(WARN ) WARNER LAMBERT CO.

Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;

WPI: 2001-257902/26.

N-PDB; AAF57559.

Competitive binding assay for screening ligands which bind a cerebral cortical voltage-dependent calcium channel alpha2delta-1 subunit, where the ligands identified are useful for treating disorders of the nervous system, including pain.

Claim 8; Page 119-122; 158pp; English.

The invention relates to a new method for screening ligands which bind a cerebral cortical voltage-dependent calcium channel alpha2delta subunit, preferably alpha2delta-1 subunit. The method comprises contacting a secreted soluble recombinant alpha2delta-1 subunit with a ligand of interest and a labelled compound which binds the subunit, followed by measuring the level of binding of the labelled compound to alpha2delta-1 subunit. The method is useful for screening ligands, preferably biologically active products that modulate a nervous system function, which bind a cerebral cortical voltage-dependent calcium channel alpha2delta-1 subunit. The ligands identified by the method are useful for treating disorders of the nervous system, including pain, epilepsy and anxiety. The present sequence represents a porcine calcium channel subunit alpha2delta-4.

Sequence 1063 AA;

Query Match 99.2%; Score 5602; DB 22; Length 1063;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MAAGCLLALTLTLPFOSLLIGPSSQEPPEPSAVTIKSWDKMOEDVTLAKTASGVNOVDI 60
DB 1 MAAGCLLALTLTLPFOSLLIGPSSQEPPEPSAVTIKSWDKMOEDVTLAKTASGVNOVDI 60
QY 61 YEKYODLTYVEPNNAQOLVEIARDIEKLNSRKALVRLALEAKYQAHHOMREDFASN 120
DB 61 YEKYODLTYVEPNNAQOLVEIARDIEKLNSRKALVRLALEAKYQAHHOMREDFASN 120
QY 121 EYVYINAKDDLPEKNDSEPGSORIKPVFIDANFGROIStYQAAVHIPDIDYEGSTIVL 180
DB 121 EYVYINAKDDLPEKNDSEPGSORIKPVFIDANFGROIStYQAAVHIPDIDYEGSTIVL 180
QY 181 NEIANTSAIDVEYFKNRREDPSLLMOVFGSATGLARYYPASPWNSRTNPKIDLYVRR 240
DB 181 NEIANTSAIDVEYFKNRREDPSLLMOVFGSATGLARYYPASPWNSRTNPKIDLYVRR 240

```

CC which bind a cerebral cortical voltage-dependent calcium channel  
 CC alpha2delta-1 subunit. The ligands identified by the method are useful  
 CC for treating disorders of the nervous system, including pain, epilepsy  
 CC and anxiety. The present sequence represents a porcine calcium channel  
 CC subunit alpha2delta-1 deletion mutant.

XX Sequence 1069 AA;

Query Match 100.0%; Score 5650; DB 22; Length 1069;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1069; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLTLEQSLIGSSQEPSPSAVTIKSWDKQKQEDLVTLAKTASGVNQLVDI 60  
 DB 1 MAAGCLLALTLTLEQSLIGSSQEPSPSAVTIKSWDKQKQEDLVTLAKTASGVNQLVDI 60  
 QY 61 YEKYQDLYTVEPNNAKQVLAARDIEKLSSNSKALVRLALAEKVOAAHQREDFASN 120  
 DB 61 YEKYQDLYTVEPNNAKQVLAARDIEKLSSNSKALVRLALAEKVOAAHQREDFASN 120  
 QY 121 EYVYVNAKDDLDPEKNSDEPSSQRIKPFVIFDDANFGROIYOHAAVHIPDIESTIYL 180  
 DB 121 EYVYVNAKDDLDPEKNSDEPSSQRIKPFVIFDDANFGROIYOHAAVHIPDIESTIYL 180  
 QY 181 NELNMTSALDEVKKNREEDPSLIMOVGSATGLAARYPPASPVWDSRTPNKIDLYDVR 240  
 DB 181 NELNMTSALDEVKKNREEDPSLIMOVGSATGLAARYPPASPVWDSRTPNKIDLYDVR 240  
 QY 241 RPYWIGQASPKDMLILYDVGSGVSGITLKITVSSEMLETISDDDFVAVAFNSNAOD 300  
 DB 241 RPYWIGQASPKDMLILYDVGSGVSGITLKITVSSEMLETISDDDFVAVAFNSNAOD 300  
 QY 301 VSCFOHLVQAVNNAKVKVLAQVNNITAKGTFDKKGFSAFEOQLNYSRACNKTIML 360  
 DB 301 VSCFOHLVQAVNNAKVKVLAQVNNITAKGTFDKKGFSAFEOQLNYSRACNKTIML 360  
 QY 361 FTDGEERRAOEIFAKYKDKKRVNFTFVSGOHNYDRGPIQWMAECENKGYEYIPISGAIR 420  
 DB 361 FTDGEERRAOEIFAKYKDKKRVNFTFVSGOHNYDRGPIQWMAECENKGYEYIPISGAIR 420  
 QY 421 INFOEYLDVIGRPVVLADGAKOVOMTVYLDALGLVITGLTPFNITGOENKNTNK 480  
 DB 421 INFOEYLDVIGRPVVLADGAKOVOMTVYLDALGLVITGLTPFNITGOENKNTNK 480  
 QY 481 NQILGVMGVDSLEDIKRLTPRTLCPNGYFAIDPENGVYLLHPNLQPNPSCQEPVTL 540  
 DB 481 NQILGVMGVDSLEDIKRLTPRTLCPNGYFAIDPENGVYLLHPNLQPNPSCQEPVTL 540  
 QY 541 DFIDAELENDIKVEIRKMKIDGESGKTFRTLVKSODERTIDKGNRTYTWPVNGTDYSL 600  
 DB 541 DFIDAELENDIKVEIRKMKIDGESGKTFRTLVKSODERTIDKGNRTYTWPVNGTDYSL 600  
 QY 601 ALVLPYTFYIKAKIETITTOARSKKGKMDSETLKPDEESGYTFIAPRYCNDLKI 660  
 DB 601 ALVLPYTFYIKAKIETITTOARSKKGKMDSETLKPDEESGYTFIAPRYCNDLKI 660  
 QY 661 SDNNTEFLNFEIDRKTPNNSCNTDLINRYLLDAGFTNELVOMYWSKOKIKCVKAR 720  
 DB 661 SDNNTEFLNFEIDRKTPNNSCNTDLINRYLLDAGFTNELVOMYWSKOKIKCVKAR 720  
 QY 721 FVYTDGQITRVYFKAGEMNQENPEYEDSFYKRSIDNDNYVTAPYFNKSGCAYESGI 780  
 DB 721 FVYTDGQITRVYFKAGEMNQENPEYEDSFYKRSIDNDNYVTAPYFNKSGCAYESGI 780  
 QY 781 MSKAVEITYOGKILKPAVVGIRIDVNSWTEENTKTSTIRPCGAPVCDCKRNSDVMCYI 840  
 DB 781 MSKAVEITYOGKILKPAVVGIRIDVNSWTEENTKTSTIRPCGAPVCDCKRNSDVMCYI 840  
 QY 841 LDDGGFLMANHDYTNQIGRFGGEIDPSLMRLHVNISYAFNKSXYDQSVCEPGAAPKQ 900  
 DB 841 LDDGGFLMANHDYTNQIGRFGGEIDPSLMRLHVNISYAFNKSXYDQSVCEPGAAPKQ 900  
 QY 901 GAGHRSAVYVSIADILHIGWMTAAAMSLIQOFLSLTFPRLLAEVEMEDDFTASLSKQ 960

DB 901 GAGHRSAVYVSIADILHIGWMTAAAMSLIQOFLSLTFPRLLAEVEMEDDFTASLSKQ 960  
 QY 961 SCITTEQTOYFENDSKSFSGVLDGCGSKRIFVEKLMNTNLIFFIVESKGTCPDTRLLI 1020  
 DB 961 SCITTEQTOYFENDSKSFSGVLDGCGSKRIFVEKLMNTNLIFFIVESKGTCPDTRLLI 1020  
 QY 1021 QAEQTSIDGPDPCDMVKOPRYRKGPVPCPDNNALDEYTCGGVSHHHHH 1069  
 DB 1021 QAEQTSIDGPDPCDMVKOPRYRKGPVPCPDNNALDEYTCGGVSHHHHH 1069

RESULT 3  
 ID AAU01030 standard; Protein; 1063 AA.

XX AAU01030;  
 DT 04-JUL-2001 (first entry)

XX Pig secreted soluble alpha2delta calcium channel subunit #4 protein.

KW Pig; secreted calcium channel alpha2delta subunit; alpha2delta-2;  
 KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;  
 KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;  
 XX filter binding assay; wheat germ lectin flashplate assay; porcine.

OS Sus scrofa.

PN WO200119870-A2.

PD 22-MAR-2001.

PF 18-SEP-2000; 2000WO-EP09137.

PR 16-SEP-1999; 99US-0397550.

PA (WARN ) WARNER LAMBERT CO.

PI Brown JP, Bertelli F;

DR WPI: 2001-235262/24.

DR N-PSDB; AAS01422.

PT Calcium channel alpha2delta subunits; useful in e.g. SPA assays.

PT Flashplate assays; Nickel Flashplate assays. Filter binding assays or

PT wheat germ lectin flashplate assays -

XX Claim 31; Page 120-124; 160pp; English.

The present sequence represents pig secreted calcium channel alpha2delta subunit #4 which is soluble and retains the functional characteristics of the full length or wild type alpha2delta subunit from which it is derived. The invention relates to truncated alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins which retain their affinity for radioactively labelled gabapentin. The alpha2delta subunit is 1 of the components of the heteromultimeric voltage-dependent calcium channel (VDCC) complexes present in neuronal and non-neuronal tissues including heart and skeletal muscle. Numerous soluble forms of the human calcium channel alpha2delta subunits (AAU01014-AAU01024 and AAU01037-AAU01038) and 5 soluble forms of the porcine calcium channel alpha2delta subunits (AAU01027-AAU01031) are described. The secreted soluble alpha2delta subunit may be used in assays e.g. scintillation proximity assay (SPA), flashplate, nickel flashplate, filter binding or wheat germ lectin flashplate assays to detect or measure the binding or interaction of a ligand (e.g. gabapentin, L-Norleucine, L-Allo-isoleucine, L-methionine, L-leucine, L-isoleucine, L-Valine, Spectrin and/or L-Phenylalanine) of a calcium channel alpha2delta subunit.

XX Sequence 1063 AA;

Query Match 99.2%; Score 5602; DB 22; Length 1063;  
 Best Local Similarity 100.0%; Pred. No. 0;

PT Wheat Germ Lectin Flashplate assays -  
 XX  
 PS Disclosure; Page 124-127; 160pp; English.  
 XX  
 CC The present sequence represents pig secreted calcium channel alpha2delta  
 CC subunit #5 which is soluble and retains the functional characteristics  
 CC of the full length or wild type alpha2delta subunit from which it is  
 CC derived. The invention relates to truncated alpha2delta-2, alpha2delta-3  
 CC or alpha2delta-4 subunit soluble proteins which retain their affinity for  
 CC radioactively labelled gabapentin. The alpha2delta subunit is 1 of the  
 CC components of the heteromultimeric voltage-dependent calcium channel  
 CC (VCC) complexes present in neuronal and non-neuronal tissues including  
 CC heart and skeletal muscle. Numerous soluble forms of the human calcium  
 CC channel alpha2delta subunits (AA01014-AA01024 and AA01032-AA01038)  
 CC and 5 soluble forms of the porcine calcium channel alpha2delta subunits  
 CC (AA01027-AA01031) are described. The secreted soluble alpha2delta  
 CC subunit may be used in assays e.g. scintillation proximity assay (SPA),  
 CC flashplate, nickel flashplate, filter binding or wheat germ lectin  
 CC flashplate assays to detect or measure the binding or interaction of a  
 CC ligand (e.g. gabapentin, L-Norleucine, L-Allo-Isoleucine, L-methionine,  
 CC L-leucine, L-Isoleucine, L-Valine, Spermine and/or L-phenylalanine) of  
 CC a calcium channel alpha2delta subunit.  
 XX  
 XX

Sequence 1069 AA:

Query Match 100.0%; Score 5650; DB 22; Length 1069;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1069; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLALTLTLTQSLIGSSQEPSPSATYIKSWDKMEDLVTLAKTSQVQLVDI 60  
 DB 1 MAAGCLALTLTLTQSLIGSSQEPSPSATYIKSWDKMEDLVTLAKTSQVQLVDI 60  
 QY 61 YEKYODLTVEPNNAQQLVEIAARDIEKLISNRKALVRLALEAKVOAQMREDFASN 120  
 DB 61 YEKYODLTVEPNNAQQLVEIAARDIEKLISNRKALVRLALEAKVOAQMREDFASN 120  
 QY 121 EYVYTNADKDDLPKNDSEPSQRIKPVFIDANFGROIYQHAHVHPDIIYEGSTIVL 180  
 DB 121 EYVYTNADKDDLPKNDSEPSQRIKPVFIDANFGROIYQHAHVHPDIIYEGSTIVL 180  
 QY 161 NELNMTSALDVEFKKRNREDPSLLMOVGSATGLARYPAAPWVNDNSTPKIDLYDVR 240  
 DB 161 NELNMTSALDVEFKKRNREDPSLLMOVGSATGLARYPAAPWVNDNSTPKIDLYDVR 240  
 QY 241 RFWYIOGAASPKDMLILDVSGSVGLTLKLRISVSEMLETISDDPVDVNAASEFNSAD 300  
 DB 241 RFWYIOGAASPKDMLILDVSGSVGLTLKLRISVSEMLETISDDPVDVNAASEFNSAD 300  
 QY 301 VSCFOHLVQAVNRKKVLDKAVNNITAKGIDYKKGSFAFEQLNIVNSRANCKIIML 360  
 DB 301 VSCFOHLVQAVNRKKVLDKAVNNITAKGIDYKKGSFAFEQLNIVNSRANCKIIML 360  
 QY 361 FPDGGEERAEQELFAKYNKDKRVFTSVGQHNDRGIQMACENKYYEISIGAIR 420  
 DB 361 FPDGGEERAEQELFAKYNKDKRVFTSVGQHNDRGIQMACENKYYEISIGAIR 420  
 QY 421 INTQYLDVLAGHPVLAGDKAKOVMTNVYDALELGIVITGLPVEITQONENKKTMLK 480  
 DB 421 INTQYLDVLAGHPVLAGDKAKOVMTNVYDALELGIVITGLPVEITQONENKKTMLK 480  
 QY 481 NOLILGVNGVDVSLIEDIKRLPRTFLCPNGYGFALDPNGVYLLHPNLOPKNPKSQEPVTL 540  
 DB 481 NOLILGVNGVDVSLIEDIKRLPRTFLCPNGYGFALDPNGVYLLHPNLOPKNPKSQEPVTL 540  
 QY 541 DELDALENDIKVEITRNKMDIGESGEKTFRLVKSQDERYIDKGRYTTWTPVNGTDSL 600  
 DB 541 DELDALENDIKVEITRNKMDIGESGEKTFRLVKSQDERYIDKGRYTTWTPVNGTDSL 600  
 QY 601 ALVLPYTFYVYIKAKIEETIQARSKKGMKDSLETLPKDPNEESGYPFIAPRDYCNLDKI 660  
 DB 601 ALVLPYTFYVYIKAKIEETIQARSKKGMKDSLETLPKDPNEESGYPFIAPRDYCNLDKI 660

QY 661 SDNTEFLNENEFIDKTPPNNSCNTDLINRYLLDAGFTNELVQWMSKQKNIKGVKAR 720  
 DB 661 SDNTEFLNENEFIDKTPPNNSCNTDLINRYLLDAGFTNELVQWMSKQKNIKGVKAR 720  
 QY 721 FVYTDGIFRVYKKEGEMNENPTEDESFYKRSIDNNYFTAYFNKSGRGATGESI 780  
 DB 721 FVYTDGIFRVYKKEGEMNENPTEDESFYKRSIDNNYFTAYFNKSGRGATGESI 780  
 QY 781 MFKAVEITYQGLKLPAYVGIKIDVNSWIENTKTSIRDPCAGPYCDCKRNSDVMDYI 840  
 DB 781 MFKAVEITYQGLKLPAYVGIKIDVNSWIENTKTSIRDPCAGPYCDCKRNSDVMDYI 840  
 QY 841 LDGGEFLMANHDDYNTQIGRFEGEIDPSLMRLVNIYVAENKSTDYOSCEPGAAPKQ 900  
 DB 841 LDGGEFLMANHDDYNTQIGRFEGEIDPSLMRLVNIYVAENKSTDYOSCEPGAAPKQ 900  
 QY 901 GAGHRSAYVPSIADILHIGMMATRAAMSIIQOPLSLTFRPLEAVEMEDDDFTASLSKQ 960  
 DB 901 GAGHRSAYVPSIADILHIGMMATRAAMSIIQOPLSLTFRPLEAVEMEDDDFTASLSKQ 960  
 QY 961 SCITEQYQYFFNDKSKSFSGVLDCGNCSTRIFHYEKLMTNLLFIWVESKGTCPDTRLLI 1020  
 DB 961 SCITEQYQYFFNDKSKSFSGVLDCGNCSTRIFHYEKLMTNLLFIWVESKGTCPDTRLLI 1020  
 QY 1021 QABQTSDEPDCPMKOPRYRKGPDYCFDNNALDEYTDGCGVSHHHHH 1069  
 DB 1021 QABQTSDEPDCPMKOPRYRKGPDYCFDNNALDEYTDGCGVSHHHHH 1069

# RESULT 2

AA062255 standard; Protein: 1069 AA.

AA062255;

11-JUN-2001 (first entry)

Porcine calcium channel subunit alpha2delta-1 deletion mutant.

Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;

nerve system disorder; pain; epilepsy; anxiety; pig; mutant.

Sus scrofa.

MO200120336-A2.

22-MAR-2001.

18-SEP-2000; 2000MO-EP09136.

16-SEP-1999; 99US-0397549.

(WARN ) WARNER LAMBERT CO.

Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;

WPI; 2001-257902/26.

Competitive binding assay for screening ligands which bind a cerebral  
 cortical voltage-dependent calcium channel alpha2delta-1 subunit,  
 where the ligands identified are useful for treating disorders of the  
 nervous system, including pain -

Claim 8; Page 122-126; 158pp; English.

The invention relates to a new method for screening ligands which bind a  
 cerebral cortical voltage-dependent calcium channel alpha2delta subunit,  
 preferably alpha2delta-1 subunit. The method comprises contacting a  
 secreted soluble recombinant alpha2delta-1 subunit with a ligand of  
 interest and a labelled compound which binds the subunit, followed by  
 CC measuring the level of binding of the labelled compound to alpha2delta-1  
 CC subunit. The method is useful for screening ligands, preferably  
 biologically active products that modulate a nervous system function,

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 10, 2003, 14:13:50 ; Search time 34.6916 Seconds

(without alignments)  
4106.031 Million cell updates/sec

Title: US-10-090-827-9

Sequence: 1 MAACGLALTLTLFQSLILG.....NNALEDYWDGCVSHHHHH 1069

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : A.GeneSeq.101002:\*

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2: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1981.DAT:\*  
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8: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1987.DAT:\*  
9: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1988.DAT:\*  
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19: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1998.DAT:\*  
20: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1999.DAT:\*  
21: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA2000.DAT:\*  
22: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA2001.DAT:\*  
23: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5650	100.0	1069	22 AAU01031	Pig secreted solub
2	5650	100.0	1069	22 AAB62255	Porcine calcium ch
3	5602	99.2	1063	22 AAU01030	Pig secreted solub
4	5602	99.2	1063	22 AAB62254	Porcine calcium ch
5	5602	99.2	1091	22 AAU01027	Pig secreted solub
6	5602	99.2	1091	22 AAB62251	Porcine calcium ch
7	5532	97.9	1063	22 AAU01034	Human secreted sol
8	5532	97.9	1063	22 AAB62258	Human secreted sol
9	5532	97.9	1091	16 AAR71011	Human neuronal cal
10	5532	97.9	1091	19 AAW63145	Human calcium chan

11	5532	97.9	1091	21 AAB10576	Human calcium chan
12	5532	97.9	1091	22 AAU01035	Human secreted sol
13	5532	97.9	1091	22 AAB62259	Porcine calcium ch
14	5528	97.8	1091	19 AAB37879	Human calcium chan
15	5526	97.8	1091	14 AAR33553	Sequence of the al
16	5512.5	97.6	1110	19 AAW63148	Human calcium chan
17	5492.5	97.2	1086	16 AAR71013	Human neuronal cal
18	5492.5	97.2	1086	16 AAW63153	Human neuronal cal
19	5492.5	97.2	1086	21 AAB10587	Human calcium chan
20	5475.5	96.9	1084	16 AAR71015	Human neuronal chan
21	5475.5	96.9	1084	19 AAW63155	Human calcium chan
22	5475.5	96.9	1084	19 AAB10589	Human neuronal chan
23	5456	96.6	1103	16 AAR71012	Human neuronal cal
24	5456	96.6	1103	19 AAW63151	Human calcium chan
25	5456	96.6	1103	21 AAB10586	Human calcium chan
26	5446	96.4	1036	22 AAU01029	Human calcium chan
27	5446	96.4	1036	22 AAB62253	Pig secreted solub
28	5436	96.2	1079	19 AAW63154	Porcine calcium ch
29	5436	96.2	1079	21 AAB10588	Human calcium chan
30	5430	96.1	1079	16 AAR71014	Human neuronal cal
31	5410.5	95.8	1106	18 AAW7712	Rabbit skeletal cal
32	5410.5	95.8	1106	18 AAW7712	Rabbit skeletal cal
33	5410.5	95.8	1106	18 AAW7712	Rabbit skeletal cal
34	5389.5	95.4	1106	16 AAR73056	Rabbit skeletal ca
35	5380	95.2	1036	22 AAU01033	Human secreted sol
36	5380	95.2	1036	22 AAB62257	Porcine calcium ch
37	5349	94.7	1018	22 AAU01028	Human secreted sol
38	5349	94.7	1018	22 AAB62252	Porcine calcium ch
39	5288	93.6	1018	22 AAU01032	Human secreted sol
40	5288	93.6	1018	22 AAB62256	Porcine calcium ch
41	5282.5	93.5	1100	10 AAP95644	Rabbit skeletal mus
42	3069.5	54.3	1115	22 AAU01025	Human wild type al
43	3069.5	54.3	1115	22 AAB62249	Human calcium chan
44	3025.5	53.5	1109	22 AAU01016	Human secreted sol
45	3025.5	53.5	1109	22 AAB62240	Human calcium chan

#### ALIGNMENTS

RESULT 1  
AAU01031  
ID AAU01031 standard; Protein; 1069 AA.  
XX  
AC AAU01031;  
XX  
XX  
04-JUL-2001 (first entry)  
XX  
XX Pig secreted soluble alpha2delta calcium channel subunit #5 protein.  
DE  
XX Pig: secreted calcium channel alpha2delta subunit; alpha2delta-2;  
KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;  
KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;  
KW filter binding assay; wheat germ lectin flashplate assay; porcine.  
XX  
XX Sus scrofa.  
XX  
XX WO200119870-A2.  
XX  
XX 22-MAR-2001.  
XX  
XX 18-SEP-2000; 2000WC-EP09137.  
XX  
XX 16-SEP-1999; 99US-0397550.  
XX  
XX (WARN) WARNER LAMBERT CO.  
XX  
XX Brown JP, Bertelli F;  
XX WPI; 2001-235262/24.  
XX  
XX Calcium channel alpha2delta subunits, useful in e.g. SPA assays,  
XX Flashplate assays, Nickel Flashplate assays, Filter binding assays or

— — — — —







## RESULT 13

US-08-455-543A-55  
Sequence 55, Application US/08455543A  
Patent No. 5792846  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,543A  
FILING DATE: May 31, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/223,305  
FILING DATE: April 4, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/869,354  
FILING DATE: April 10, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-52517  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1079 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-455-543A-55

Query Match 96.2%; Score 5436; DB 1; Length 1079;  
Best Local Similarity 97.5%; Pred. No. 0;  
Matches 1036; Conservative 6; Mismatches 9; Indels 12; Gaps 2;

QY 1 MAAGCLLALTLTLFOSLLIGPSSOEPPSAVTIKSWDKMOEDLYTLAKTASGVNQLVDI 60  
DB 1 MAAGCLLALTLTLFOSLLIGPSSOEPPSAVTIKSWDKMOEDLYTLAKTASGVNQLVDI 60  
QY 61 YERYODLYTEPNNAQVLEIARDIEKLLNSRKALVRLALEAKVOAHHQMRDFASN 120  
DB 61 YERYODLYTEPNNAQVLEIARDIEKLLNSRKALVRLALEAKVOAHHQMRDFASN 120  
QY 121 EYVYNAKDDLPPEKNDSESGSQRIRKPVTEIDANGROISYQAAVHPTDIEESTIVL 180  
DB 121 EYVYNAKDDLPPEKNDSESGSQRIRKPVTEIDANGROISYQAAVHPTDIEESTIVL 180  
QY 181 NELMTSALDEVEFKKREDEPSLLMQVFSATGLARYYPASPMVNSRTPNKTIDYVR 240  
DB 181 NELMTSALDEVEFKKREDEPSLLMQVFSATGLARYYPASPMVNSRTPNKTIDYVR 240  
QY 241 RPYVIGGAASPKDMLILVDSVSGSLTKLIRTSVSEMLETSLDDPVNVAFSNAD 300  
DB 241 RPYVIGGAASPKDMLILVDSVSGSLTKLIRTSVSEMLETSLDDPVNVAFSNAD 300  
QY 301 VSCFOHLVQANRNKKVLDVANNITAKGITDYKKGSFAFQOLLNYSRANCKITML 360  
DB 301 VSCFOHLVQANRNKKVLDVANNITAKGITDYKKGSFAFQOLLNYSRANCKITML 360  
QY 361 FTDGGERAQEITFAKYNKDKKRVFTFSVQHNDRGPLOMACENKGYEIPISGAIR 420  
DB 361 FTDGGERAQEITFAKYNKDKKRVFTFSVQHNDRGPLOMACENKGYEIPISGAIR 420  
QY 421 INTQEYLDVLRPMVLASGAKAOVQNTNYLDALBLGLVITGTLPEVFNITGONENKTNL 480  
DB 421 INTQEYLDVLRPMVLASGAKAOVQNTNYLDALBLGLVITGTLPEVFNITGONENKTNL 480  
QY 481 NQILIGVMGVDSLEDKRLTFRFTLCBPNGYFAIDPNQVYLHNLDPKNKSOSEPTL 540  
DB 481 NQILIGVMGVDSLEDKRLTFRFTLCBPNGYFAIDPNQVYLHNLDPKNKSOSEPTL 540  
QY 541 DFLDAELENDIKVEIRNKMIDGSEGEPTRTLVKSODERYIDKGRNTYTWTPVNGTDSL 600  
DB 541 DFLDAELENDIKVEIRNKMIDGSEGEPTRTLVKSODERYIDKGRNTYTWTPVNGTDSL 600  
QY 596 ALVLPYTSFYIYKAKTEITTOARSKKGMKSEITLKPNEFESGTYTAPADYCNDLKI 660  
DB 596 ALVLPYTSFYIYKAKTEITTOARSKKGMKSEITLKPNEFESGTYTAPADYCNDLKI 660  
QY 601 ALVLPYTSFYIYKAKTEITTOARSKKGMKSEITLKPNEFESGTYTAPADYCNDLKI 660  
DB 601 ALVLPYTSFYIYKAKTEITTOARSKKGMKSEITLKPNEFESGTYTAPADYCNDLKI 660  
QY 661 SDNTEFLNFEIDRKTTPNPSCNTDLINRYLDAGTNEIYVONYSKONINGVAR 720  
DB 661 SDNTEFLNFEIDRKTTPNPSCNTDLINRYLDAGTNEIYVONYSKONINGVAR 720  
QY 709 FVYTDGITRVYPKEAGENWQENPETYEDSFYKRSIDNDNYVFTAPYFNKSGPAYESGI 768  
DB 709 FVYTDGITRVYPKEAGENWQENPETYEDSFYKRSIDNDNYVFTAPYFNKSGPAYESGI 768  
QY 781 MYSKAVEIYIQGLKLPAYVGIKIDVNSWIEFTKTSINDPAGAPVCCDKRNSDVMDCVI 840  
DB 781 MYSKAVEIYIQGLKLPAYVGIKIDVNSWIEFTKTSINDPAGAPVCCDKRNSDVMDCVI 840  
QY 841 LDGCGFLMANHDDYTNQIGRFGFIDPSLMRLVNI SYAANKSVDYOSVEPPAAPKO 900  
DB 841 LDGCGFLMANHDDYTNQIGRFGFIDPSLMRLVNI SYAANKSVDYOSVEPPAAPKO 900  
QY 889 GAGHRSAVYPSVADIIQIGMATAAAMSIIOQFLSLTFPRLLAEVEMDDFTASLSKQ 948  
DB 889 GAGHRSAVYPSVADIIQIGMATAAAMSIIOQFLSLTFPRLLAEVEMDDFTASLSKQ 948  
QY 961 SCITTEOTYFFNDKSKSFGVLDGCKSKLIFHEVEKLMNTNLFIVYESGTCPCDTRLLI 1020  
DB 961 SCITTEOTYFFNDKSKSFGVLDGCKSKLIFHEVEKLMNTNLFIVYESGTCPCDTRLLI 1020  
QY 1021 QAEOTSDGPPCDPMVKOPRRYRKGPDVCFDNNALLEDYTDGGSYS 1063  
DB 1021 QAEOTSDGPPCDPMVKOPRRYRKGPDVCFDNNALLEDYTDGGSYS 1063

Sequence 53, Application US/08223305C  
 Patent No. 5851824  
 GENERAL INFORMATION:  
 APPLICANT: Harpold, Michael  
 APPLICANT: Ellis, Steven  
 APPLICANT: Williams, Mark  
 APPLICANT: Feldman, Daniel  
 APPLICANT: McCue, Ann  
 APPLICANT: Brenner, Robert  
 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
 TITLE OF INVENTION: METHODS  
 NUMBER OF SEQUENCES: 57  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Brown, Martin, Haller & McClain  
 STREET: 1660 Union Street  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92101-2926  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/223,305C  
 FILING DATE: April 4, 1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/868,354  
 FILING DATE: April 10, 1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/745,206  
 FILING DATE: 15-AUG-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/620,250  
 FILING DATE: 30-NOV-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/482,384  
 FILING DATE: 20-FEB-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/603,751  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/US89/01408  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/176,899  
 FILING DATE: 04-APR-1988  
 AUTHOR/AGENT INFORMATION:  
 NAME: Seidman, Stephanie L.  
 REGISTRATION NUMBER: 33,779  
 REFERENCE/DOCKET NUMBER: 52516 (P519739)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 238-0999  
 TELEFAX: (619) 238-0062  
 INFORMATION FOR SEQ ID NO: 53:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1103 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-223-305C-53

Query Match 96.6%; Score 5456; DB 2; Length 1103;  
 Best Local Similarity 96.2%; Pred. No. 0;  
 Matches 1041; Conservative 6; Mismatches 9; Indels 26; Gaps 2;

QY 1 MAAGCLLAATTTTFOSSLIGSSQEPSPASVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60  
 DB 1 MAAGCLLAATTTTFOSSLIGSSQEPSPASVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60

QY 61 YEKYODLVTVPEENNAKROLVETIARDIEKLLNSRSKALVRLALEAKVQAQAQWREDFASN 120  
 DB 61 YEKYODLVTVPEENNAKROLVETIARDIEKLLNSRSKALVRLALEAKVQAQAQWREDFASN 120  
 QY 121 EYVYNAKDDLDPEKNDSPPGSSORIKPVEIDPANGROISVOHAIVH1PTDIEGSTVL 180  
 DB 121 EYVYNAKDDLDPEKNDSPPGSSORIKPVEIDPANGROISVOHAIVH1PTDIEGSTVL 180  
 QY 181 NELNMTSALDEVFKKREEDPSLLWQVGSATGLARYYPASPMVDSRTPKIDLYDVR 240  
 DB 181 NELNMTSALDEVFKKREEDPSLLWQVGSATGLARYYPASPMVDSRTPKIDLYDVR 240  
 QY 241 RPYITOGAASPRDMLLVVSGSVSLTKLIRTSVSEMLETLSDDDVYVNASFNSNOD 300  
 DB 241 RPYITOGAASPRDMLLVVSGSVSLTKLIRTSVSEMLETLSDDDVYVNASFNSNOD 300  
 QY 301 VSCFOHLVQANRNKKVLKDAVNNITAKITDYKGFSAFQOLLNVYSRANCKIIML 360  
 DB 301 VSCFOHLVQANRNKKVLKDAVNNITAKITDYKGFSAFQOLLNVYSRANCKIIML 360  
 QY 361 FTDGGEERAQEIFAKYNNKDKKRVFTFSVGHNYDRGP1QWNAKCNKGYEIPSIGAIR 420  
 DB 361 FTDGGEERAQEIFAKYNNKDKKRVFTFSVGHNYDRGP1QWNAKCNKGYEIPSIGAIR 420  
 QY 421 INTQEVLDVLRPMVLAGKAKOVQWNTNVLDALEGLVITTLVFNNTGQENKTNLK 480  
 DB 421 INTQEVLDVLRPMVLAGKAKOVQWNTNVLDALEGLVITTLVFNNTGQENKTNLK 480  
 QY 481 NQILGVMGVDSVLEEDIKLTPFTLCPNGYFAIDPNGYVLLHNPLOPK----- 530  
 DB 481 NQILGVMGVDSVLEEDIKLTPFTLCPNGYFAIDPNGYVLLHNPLOPK----- 530  
 QY 531 -----NPKSQEPVTLDFDLAELNDIKVEIRNMKIDSGEGTEFTLVKSODERYI 581  
 DB 531 -----NPKSQEPVTLDFDLAELNDIKVEIRNMKIDSGEGTEFTLVKSODERYI 581  
 QY 581 LKRRPNIONPKSQEPVTLDFDLAELNDIKVEIRNMKIDSGEGTEFTLVKSODERYI 600  
 DB 581 LKRRPNIONPKSQEPVTLDFDLAELNDIKVEIRNMKIDSGEGTEFTLVKSODERYI 600  
 QY 601 DKGNRTYTWTPVNGTYSALVLPYTSFYIKAKIETTORSKKMGKDESETLKPDNF 641  
 DB 601 DKGNRTYTWTPVNGTYSALVLPYTSFYIKAKIETTORSKKMGKDESETLKPDNF 641  
 QY 642 EESGYTFIAPRDYCNLDKISDNTTEFLNFEIDRKTNNPNSCNTDLINRYLDAGFTN 701  
 DB 642 EESGYTFIAPRDYCNLDKISDNTTEFLNFEIDRKTNNPNSCNTDLINRYLDAGFTN 701  
 QY 702 ELVQNTWSKOKNIKGYKARVYTDGITRYYPKEAGEENQENPEYEDSFYKRSLDNMY 761  
 DB 702 ELVQNTWSKOKNIKGYKARVYTDGITRYYPKEAGEENQENPEYEDSFYKRSLDNMY 761  
 QY 762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKRAVVGIKIDVMSWLENFTKTSIRDP 821  
 DB 762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKRAVVGIKIDVMSWLENFTKTSIRDP 821  
 QY 822 CAGPVCDCRNSDVMDCVILDDGGFLLMANHDDYTNQIRFGEIDPSIMRLVNI SYVA 881  
 DB 822 CAGPVCDCRNSDVMDCVILDDGGFLLMANHDDYTNQIRFGEIDPSIMRLVNI SYVA 881  
 QY 882 FNSYDQVSCYCEGAPKQAGHRSAYVPSADILIIIGMMATTAASIIIOFLSTFPR 941  
 DB 882 FNSYDQVSCYCEGAPKQAGHRSAYVPSADILIIIGMMATTAASIIIOFLSTFPR 941  
 QY 942 LLEAVEMEDDFTASLSKQSCITEQTYFEDNDSKFSGLVDCGNSRIFFHEKILMNTL 1001  
 DB 942 LLEAVEMEDDFTASLSKQSCITEQTYFEDNDSKFSGLVDCGNSRIFFHEKILMNTL 1001  
 QY 1001 IFIIVESKGTCPDTRILLIOAEOISDGPDCDMVWKPRIKKGPDVCFDNNALLEDYDCCG 1061  
 DB 1001 IFIIVESKGTCPDTRILLIOAEOISDGPDCDMVWKPRIKKGPDVCFDNNALLEDYDCCG 1061  
 QY 1062 VS 1063  
 DB 1062 VS 1063  
 QY 1074 VS 1075  
 DB 1074 VS 1075

APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,543A  
FILING DATE: May 31, 1995  
APPLICATION NUMBER: 08/223,305  
FILING DATE: April 4, 1994  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-52517  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1103 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-455-543A-53

Query March 96.64; Score 5456; DB 1; Length 1103;  
Best Local Similarity 96.28; Pred. No. 0;  
Matches 1041; Conservative 6; Mismatches 9; Indels 26; Gaps 2;

QY 1 MAACGLATLTTLTSSQSSQPPSAVTIKSWTDKMOEDVTLAKTASGVNQLVDI 60  
Db 1 MAACGLATLTTLTSSQSSQPPSAVTIKSWTDKMOEDVTLAKTASGVNQLVDI 60  
QY 61 YEKQDLYTVEPNNAQVETIARDIEKLNSKALVRLALEAKVOAHHQREDFASN 120

Db 61 YEKQDLYTVEPNNAQVETIARDIEKLNSKALVRLALEAKVOAHHQREDFASN 120  
QY 121 EVVYNAKDDLDPEKNDSPEQSRIKPVETIDANFGROISYOAHAHVIPTDIYEGSTIVL 180  
Db 121 EVVYNAKDDLDPEKNDSPEQSRIKPVETIDANFGROISYOAHAHVIPTDIYEGSTIVL 180  
QY 181 NELNMTSALDEVEFKKNREDEPSLLMOVFGSATGLARIYPASPVWDSNRTPKIDLYVRR 240  
Db 181 NELNMTSALDEVEFKKNREDEPSLLMOVFGSATGLARIYPASPVWDSNRTPKIDLYVRR 240  
QY 241 RPPWYIQAASPKDMLITVDVSGSVGLTKLIPISVSMLETTSDDDPFVNAVSPNSAOD 300  
Db 241 RPPWYIQAASPKDMLITVDVSGSVGLTKLIPISVSMLETTSDDDPFVNAVSPNSAOD 300  
QY 301 VSCFOHLVQAVNRKKVYLKDAVNNITAKGJTDYKGFSAFEOILLNVSRANCKIIML 360  
Db 301 VSCFOHLVQAVNRKKVYLKDAVNNITAKGJTDYKGFSAFEOILLNVSRANCKIIML 360  
QY 361 FTDGEERAQRIIFAKYNNKDKRVFETFSVGONHNRDGPIDGMACENKGYEETIPISIGAIR 420  
Db 361 FTDGEERAQRIIFAKYNNKDKRVFETFSVGONHNRDGPIDGMACENKGYEETIPISIGAIR 420  
QY 421 INTQEYLDVIGRPVYLAGDRAKQVQWNTNVLDALEGLVITGLPVNITGONENKTNLK 480  
Db 421 INTQEYLDVIGRPVYLAGDRAKQVQWNTNVLDALEGLVITGLPVNITGONENKTNLK 480  
QY 481 NOLLIGVWGVVSLIEDIKRLTPRTLCPPNGYFPAIDPNGVYLLHPNLQPK----- 530  
Db 481 NOLLIGVWGVVSLIEDIKRLTPRTLCPPNGYFPAIDPNGVYLLHPNLQPK----- 530  
QY 531 -----NPKSQEPTLDFLDALEENDIKVEIRNNMIDGSEGETFRTLYSODERTY 581  
Db 531 -----NPKSQEPTLDFLDALEENDIKVEIRNNMIDGSEGETFRTLYSODERTY 581  
QY 582 DKGRITVTPVNGTDSIALVLPYSFYIKAKIEETIQAASKKGMKMDSETLPDNF 641  
Db 582 DKGRITVTPVNGTDSIALVLPYSFYIKAKIEETIQAASKKGMKMDSETLPDNF 641  
QY 601 DKGNRTYTWTPVNGTDSIALVLPYSFYIKAKIEETIQAASKKGMKMDSETLPDNF 653  
Db 601 DKGNRTYTWTPVNGTDSIALVLPYSFYIKAKIEETIQAASKKGMKMDSETLPDNF 653  
QY 642 EESGTFIAPRDYCNLDKISDNNTEFLNPNEDIDKTPNPNPCNDLIRVYLDAGFTN 701  
Db 642 EESGTFIAPRDYCNLDKISDNNTEFLNPNEDIDKTPNPNPCNDLIRVYLDAGFTN 701  
QY 702 ELVQNTWSKQNTIKGVKARFVTDGITRYYPKEAGENMOENETEDSEFYKSLDNDNY 761  
Db 702 ELVQNTWSKQNTIKGVKARFVTDGITRYYPKEAGENMOENETEDSEFYKSLDNDNY 761  
QY 762 VFTAPYFNKSGPRAYESGIMVSKAVEIYIOGKILKPAVVGIKIDVNSWIENTFTSIRDP 821  
Db 762 VFTAPYFNKSGPRAYESGIMVSKAVEIYIOGKILKPAVVGIKIDVNSWIENTFTSIRDP 821  
QY 822 CAGPVCDCRNSDVMDCVIIDDGFLMANHDDYTQIGRFGETIDPSIMRHLVNTSYVA 881  
Db 822 CAGPVCDCRNSDVMDCVIIDDGFLMANHDDYTQIGRFGETIDPSIMRHLVNTSYVA 881  
QY 882 FNSKSYDQSVCEGPAAPKOGAGHRSAYVPSIADILHIGMWATAAAMSIIQOGLLSITFPR 941  
Db 882 FNSKSYDQSVCEGPAAPKOGAGHRSAYVPSIADILHIGMWATAAAMSIIQOGLLSITFPR 941  
QY 942 LLEAVEMEDDDFTASLSKQSCITEQYQFPFNDKSFSSVLDCCGNSRIFHEKIMLNTNL 1001  
Db 942 LLEAVEMEDDDFTASLSKQSCITEQYQFPFNDKSFSSVLDCCGNSRIFHEKIMLNTNL 1001  
QY 1002 IFIMVSKGTCPCDPTRLILQAEQTSIDGPPCDMVVQPRYRKPDVCFDNNALIEDYTDGCG 1061  
Db 1002 IFIMVSKGTCPCDPTRLILQAEQTSIDGPPCDMVVQPRYRKPDVCFDNNALIEDYTDGCG 1061  
QY 1062 VS 1063  
Db 1062 VS 1063  
QY 1074 VS 1075  
Db 1074 VS 1075

RESULT 12  
US-08-223-305C-53

APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/223,305C  
FILING DATE: April 4, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 52516 (P519739)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1084 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-223-305C-56

Query Match 96.9%; Score 5475.5; DB 2; Length 1084;  
Best Local Similarity 97.9%; Pred. No. 0;  
Matches 1041; Conservative 6; Mismatches 9; Indels 7; Gaps 1;

QY 1 MAAGCLALTLTFLQSLIGPSSQEPSPSAVTIKSWDKQMEDLVTTAKTASGVNQLVDI 60  
DB 1 MAAGCLALTLTFLQSLIGPSSQEPSPSAVTIKSWDKQMEDLVTTAKTASGVNQLVDI 60  
QY 61 YEKYODLTVEPNNAKQIVETIARDIEKLNSRKALVRLALEAKVQAIAHQWREDFASN 120  
DB 61 YEKYODLTVEPNNAKQIVETIARDIEKLNSRKALVRLALEAKVQAIAHQWREDFASN 120

QY 121 EYVYNNAKDDLDEPKNDSEPSQRIKPFVIDANFGQISYQAAVHIPDIYEGSTIVL 180  
DB 121 EYVYNNAKDDLDEPKNDSEPSQRIKPFVIDANFGQISYQAAVHIPDIYEGSTIVL 180  
QY 181 NELNMTSALDEVRKKNREEDPSLLMOVFGSATGLARYYPASPVWDSRPNNKIDLYDVR 240  
DB 181 NELNMTSALDEVRKKNREEDPSLLMOVFGSATGLARYYPASPVWDSRPNNKIDLYDVR 240  
QY 241 RPWYIOGAASPKDMLILVDYSGSVGLTLKIRTSVSEMETLSDDDFNVVASFNSNAD 300  
DB 241 RPWYIOGAASPKDMLILVDYSGSVGLTLKIRTSVSEMETLSDDDFNVVASFNSNAD 300  
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITYDKKGSEFAEQLLYNVSRANCKIIML 360  
DB 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITYDKKGSEFAEQLLYNVSRANCKIIML 360  
QY 361 FTDGEERAQEIYAKYKDKKVRFTFVSQOHNYDRGPIOMACENKGYEIEPSIGAIR 420  
DB 361 FTDGEERAQEIYAKYKDKKVRFTFVSQOHNYDRGPIOMACENKGYEIEPSIGAIR 420  
QY 421 INFOEYLDVGRPVYLAGDKAKOVMTNVLDALELGIVTGTLPVFNITGQENKTNLK 480  
DB 421 INFOEYLDVGRPVYLAGDKAKOVMTNVLDALELGIVTGTLPVFNITGQENKTNLK 480  
QY 481 NQILIGVGVDSLEDIKRLTPRETLCPNGYFPAIDPNCYVLLHPNLOPKNPSQEPVTL 540  
DB 481 NQILIGVGVDSLEDIKRLTPRETLCPNGYFPAIDPNCYVLLHPNLOPKNPSQEPVTL 540  
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DB 541 DFLDALELNDIKVEIKNMKIDSGSEKTFRLVKSODERYIDKGNRTYWTVPNGTDSL 600  
QY 601 ALVLPYTSFYIKAKIETITTOARSKKGMKDESETLKPOMEESGTFIAPRYCNDLAI 660  
DB 601 ALVLPYTSFYIKAKIETITTOARSKKGMKDESETLKPOMEESGTFIAPRYCNDLAI 660  
QY 661 SDNTEFLNENEFIDKRTPNPNSCNTDLINRYLDAGFNLVQYWSKOKNIKGVKAR 720  
DB 661 SDNTEFLNENEFIDKRTPNPNSCNTDLINRYLDAGFNLVQYWSKOKNIKGVKAR 720  
QY 721 FVYTDGCTIRYVREKAGENNQENPEYEDSFYKRSIDNDNYVTAPYFNKSGGAYESGI 780  
DB 721 FVYTDGCTIRYVREKAGENNQENPEYEDSFYKRSIDNDNYVTAPYFNKSGGAYESGI 780  
QY 781 MVSRAVEIYIOGKLKRAYVGIRKIDVNSWTEFTKTSIRPCAGPVCDCKRNSDVMDCVI 840  
DB 781 MVSRAVEIYIOGKLKRAYVGIRKIDVNSWTEFTKTSIRPCAGPVCDCKRNSDVMDCVI 840  
QY 841 LDDGFLMANHDDYTNOIGRFGELIDPSLMRLVINSYVAFNKSVDYQSVCEPGAAPQ 900  
DB 841 LDDGFLMANHDDYTNOIGRFGELIDPSLMRLVINSYVAFNKSVDYQSVCEPGAAPQ 900  
QY 901 GAGHRSAYVPSIADILHIGWMTAAAMSIIQOFLSLTFRLLAEVEMEDDFTASLSQ 960  
DB 901 GAGHRSAYVPSIADILHIGWMTAAAMSIIQOFLSLTFRLLAEVEMEDDFTASLSQ 960  
QY 961 SCITEQOYFFENDSKSFSGLDGCNCSRFHEHEKLMNTLFIIMVESGTCGCDTRILLI 1020  
DB 961 SCITEQOYFFENDSKSFSGLDGCNCSRFHEHEKLMNTLFIIMVESGTCGCDTRILLI 1020  
QY 1021 QAEQTSIDGPPDCMVKQPRYRKGPVOCFNNALDEYTDGCVS 1063  
DB 1021 QAEQTSIDGPPDCMVKQPRYRKGPVOCFNNALDEYTDGCVS 1063  
QY 1014 QAEQTSIDGPPDCMVKQPRYRKGPVOCFNNALDEYTDGCVS 1056  
DB 1014 QAEQTSIDGPPDCMVKQPRYRKGPVOCFNNALDEYTDGCVS 1056

RESULT 11  
US-08-455-543A-53  
Sequence 53; Application us/08455543A  
Patent No. 5792846  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven

APPLICANT: Ellis, Steven  
 APPLICANT: Williams, Mark  
 APPLICANT: Feldman, Daniel  
 APPLICANT: McCue, Ann  
 APPLICANT: Brenner, Robert  
 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
 NUMBER OF SEQUENCES: 57  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Brown, Martin, Haller & McClain  
 STREET: 1660 Union Street  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92101-2926  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/455,543A  
 FILING DATE: May 31, 1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/223,305  
 FILING DATE: April 4, 1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/868,354  
 FILING DATE: April 10, 1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/745,206  
 FILING DATE: 15-AUG-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/620,250  
 FILING DATE: 30-NOV-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/482,384  
 FILING DATE: 20-FEB-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/603,751  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/US89/01408  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/176,899  
 FILING DATE: 04-APR-1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie L.  
 REGISTRATION NUMBER: 33,779  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619)238-0999  
 TELEFAX: (619)238-0062  
 INFORMATION FOR SEQ ID NO: 56:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1084 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-455-543A-56

Query Match 96.9%; Score 5475.5; DB 1; Length 1084;  
 Best Local Similarity 97.9%; Pred. No. 0;  
 Matches 1041; Conservative 6; Mismatches 9; Indels 7; Gaps 1;

QY 1 MAAGCLATLTLFOSLLIGSSQEPFSPAVITKSWDKMOEDLVYLAKTASGVNOLVDI 60  
 Db 1 MAAGCLATLTLFOSLLIGSSQEPFSPAVITKSWDKMOEDLVYLAKTASGVNOLVDI 60  
 QY 61 YEKYODLYVEPNNAQVLEIAARDIEKLISNRKALVRLALEAEKVQAHQWREDPASN 120

Db 61 YEKYODLYVEPNNAQVLEIAARDIEKLISNRKALVRLALEAEKVQAHQWREDPASN 120  
 QY 121 EYVYNAKADDDPEKNDSEPSORIKPFVIDANGROISYQAAVHPPTIYSGSTIVL 180  
 Db 121 EYVYNAKADDDPEKNDSEPSORIKPFVIDANGROISYQAAVHPPTIYSGSTIVL 180  
 QY 181 NELNMTSALDEYFKKKNREDEPSLLMQVPGSATGLARYYPASPWNDRTPNKIDLYVNR 240  
 Db 181 NELNMTSALDEYFKKKNREDEPSLLMQVPGSATGLARYYPASPWNDRTPNKIDLYVNR 240  
 QY 241 RPYITQGAASPRKMLILVDGSGVSGTLKILRISVSMELETSLDDDFVYNVANSNAOD 300  
 Db 241 RPYITQGAASPRKMLILVDGSGVSGTLKILRISVSMELETSLDDDFVYNVANSNAOD 300  
 QY 301 VSCFOHLVQANRANKVLDKAVNNNTAGITDYKGFSAFEOQLNNTVSNRANKIIML 360  
 Db 301 VSCFOHLVQANRANKVLDKAVNNNTAGITDYKGFSAFEOQLNNTVSNRANKIIML 360  
 QY 361 FTDGGEERAQELIPAKYNNKRVKRVFTFSVGOHNDRGP10MACENKGYEIPISGAIR 420  
 Db 361 FTDGGEERAQELIPAKYNNKRVKRVFTFSVGOHNDRGP10MACENKGYEIPISGAIR 420  
 QY 421 INTQGYLLVLRPMVLAQDAKQOVQWTVYLDALGLVITGTLVPRNITGQNKNTNLK 480  
 Db 421 INTQGYLLVLRPMVLAQDAKQOVQWTVYLDALGLVITGTLVPRNITGQNKNTNLK 480  
 QY 481 NOLIIGVGVDSLEDIRLTPRFTLCPNGYFFAIDPAGYLLPNLOPKPKSOEPTL 540  
 Db 481 NOLIIGVGVDSLEDIRLTPRFTLCPNGYFFAIDPAGYLLPNLOPKPKSOEPTL 540  
 QY 541 DELDAELNDIKVELIRNMKIDGSEGEKTRLVNSODERYIDKGNRTYTWTPVNGTYSL 600  
 Db 541 DELDAELNDIKVELIRNMKIDGSEGEKTRLVNSODERYIDKGNRTYTWTPVNGTYSL 600  
 QY 601 ALVLTYSFYITKAKIETITQANSKKGMKDSFTLAKDNFEESGYTFIAPRDYCNLDKI 660  
 Db 601 ALVLTYSFYITKAKIETITQANSKKGMKDSFTLAKDNFEESGYTFIAPRDYCNLDKI 660  
 QY 661 SDNNTPEFLNNEFTDRKTPNNPSCNTDLINRVLLDAGFTLQVNTVWSKKNIKGYKAR 720  
 Db 661 SDNNTPEFLNNEFTDRKTPNNPSCNTDLINRVLLDAGFTLQVNTVWSKKNIKGYKAR 720  
 QY 721 FVYTDGGLTRVYPKKEGEMOENPETYEDSFYKRSLDNDNVVTPAPFNKSGPAYESGI 780  
 Db 721 FVYTDGGLTRVYPKKEGEMOENPETYEDSFYKRSLDNDNVVTPAPFNKSGPAYESGI 780  
 QY 781 MYSKAVEITYIOGKLKPAVVGIKIDVNSWINEFTKTSIRDPACGAPVDCRNSVMDCVI 840  
 Db 781 MYSKAVEITYIOGKLKPAVVGIKIDVNSWINEFTKTSIRDPACGAPVDCRNSVMDCVI 840  
 QY 841 LDDGGFLMANNDVYTNIGRFFGEIDPSLMRHLVNTISVYFNFNSYDQSCGEGAAAPKQ 900  
 Db 841 LDDGGFLMANNDVYTNIGRFFGEIDPSLMRHLVNTISVYFNFNSYDQSCGEGAAAPKQ 900  
 QY 901 GAGHSAYVPSIADILHIGMATAAAMSIILOOFLSTLFPRLBAVEMEDDFTASLSKQ 960  
 Db 901 GAGHSAYVPSIADILHIGMATAAAMSIILOOFLSTLFPRLBAVEMEDDFTASLSKQ 960  
 QY 961 SCITQOTQYFFPDNDKSKSSGVLDGNCGRIRHVEKLMNTNLIIFIMWSKGTCPDTRLLI 1020  
 Db 961 SCITQOTQYFFPDNDKSKSSGVLDGNCGRIRHVEKLMNTNLIIFIMWSKGTCPDTRLLI 1020  
 QY 1021 QAEQTSIDGPNPCDMVKQPRYRKGPVYCFDNNVLEDTYDCGVS 1056  
 Db 1021 QAEQTSIDGPNPCDMVKQPRYRKGPVYCFDNNVLEDTYDCGVS 1056

RESULT 10  
 US-08-223-305C-56  
 ; Sequence 56 Application US/08223305C  
 ; Patent No. 5651824  
 ; GENERAL INFORMATION:

GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
ZIP: 92101-2926  
COUNTRY: USA  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/223,305C  
FILING DATE: April 4, 1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET INFORMATION: 52516 (P519739)  
TELEPHONE: (619)238-0062  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1086 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-223-305C-54

Query Match 97.2%; Score 5492.5; DB 2; Length 1086;  
Best Local Similarity 98.2%; Pred. No. 0;  
Matches 1044; Conservative 6; Mismatches 8; Indels 5; Gaps 1.

QY 1 MAAGCLLALTLTLFOSLLIGPSSQEPFSAVTIKSWDKMDELYTLAKTASGVNQLVDI 60  
DB 1 MAAGCLLALTLTLFOSLLIGPSSQEPFSAVTIKSWDKMDELYTLAKTASGVNQLVDI 60  
QY 61 YEKYQDLTYVEPNNAQQLVEIAARDIEKLNSKALVSLALEAEKYQAAHQNRDEFSAN 120

DB 61 YEKYQDLTYVEPNNAQQLVEIAARDIEKLNSKALVSLALEAEKYQAAHQNRDEFSAN 120  
QY 121 EVVYYNNAKDDLDPEKNSPEQSQRIRKPVFIIDANFGHIOYQAAVHIPDIYEGSTIYL 180  
DB 121 EVVYYNNAKDDLDPEKNSPEQSQRIRKPVFIIDANFGHIOYQAAVHIPDIYEGSTIYL 180  
QY 181 NELNMTSALDEVEFKKNEDEPSLLIMOVGSATGLARYPASPVWDSRPNKIDLYDVR 240  
DB 181 NELNMTSALDEVEFKKNEDEPSLLIMOVGSATGLARYPASPVWDSRPNKIDLYDVR 240  
QY 241 RPYWIOGAASPKDMLILVDVSGSYGLTLKILIRSVSEMELETJSDDEPVVASFNSAOD 300  
DB 241 RPYWIOGAASPKDMLILVDVSGSYGLTLKILIRSVSEMELETJSDDEPVVASFNSAOD 300  
QY 301 VSCFOHLVQAVNRKRVKYLKADVNNITAKGJTDYKKGFSFAEQLNANVSRAONKIIML 360  
DB 301 VSCFOHLVQAVNRKRVKYLKADVNNITAKGJTDYKKGFSFAEQLNANVSRAONKIIML 360  
QY 361 FTDGGEERADEIFAKYKNDKKVRFVTSVGOHNDRGPIDWMAECENKGYEIPISGAIR 420  
DB 361 FTDGGEERADEIFAKYKNDKKVRFVTSVGOHNDRGPIDWMAECENKGYEIPISGAIR 420  
QY 421 INTQEVYLDVGRPMVLAGDKAKOVQWNTNYIDALELGLVITGLTPVFNITGONENKTNLK 480  
DB 421 INTQEVYLDVGRPMVLAGDKAKOVQWNTNYIDALELGLVITGLTPVFNITGONENKTNLK 480  
QY 481 NQLILGVKGVVSLIEDIKRLPRFTLCPNGYFEAIDPNGVYLALPNLOPNKPSQEPVTL 540  
DB 481 NQLILGVKGVVSLIEDIKRLPRFTLCPNGYFEAIDPNGVYLALPNLOPNKPSQEPVTL 540  
QY 541 DFLDAELNDIKVEIRKMKIDGESGKFTFLVKSQDERYIDKGNRTYTTPVNGTIDYSL 600  
DB 541 DFLDAELNDIKVEIRKMKIDGESGKFTFLVKSQDERYIDKGNRTYTTPVNGTIDYSL 600  
QY 601 ALVLPYSFYIKAKIEETITQARSKKGMKDSFTLKPDPESGYEFLAPROYCNDLKI 660  
DB 601 ALVLPYSFYIKAKIEETITQARSKKGMKDSFTLKPDPESGYEFLAPROYCNDLKI 660  
QY 661 SDNNTFELNPFIDRKTNPNSCNTDLINRYLLDAGFTNELVQWNSKOKNIKGVKAR 720  
DB 661 SDNNTFELNPFIDRKTNPNSCNTDLINRYLLDAGFTNELVQWNSKOKNIKGVKAR 720  
QY 721 FVYTDGGITRYPKEAGENMOENPETEYEDSFYKSLDNDYVFTAPYFNKSGPANESEGI 780  
DB 721 FVYTDGGITRYPKEAGENMOENPETEYEDSFYKSLDNDYVFTAPYFNKSGPANESEGI 780  
QY 781 MYSKAVEIYIOGKLLKPAVVGIRKIDVNSWTEFNFTKTSIRDPACGAPVDCCKRNSDVMCVI 840  
DB 781 MYSKAVEIYIOGKLLKPAVVGIRKIDVNSWTEFNFTKTSIRDPACGAPVDCCKRNSDVMCVI 840  
QY 841 LDDGCFLLMANHDDYTNQIGRFGEIDPSLMRHLVNISVYAFNKSXYQSGVCEGAPAKQ 900  
DB 841 LDDGCFLLMANHDDYTNQIGRFGEIDPSLMRHLVNISVYAFNKSXYQSGVCEGAPAKQ 900  
QY 901 GAGHRSATVPSIAIDILHIGWMTAAAMSILQOFLSLTFPRLLAEVMEDDDTFASLSKQ 960  
DB 901 GAGHRSATVPSIAIDILHIGWMTAAAMSILQOFLSLTFPRLLAEVMEDDDTFASLSKQ 960  
QY 961 SCITEOIOYFFDNDNSKSPSGVLDGNCSTRIFHYEKLKLNNTNLIIFMWSKGCPCPDFTLLI 1020  
DB 961 SCITEOIOYFFDNDNSKSPSGVLDGNCSTRIFHYEKLKLNNTNLIIFMWSKGCPCPDFTLLI 1020  
QY 1021 QAEQTSDBGPDPCDMVKOPRYRKGPVCFDNNALADYTDGCGVS 1063  
DB 1021 QAEQTSDBGPDPCDMVKOPRYRKGPVCFDNNALADYTDGCGVS 1063  
QY 1016 QAEQTSDBGPDPCDMVKOPRYRKGPVCFDNNALADYTDGCGVS 1098  
DB 1016 QAEQTSDBGPDPCDMVKOPRYRKGPVCFDNNALADYTDGCGVS 1098

RESULT 9  
US-08-455-543A-56  
Sequence 56, Application US/08455543A  
Patent No. 5792846  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael

APPLICANT: Harpold, Michael  
 APPLICANT: Ellis, Steven  
 APPLICANT: Williams, Mark  
 APPLICANT: Feldman, Daniel  
 APPLICANT: McCue, Ann  
 APPLICANT: Brenner, Robert  
 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
 NUMBER OF SEQUENCES: 57  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Brown, Martin, Haller & McClain  
 STREET: 1660 Union Street  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92101-2926  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/455,543A  
 FILING DATE: May 31, 1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/223,305  
 FILING DATE: April 4, 1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/868,354  
 FILING DATE: April 10, 1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/745,206  
 FILING DATE: 15-AUG-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/620,250  
 FILING DATE: 30-NOV-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/482,384  
 FILING DATE: 20-FEB-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/603,751  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/US89/01408  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/176,899  
 FILING DATE: 04-APR-1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie L.  
 REGISTRATION NUMBER: 33,779  
 REFERENCE/DOCKET NUMBER: 6362-52517  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619)238-0999  
 TELEFAX: (619)238-0062  
 INFORMATION FOR SEQ ID NO: 54:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1086 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-455-543A-54

Query Match 97.2%; Score 5492.5; DB 1; Length 1086;  
 Best Local Similarity 98.2%; Pred. No. 0;  
 Matches 1044; Conservative 6; Mismatches 8; Indels 5; Gaps 1;

QY 1 MAAGCLATLTLFOSLLIGSSQSPPPSAVTIKSWDKMOEDLVTLAKTAGSVNOLVDI 60  
 DB 1 MAAGCLATLTLFOSLLIGSSQSPPPSAVTIKSWDKMOEDLVTLAKTAGSVNOLVDI 60

QY 61 YEKYODLYTEBNNAROLVEIARDIEKLLSNRSKALVRLALEAKVOAHOQREDFASN 120  
 DB 61 YEKYODLYTEBNNAROLVEIARDIEKLLSNRSKALVRLALEAKVOAHOQREDFASN 120  
 QY 121 EYVYNAKDDLPBKNDSFSGSQRITKPFVIDANANGROISTOHAAVHPTDIYEGSTVL 180  
 DB 121 EYVYNAKDDLPBKNDSFSGSQRITKPFVIDANANGROISTOHAAVHPTDIYEGSTVL 180  
 QY 181 NELNMTSALDEYFKKREDDPSLIMOVGSATGLRKYVPASPVWNSPTPKTIDLYDVR 240  
 DB 181 NELNMTSALDEYFKKREDDPSLIMOVGSATGLRKYVPASPVWNSPTPKTIDLYDVR 240  
 QY 241 RPYITOGAASPMDLILVDVSGSVGLTKLIRTSVSEMLETLLSDDDPVNVAFSFNQAD 300  
 DB 241 RPYITOGAASPMDLILVDVSGSVGLTKLIRTSVSEMLETLLSDDDPVNVAFSFNQAD 300  
 QY 301 VSGFQHLVQANVRNKKVYLKDAVNNITAKGIDYKKGFSAFEOQLINYNVSRANCKITML 360  
 DB 301 VSGFQHLVQANVRNKKVYLKDAVNNITAKGIDYKKGFSAFEOQLINYNVSRANCKITML 360  
 QY 361 FTDGGERAOELFAKYNKKRVFTFSYGOHNNYRGPLOMMACBCKGYEIPISGAIR 420  
 DB 361 FTDGGERAOELFAKYNKKRVFTFSYGOHNNYRGPLOMMACBCKGYEIPISGAIR 420  
 QY 421 INTQYLDVLAGRPVYLAGDKAKOVQNTNYLDALGLVITGTLPEVNTGQNEKNTMLK 480  
 DB 421 INTQYLDVLAGRPVYLAGDKAKOVQNTNYLDALGLVITGTLPEVNTGQNEKNTMLK 480  
 QY 481 NOLITGVKGVDSLEDIRKLTFRFLCPNGYFFAIDPNGYVYLHPNLOPKMKSOEPTVL 540  
 DB 481 NOLITGVKGVDSLEDIRKLTFRFLCPNGYFFAIDPNGYVYLHPNLOPKMKSOEPTVL 540  
 QY 541 DELDAELNDIYELRNKKIDGESGKFTPTLVKQODRYIDKGRRTWTWVPVNGTDSL 600  
 DB 541 DELDAELNDIYELRNKKIDGESGKFTPTLVKQODRYIDKGRRTWTWVPVNGTDSL 600  
 QY 596 ALVLPYSRYIKAKLEETITQARSKKMKSEFLKPDNEESGYTPIADRYCNDLKI 655  
 DB 596 ALVLPYSRYIKAKLEETITQARSKKMKSEFLKPDNEESGYTPIADRYCNDLKI 655  
 QY 601 ALVLPYSRYIKAKLEETITQARSKKMKSEFLKPDNEESGYTPIADRYCNDLKI 660  
 DB 601 ALVLPYSRYIKAKLEETITQARSKKMKSEFLKPDNEESGYTPIADRYCNDLKI 660  
 QY 661 SONNTEFLNFEFTDRKTPNPNPSCNTDLINRVLLDAQFTNELVQNTYRSKKNIKGVKAR 720  
 DB 661 SONNTEFLNFEFTDRKTPNPNPSCNTDLINRVLLDAQFTNELVQNTYRSKKNIKGVKAR 720  
 QY 715 SONNTEFLNFEFTDRKTPNPNPSCNTDLINRVLLDAQFTNELVQNTYRSKKNIKGVKAR 715  
 DB 715 SONNTEFLNFEFTDRKTPNPNPSCNTDLINRVLLDAQFTNELVQNTYRSKKNIKGVKAR 715  
 QY 721 FVYTDGGLTRVYKKEGEMQENPFTYEDSFYKSLDNDNVFAPYRNKSGPAYESGI 780  
 DB 721 FVYTDGGLTRVYKKEGEMQENPFTYEDSFYKSLDNDNVFAPYRNKSGPAYESGI 780  
 QY 716 FVYTDGGLTRVYKKEGEMQENPFTYEDSFYKSLDNDNVFAPYRNKSGPAYESGI 775  
 DB 716 FVYTDGGLTRVYKKEGEMQENPFTYEDSFYKSLDNDNVFAPYRNKSGPAYESGI 775  
 QY 781 MYSKAVEITYIOGKLLKPAVAVGIKIDVNSWIENFTKTSIRDCAGPYCDCKRNSDVCVI 840  
 DB 781 MYSKAVEITYIOGKLLKPAVAVGIKIDVNSWIENFTKTSIRDCAGPYCDCKRNSDVCVI 840  
 QY 776 MYSKAVEITYIOGKLLKPAVAVGIKIDVNSWIENFTKTSIRDCAGPYCDCKRNSDVCVI 835  
 DB 776 MYSKAVEITYIOGKLLKPAVAVGIKIDVNSWIENFTKTSIRDCAGPYCDCKRNSDVCVI 835  
 QY 841 LDDGFFLLMANNDVTTNOIGRFGELDPSLMARHLVNIYVAFPNKSYDQSCFEGAAPQ 900  
 DB 841 LDDGFFLLMANNDVTTNOIGRFGELDPSLMARHLVNIYVAFPNKSYDQSCFEGAAPQ 900  
 QY 836 LDDGFFLLMANNDVTTNOIGRFGELDPSLMARHLVNIYVAFPNKSYDQSCFEGAAPQ 895  
 DB 836 LDDGFFLLMANNDVTTNOIGRFGELDPSLMARHLVNIYVAFPNKSYDQSCFEGAAPQ 895  
 QY 901 GAGHSAYVPSIADILHIGWMTAAWASIILOOFLSTLFPRLLEVEHEDDPFASLSKO 960  
 DB 901 GAGHSAYVPSIADILHIGWMTAAWASIILOOFLSTLFPRLLEVEHEDDPFASLSKO 960  
 QY 896 GAGHSAYVPSIADILHIGWMTAAWASIILOOFLSTLFPRLLEVEHEDDPFASLSKO 955  
 DB 896 GAGHSAYVPSIADILHIGWMTAAWASIILOOFLSTLFPRLLEVEHEDDPFASLSKO 955  
 QY 961 SCITEQOTYFEDNDSKFSFGLDGCNCSRIHFVEKLMNTNLIIFTNVESEKTCPCDTRLII 1020  
 DB 961 SCITEQOTYFEDNDSKFSFGLDGCNCSRIHFVEKLMNTNLIIFTNVESEKTCPCDTRLII 1020  
 QY 956 SCITEQOTYFEDNDSKFSFGLDGCNCSRIHFVEKLMNTNLIIFTNVESEKTCPCDTRLII 1015  
 DB 956 SCITEQOTYFEDNDSKFSFGLDGCNCSRIHFVEKLMNTNLIIFTNVESEKTCPCDTRLII 1015  
 QY 1021 QAEQTSDDGPDPCDMYKQPRYRKGPVYCDNNALBXYTTCGCVS 1063  
 DB 1021 QAEQTSDDGPDPCDMYKQPRYRKGPVYCDNNALBXYTTCGCVS 1058

RESULT 8  
 US-08-223-305C-54  
 ; Sequence No. 54, Application US/08223305C  
 ; Patent No. 5851824



Db 781 MYSKAVEIYIGKILKPAVVGIKIDVNSWIENTKTSIRDPACGPVCDCKRNSDVMDCVI 840  
QY 841 LDDGFLMANHDDYTNOIGRFFGEIDPSLMRHLVINSVYAFNKSYDYOSVCEGPAAPQ 900  
Db 841 LDDGFLMANHDDYTNOIGRFFGEIDPSLMRHLVINSVYAFNKSYDYOSVCEGPAAPQ 900  
QY 901 GAGHSAYVPSIADILHIGMATAAWSILOQFLSLTFPRLLAEVEMEDDFTASLSKQ 960  
Db 901 GAGHSAYVPSIADILHIGMATAAWSILOQFLSLTFPRLLAEVEMEDDFTASLSKQ 960  
QY 961 SCITEOTQYFFNDKSFSGVLDGNCNSRIFHEKLMNTLIFIVESKGTCPDTRLI 1020  
Db 961 SCITEOTQYFFNDKSFSGVLDGNCNSRIFHEKLMNTLIFIVESKGTCPDTRLI 1020  
QY 1021 QAEQTSDEGPPCDMVKOPRYRKGPVCFDNNALIEDYTDGCVS 1063  
Db 1021 QAEQTSDEGPPCDMVKOPRYRKGPVCFDNNALIEDYTDGCVS 1063

## RESULT 6

US-09-452-007-4  
; Sequence 4, Application US/09452007  
; Patent No. 6140485

## GENERAL INFORMATION:

APPLICANT: Franco, Rodrigo  
APPLICANT: Sun Chen, Ai Ru  
APPLICANT: Suey, David J.  
TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Millicia Drive  
CITY: Lexington  
STATE: MA

COUNTRY: USA  
ZIP: 02173-4799

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/452,007  
FILING DATE:

## CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/713,118  
FILING DATE: 16-SEP-1996

## ATTORNEY/AGENT INFORMATION:

NAME: Mata, Elizabeth W.  
REGISTRATION NUMBER: 38,236

REFERENCE/DOCKET NUMBER: ACC96-01  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1091 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-452-007-4

Query Match 97.8%; Score 5528; DB 4; Length 1091;  
Best Local Similarity 98.6%; Pred. No. 0;

Matches 1048; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 MAAGCLALITLTQSLIGPSQPPPSAVTIKSWDKMOEDIVTLAKTASGVNOIYDI 60  
Db 1 MAAGCLALITLTQSLIGPSQPPPSAVTIKSWDKMOEDIVTLAKTASGVNOIYDI 60  
QY 61 YEKYODLYTVEPNNAKQVEIAARDIEKLISNRSKALVRLALEAKVQAHQWEDFASN 120

Db 61 YEKYODLYTVEPNNAKQVEIAARDIEKLISNRSKALVRLALEAKVQAHQWEDFASN 120  
QY 121 EVVYNNKADLDLPPKKNSEPGSORIKPVPIDDPANFGQISYQAAHHPIDDIESTIYL 180  
Db 121 EVVYNNKADLDLPPKKNSEPGSORIKPVPIDDPANFGQISYQAAHHPIDDIESTIYL 180  
QY 181 NELNMTSALDEVEFKKNEEDPSLMQVFGSATGLARYPASPVWDNSRPNKIDLYDVR 240  
Db 181 NELNMTSALDEVEFKKNEEDPSLMQVFGSATGLARYPASPVWDNSRPNKIDLYDVR 240  
QY 241 RPYTQGAASEKDMILIVDYSVSGTLTKLIRTSVEMLETSLDDFVNVASFNSNAOD 300  
Db 241 RPYTQGAASEKDMILIVDYSVSGTLTKLIRTSVEMLETSLDDFVNVASFNSNAOD 300  
QY 301 VSCFOHLVOANVRKAYLKAIVNNITAKGTDYDKKGSFAFEBOLVANNRACNKLIML 360  
Db 301 VSCFOHLVOANVRKAYLKAIVNNITAKGTDYDKKGSFAFEBOLVANNRACNKLIML 360  
QY 361 FTDGEEERAOEIFAKYNNKDKRVYFTEVSGOHYDRGPIDMMACENKGYEIEPSIGAIR 420  
Db 361 FTDGEEERAOEIFAKYNNKDKRVYFTEVSGOHYDRGPIDMMACENKGYEIEPSIGAIR 420  
QY 421 INTQYEDVIGRPVYLAGDKAKOYQNTNVTLDLDELGLVITGTLVPVFNITGQENKNTLK 480  
Db 421 INTQYEDVIGRPVYLAGDKAKOYQNTNVTLDLDELGLVITGTLVPVFNITGQENKNTLK 480  
QY 481 NOLILGVAGVDSLEDIKRLTPRTLCPNGYFAIDPNCVLLHPNLOPNPSSQSPVL 540  
Db 481 NOLILGVAGVDSLEDIKRLTPRTLCPNGYFAIDPNCVLLHPNLOPNPSSQSPVL 540  
QY 541 DFLDALENDIKVEIRKMKIDGESGKTFRTLVKSODERYIDKNGNTYTWTPYNGTDSL 600  
Db 541 DFLDALENDIKVEIRKMKIDGESGKTFRTLVKSODERYIDKNGNTYTWTPYNGTDSL 600  
QY 601 ALVLPYTSFYIRAKLEETITQARSKKGMKDETLKPDNFESGYTFLAPRDYCDLKI 660  
Db 601 ALVLPYTSFYIRAKLEETITQARSKKGMKDETLKPDNFESGYTFLAPRDYCDLKI 660  
QY 661 SDNTEFLNPNFIDKRTPNNSCNTDLINRYLLDAGFNELVQVWYWSKOKIKGVKAR 720  
Db 661 SDNTEFLNPNFIDKRTPNNSCNTDLINRYLLDAGFNELVQVWYWSKOKIKGVKAR 720  
QY 721 FVYTDGIGITRYPREAGENQENPETEYEDSFYKRSIDNDNYVTAFYFNKSGGAYESGI 780  
Db 721 FVYTDGIGITRYPREAGENQENPETEYEDSFYKRSIDNDNYVTAFYFNKSGGAYESGI 780  
QY 781 MYSKAVEIYIGKILKPAVVGIRKIDVNSWIENTKTSIRDPACGPVCDCKRNSDVMDCVI 840  
Db 781 MYSKAVEIYIGKILKPAVVGIRKIDVNSWIENTKTSIRDPACGPVCDCKRNSDVMDCVI 840  
QY 841 LDDGFLMANHDDYTNOIGRFFGEIDPSLMRHLVINSVYAFNKSYDYOSVCEGPAAPQ 900  
Db 841 LDDGFLMANHDDYTNOIGRFFGEIDPSLMRHLVINSVYAFNKSYDYOSVCEGPAAPQ 900  
QY 901 GAGHSAYVPSIADILHIGMATAAWSILOQFLSLTFPRLLAEVEMEDDFTASLSKQ 960  
Db 901 GAGHSAYVPSIADILHIGMATAAWSILOQFLSLTFPRLLAEVEMEDDFTASLSKQ 960  
QY 961 SCITEOTQYFFNDKSFSGVLDGNCNSRIFHEKLMNTLIFIVESKGTCPDTRLI 1020  
Db 961 SCITEOTQYFFNDKSFSGVLDGNCNSRIFHEKLMNTLIFIVESKGTCPDTRLI 1020  
QY 1021 QAEQTSDEGPPCDMVKOPRYRKGPVCFDNNALIEDYTDGCVS 1063  
Db 1021 QAEQTSDEGPPCDMVKOPRYRKGPVCFDNNALIEDYTDGCVS 1063

## RESULT 7

US-08-455-543A-54  
; Sequence 54, Application US/08455543A  
; Patent No. 5792846

## GENERAL INFORMATION:

QY 421 INFOEYLDVGRPMVLADGKAKOVMTNYLDALGLVITGTLPEVNTIGONENKTNLK 480  
 DB 421 INFOEYLDVGRPMVLADGKAKOVMTNYLDALGLVITGTLPEVNTIGONENKTNLK 480  
 QY 481 NOILIGVMGVDSLEDIKRLTPRFTLCPNGYFAIDPNGVYLLHPNLOPKPKSOEPTVL 540  
 DB 481 NOILIGVMGVDSLEDIKRLTPRFTLCPNGYFAIDPNGVYLLHPNLOPKPKSOEPTVL 540  
 QY 541 DFLDAELENDIKVEIRNKKMIDGSGEKTFTLVKSQDERIDKGNRTYWTPTVNGTDSL 600  
 DB 541 DFLDAELENDIKVEIRNKKMIDGSGEKTFTLVKSQDERIDKGNRTYWTPTVNGTDSL 600  
 QY 601 ALVLPYTFYIKAKIETITQARSKKGMKQSEITLKPDEESGYTEIAPRYCNDLKI 660  
 DB 601 ALVLPYTFYIKAKIETITQARSKKGMKQSEITLKPDEESGYTEIAPRYCNDLKI 660  
 QY 661 SDNTEFLNFEIDRKTNNPSCNTDLINRVLLDAGFTNELVONYWSKOKNIKGVAKR 720  
 DB 661 SDNTEFLNFEIDRKTNNPSCNTDLINRVLLDAGFTNELVONYWSKOKNIKGVAKR 720  
 QY 721 FVYTDGGITRVYKKEAGENQENPEYEDSFYKSLDNDNYVTAPYFNKSGGAYESGI 780  
 DB 721 FVYTDGGITRVYKKEAGENQENPEYEDSFYKSLDNDNYVTAPYFNKSGGAYESGI 780  
 QY 781 MVSFAVEITYOGKLLKPAVVGIKIDVNSWIENTFTSIRDPGAGPCDCCKRNSDVMDCVI 840  
 DB 781 MVSFAVEITYOGKLLKPAVVGIKIDVNSWIENTFTSIRDPGAGPCDCCKRNSDVMDCVI 840  
 QY 841 LDGGLFLMANHDDYTNQIGRFFGEIDPSLMRLVNI SYVAFNKSVDYOSVCEPGAAPKQ 900  
 DB 841 LDGGLFLMANHDDYTNQIGRFFGEIDPSLMRLVNI SYVAFNKSVDYOSVCEPGAAPKQ 900  
 QY 901 GAGRSAYVSIADLIHIGMMATAAWSILQOFLSLTFPRLLAEVEMEDDDTASLSKQ 960  
 DB 901 GAGRSAYVSIADLIHIGMMATAAWSILQOFLSLTFPRLLAEVEMEDDDTASLSKQ 960  
 QY 961 SCITEQYQYFFDNDKSFSGVLDGNCSTRIFHEKLMNTNLIIFIMVESKGTCPDTRLILI 1020  
 DB 961 SCITEQYQYFFDNDKSFSGVLDGNCSTRIFHEKLMNTNLIIFIMVESKGTCPDTRLILI 1020  
 QY 1021 QABEYSDGPDPCKMVKOPRYRKGPDYCFDNNVLEDYTDGCGVS 1063  
 DB 1021 QABEYSDGPDPCKMVKOPRYRKGPDYCFDNNVLEDYTDGCGVS 1063  
 RESULT 5  
 US-08-713-118-4  
 ; Sequence 4, Application US/08713118  
 ; Patent No. 6040436  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Franco, Rodrigo  
 ; APPLICANT: Sun Chen, Ai Ru  
 ; APPLICANT: Suey, David J.  
 ; TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL  
 ; NUMBER OF SEQUENCES: 6  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
 ; STREET: Two Militia Drive  
 ; CITY: Lexington  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02173-4799  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/713,118  
 ; FILING DATE: 16-SEP-1996  
 ; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
 NAME: Mata, Elizabeth W.  
 REGISTRATION NUMBER: 38,236  
 REFERENCE/DOCKET NUMBER: ACC96-01  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-861-6240  
 TELEFAX: 617-861-9540  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1091 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-713-118-4  
 Query Match 97.8%; Score 5528; DB 3; Length 1091;  
 Best Local Similarity 98.6%; Pred. No. 0;  
 Matches 1048; Conservative 6; Mismatches 9; Indels 0; Gaps 0;  
 QY 1 MAGCLLALTLFLFOSLIGSPSSQPPSAVTIKSWDKMEDVTLAKTASGVNQLVDI 60  
 DB 1 MAGCLLALTLFLFOSLIGSPSSQPPSAVTIKSWDKMEDVTLAKTASGVNQLVDI 60  
 QY 61 YEKYODLYVEPNNAQVEIARDIEKLLNSKALVRLALEAKYQAAHQWREDFASN 120  
 DB 61 YEKYODLYVEPNNAQVEIARDIEKLLNSKALVRLALEAKYQAAHQWREDFASN 120  
 QY 121 EYVYTNAKDDLDPERNDSPGQRIKPVFIIDANRGROIYQHAANHPTDIYEGSTVL 180  
 DB 121 EYVYTNAKDDLDPERNDSPGQRIKPVFIIDANRGROIYQHAANHPTDIYEGSTVL 180  
 QY 181 NELNMTSALDEYFKKRNREDEPSLQVFGSATGLARYYPASPMWNSRTPPKIDLYDVR 240  
 DB 181 NELNMTSALDEYFKKRNREDEPSLQVFGSATGLARYYPASPMWNSRTPPKIDLYDVR 240  
 QY 241 RPYWYIOGAASPRDMLLVDSGVSGLTLKIRTSVSEMLETSLDDDFVNAASFNSAQD 300  
 DB 241 RPYWYIOGAASPRDMLLVDSGVSGLTLKIRTSVSEMLETSLDDDFVNAASFNSAQD 300  
 QY 301 VSCFOHLYOVANRNKKVYLKDAVNNITAKGIDYKKGFSAFROLLINYNVSRANCKIIML 360  
 DB 301 VSCFOHLYOVANRNKKVYLKDAVNNITAKGIDYKKGFSAFROLLINYNVSRANCKIIML 360  
 QY 361 FTDGGEERAQELFAKYNKDKKRVFTFSVGHNYDRGFTIOWMACENKGYEIRISGAIR 420  
 DB 361 FTDGGEERAQELFAKYNKDKKRVFTFSVGHNYDRGFTIOWMACENKGYEIRISGAIR 420  
 QY 421 INFOEYLDVGRPMVLADGKAKOVMTNYLDALGLVITGTLPEVNTIGONENKTNLK 480  
 DB 421 INFOEYLDVGRPMVLADGKAKOVMTNYLDALGLVITGTLPEVNTIGONENKTNLK 480  
 QY 481 NOILIGVMGVDSLEDIKRLTPRFTLCPNGYFAIDPNGVYLLHPNLOPKPKSOEPTVL 540  
 DB 481 NOILIGVMGVDSLEDIKRLTPRFTLCPNGYFAIDPNGVYLLHPNLOPKPKSOEPTVL 540  
 QY 541 DFLDAELENDIKVEIRNKKMIDGSGEKTFTLVKSQDERIDKGNRTYWTPTVNGTDSL 600  
 DB 541 DFLDAELENDIKVEIRNKKMIDGSGEKTFTLVKSQDERIDKGNRTYWTPTVNGTDSL 600  
 QY 601 ALVLPYTFYIKAKIETITQARSKKGMKQSEITLKPDEESGYTEIAPRYCNDLKI 660  
 DB 601 ALVLPYTFYIKAKIETITQARSKKGMKQSEITLKPDEESGYTEIAPRYCNDLKI 660  
 QY 661 SDNTEFLNFEIDRKTNNPSCNTDLINRVLLDAGFTNELVONYWSKOKNIKGVAKR 720  
 DB 661 SDNTEFLNFEIDRKTNNPSCNTDLINRVLLDAGFTNELVONYWSKOKNIKGVAKR 720  
 QY 721 FVYTDGGITRVYKKEAGENQENPEYEDSFYKSLDNDNYVTAPYFNKSGGAYESGI 780  
 DB 721 FVYTDGGITRVYKKEAGENQENPEYEDSFYKSLDNDNYVTAPYFNKSGGAYESGI 780  
 QY 781 MVSFAVEITYOGKLLKPAVVGIKIDVNSWIENTFTSIRDPGAGPCDCCKRNSDVMDCVI 840  
 DB 781 MVSFAVEITYOGKLLKPAVVGIKIDVNSWIENTFTSIRDPGAGPCDCCKRNSDVMDCVI 840

DR SMART: SM00327; WVA; 1. 1.  
 DR PROSITE; PS50234; WVA; 1.  
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;  
 KW Calcium channel; Glycoprotein; Phosphorylation; Signal;  
 KW Alternative splicing.  
 FT SIGNAL 1 24  
 FT CHAIN 25 944  
 FT CHAIN 945 1091  
 FT TRANSMEM 445 468  
 FT TRANSMEM 906 930  
 FT TRANSMEM 1067 1086  
 FT DOMAIN 252 429  
 FT CARBOHYD 92 92  
 FT CARBOHYD 136 136  
 FT CARBOHYD 184 184  
 FT CARBOHYD 323 323  
 FT CARBOHYD 347 347  
 FT CARBOHYD 474 474  
 FT CARBOHYD 584 584  
 FT CARBOHYD 593 593  
 FT CARBOHYD 663 663  
 FT CARBOHYD 769 769  
 FT CARBOHYD 812 812  
 FT CARBOHYD 876 876  
 FT CARBOHYD 883 883  
 FT CARBOHYD 973 973  
 FT CARBOHYD 986 986  
 FT MOD\_RES 500 500  
 FT MOD\_RES 833 833  
 SQ SEQUENCE 1091 AA; 123822 MW; 7054907D9D343B34 CRC64;

Query Match 96.7%; Score 5174; DB 1; Length 1091;

Best Local Similarity 96.3%; Pred. No. 1.1e-300;

Matches 981; Conservative 22; Mismatches 14; Indels 2; Gaps 2;

QY 1 MAAGCLLATLTLFOSLLIGPSSQPPPSAVTIKSWDKMQEDLVLTAKTASGVNQLVDI 60  
 DB 1 MAAGCLLATLTLFOSLLIGPSSQPPPSAVTIKSWDKMQEDLVLTAKTASGVNQLADI 60  
 QY 61 YEKYQDLYTVEPNNAQOLVEIAARDIEKLLNSRSKALVRLALEAEKVQAAHOWREDFASN 120  
 DB 61 YEKYQDLYTVEPNNAQOLVEIAARDIEKLLNSRSKALVRLAMEAEKVQAAHOWREDFASN 120  
 QY 121 EYVYNAKDDLDPEKNDESGSQRIKPVFIIDANFGROISYQHAHVHTPTDIYEGSTIVL 180  
 DB 121 EYVYNAKDDLDPERNESESGSQRIKPVFIIDANFGROISYQHAHVHTPTDIYEGSTIVL 180  
 QY 181 NELNWTSALEDEVFKNREEDPSLLWVFGSATGLARYYPASPWVDSNRTPKNIDLYDVR 240  
 DB 181 NELNWTSALEDEVFKNREEDPTLLWQVF-AADRRLARYYPASPWVDSNRTPKNIDLYDVR 239  
 QY 241 RPWYIQGAASPKDMLILDVDSGVSGLTKLIRTSVSEMLETLSDDDDFVNVASPNNAQD 300  
 DB 240 RPWYIQGAASPKDMLILDVDSGVSGLTKLIRTSVSEMLETLSDDDDFVNVASPNNAQD 299  
 QY 301 VSCFOHLVQANRKKVYLKDAVNITAKGTDYKKGFSFAFEQLLNVSRANCNKIIML 360  
 DB 300 VSCFOHLVQANRKKVYLKDAVNITAKGTDYKKGFTFAFEQLLNVSRANCNKIIML 359  
 QY 361 FTDGGEERAQEIFAKYKDKKVRVFTSVGOHNYDRGPIONMACENKGYEIPISGAIR 420  
 DB 360 FTDGGEERAQEIFAKYKDKKVRVFTSVGOHNYDRGPIONMACENKGYEIPISGAIR 419  
 QY 421 INTOEYLDVLRPMVLGADKAKQVQWNTVYLDALGLVITGTLPVFNITQONFNKTNLK 480  
 DB 420 INTOEYLDVLRPMVLGADKAKQVQWNTVYLDALGLVITGTLPVFNITQONFNKTNLK 479  
 QY 481 NOLILGVMGVDVSLIEDIKLTPRTLCPNGYIFAIDPNGVYLLHPNLPKPKSQEPVTL 540  
 DB 480 NOLILGVMGVDVSLIEDIKLTPRTLCPNGYIFAIDPNGVYLLHPNLPKPKSQEPVTL 539

QY 541 DFLDAELNDIKVEIRNKMIDGESGEKTFRTLKVSQDERYIDKGNRTYTTPVNGTDYS- 599  
 DB 540 DFLDAELNDIKVEIRNKMIDGESGEKTFRTLKVSQDERYIDKGNRTYTTPVNGTDYR 599  
 QY 600 LALVLPYTSFYIYAKIEETITQARSKGKMKDSETLKPDNFEESGYTFIAPRDYCNDLK 659  
 DB 600 LALVLPYTSFYIYAKIEETITQARSKGKMKDSETLKPDNFEESGYTFIAPRDYCNDLK 659  
 QY 660 ISDNNTTELLNFNEFIDRKTPNNPNSCNTDLINRVLLDAGFTNELVQVNSKQKNIGKVA 719  
 DB 660 PSDNNTTELLNFNEFIDRKTPNNPNSCNTDLINRVLLDAGFTNELVQVNSKQKNIGKVA 719  
 QY 720 RFVVTGGITRVYPKEAGENQENPEYEDSFYKRSLDNDNYVFTAFYFNKSGPGAYESG 779  
 DB 720 RFVVTGGITRVYPKEAGENQENPEYEDSFYKRSLDNDNYVFTAFYFNKSGPGAYESG 779  
 QY 780 IMVSKAVEIYIOGKLLPVPVGIKIDVNSWIENTKTSIRDPACAGPVCDCKRNSDVMDCV 839  
 DB 780 IMVSKAVEIYIOGKLLPVPVGIKIDVNSWIENTKTSIRDPACAGPVCDCKRNSDVMDCV 839  
 QY 840 ILDDGGFLLMANHDDYTNOIGRFFGEIDPSIMRHLVNIISYAFNKSVDYQSVCEPGAAPK 899  
 DB 840 ILDDGGFLLMANHDDYTNOIGRFFGEIDPSIMRHLVNIISYAFNKSVDYQSVCEPGAAPK 899  
 QY 900 QGAGHSAYVPSIADILHIGHWATAAASIIQQFLLSLTFPRLLEAVEMEDDDFTASLSK 959  
 DB 900 QGAGHSAYVPSIADILHIGHWATAAASIIQQFLLSLTFPRLLEAVEMEDDDFTASLSK 959  
 QY 960 QSCITEQTOFFDNDSFSFGLVDCGNCGRIFHVEKLMNTNLIIFIMVESKGTGCPDTRL 1018  
 DB 960 QSCITEQTOFFDNDSFSFGLVDCGNCGRIFHVEKLMNTNLIIFIMVESKGTGCPDTRL 1018

RESULT 3

CIC2\_RABIT

ID\_CIC2\_RABIT STANDARD; PRT; 1106 AA.  
 AC PL3806;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta  
 DE subunits precursor.  
 GN CACNA2D1 OR CACNL2A OR CCHL2A.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88336904; PubMed=2458626;  
 RA Ellis S.B., Williams M.E., Ways N.R., Brenner R., Sharp A.H.,  
 RA Leung A.T., Campbell K.P., McKenna E., Koch W.J., Hui A.,  
 RA Schwartz A., Harpold M.M.;  
 RT "Sequence and expression of mRNAs encoding the alpha 1 and alpha 2  
 subunits of a DHP-sensitive calcium channel.";  
 RL Science 241:1661-1664(1988).  
 RN [2]  
 RP SEQUENCE OF 961-973.  
 RX MEDLINE=91131638; PubMed=1847144;  
 RA Jay S.D., Sharp A.H., Kahl S.D., Vedvick T.S., Harpold M.M.,  
 RA Campbell K.P.;  
 RT "Structural characterization of the dihydropyridine-sensitive calcium  
 channel alpha 2-subunit and the associated delta peptides.";  
 RL J. Biol. Chem. 266:3287-3293(1991).  
 RN [3]  
 RP SEQUENCE OF 961-975; 992-1000 AND 1033-1050.  
 RX MEDLINE=90368635; PubMed=2168391;  
 RA de Jongh K.S., Warner C., Catterall W.A.;  
 RT "Subunits of purified calcium channels. Alpha 2 and delta are encoded  
 by the same gene.";  
 RL J. Biol. Chem. 265:14738-14741(1990).  
 CC -!- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN  
 EXCITATION-CONTRACTION COUPLING.

CC -!- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:  
 CC ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS  
 CC HETERODIMERS THAT ARE DISULFIDE-LINKED.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE  
 CC SPLICING.  
 CC -!- TISSUE SPECIFICITY: SKELETAL MUSCLE.  
 CC -!- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM  
 CC A PRECURSOR FORM.  
 CC -!- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.  
 CC -!- SIMILARITY: CONTAINS 1 WFA DOMAIN.  
 CC -----  
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----

DR EMBL: M21948; AAA81562.1; -  
 DR PIR: S10579; CHRA2.  
 DR InterPro: IPR004010; Cache.  
 DR InterPro: IPR002035; WVF\_A.  
 DR Pfam: PF000092; wva; 1.  
 DR Pfam: PF02743; Cache; 1.  
 DR SMART: SM00327; WVA; 1.  
 DR PROSITE: PS0234; WVFA; 1.  
 DR Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;  
 KW Calcium channel; Glycoprotein; Phosphorylation; Signal;  
 KW Alternative splicing.  
 FT SIGNAL 1 26  
 FT CHAIN 27 960  
 FT CHAIN 961 1106  
 FT TRANSMEM 448 471  
 FT TRANSMEM 921 945  
 FT TRANSMEM 1082 1101  
 FT DOMAIN 255 432  
 FT CARBOHYD 94 94  
 FT CARBOHYD 138 138  
 FT CARBOHYD 186 186  
 FT CARBOHYD 326 326  
 FT CARBOHYD 350 350  
 FT CARBOHYD 477 477  
 FT CARBOHYD 606 606  
 FT CARBOHYD 615 615  
 FT CARBOHYD 678 678  
 FT CARBOHYD 784 784  
 FT CARBOHYD 827 827  
 FT CARBOHYD 891 891  
 FT CARBOHYD 898 898  
 FT CARBOHYD 988 988  
 FT CARBOHYD 1001 1001  
 FT MOD\_RES 503 503  
 FT MOD\_RES 848 848  
 SQ SEQUENCE 1106 AA; 125042 MW; 800DE7F3C877B618 CRC64;

Query Match 96.4%; Score 5156.5; DB 1; Length 1106;  
 Best Local Similarity 95.3%; Pred. No. 1.2e-299;  
 Matches 991; Conservative 11; Mismatches 9; Indels 29; Gaps 4;

QY 1 MAAGCULALTLTLFQS--LLIGSSQEPSPSAVTKSWYDKMQEDLVTAKTASGVNQLV 58  
 Db 1 MAAGRPLAWTLTLQAWLILIGPSSEPPSPSAVTKSWYDKMQEDLVTAKTASGVHQLV 60  
 QY 59 DIYEKQDLYTPNNAROLVETAAARDIEKLLSNRSKALVRLALEAEKQVQAAHQRDEFA 118  
 Db 61 DIYEKQDLYTPNNAROLVETAAARDIEKLLSNRSKALVRLALEAEKQVQAAHQRDEFA 120  
 QY 119 SNEWYNAKDDLDPEKNDSEPGSQRIKPVFIDDAFNFRQISYQHAHVHIPTDIYEGSTI 178  
 Db 121 SNEWYNAKDDLDPEKNDSEPGSQRIKPVFIDDAFNFRQISYQHAHVHIPTDIYEGSTI 180

QY 179 VLNLNWTISALDEVFKKREEDPSLLQVFGSATGLARYYPASPDVNDNRTNPKIDLYDV 238  
 Db 181 VLNLNWTISALDEVFKKREEDPSLLQVFGSATGLARYYPASPDVNDNRTNPKIDLYDV 240  
 QY 239 RRPWTIOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETLDSDDFVNVASNSNA 298  
 Db 241 RRPWTIOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETLDSDDFVNVASNSNA 300  
 QY 299 QDYSCFQHLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFEQLLNYSRANCNKII 358  
 Db 301 QDYSCFQHLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFEQLLNYSRANCNKII 360  
 QY 359 MLFTDGEERAQEIFAKYKNDKKVRVFTSVGOHNDYDRGPIOMMACENKGYEIPISGA 418  
 Db 361 MLFTDGEERAQEIFAKYKNDKKVRVFTSVGOHNDYDRGPIOMMACENKGYEIPISGA 420  
 QY 419 IRTNQEYLDVLRPMVLADGKAKQVQWNTNYLDALGLVITGLTPVNTIGONENKTN 478  
 Db 421 IRTNQEYLDVLRPMVLADGKAKQVQWNTNYLDALGLVITGLTPVNTIGONENKTN 480  
 QY 479 LKNOLILGVMGVDVSLIEDIKRLTPRTCLCPNGYFFAIDPNGYVLLHPNLQPK 530  
 Db 481 LKNOLILGVMGVDVSLIEDIKRLTPRTCLCPNGYFFAIDPNGYVLLHPNLQPKPIGVGPT 540  
 QY 531 -----NPKSQBPVTLDFDLAELENDIKVEIRNKMIDGESGEKTPRTLVSQDER 579  
 Db 541 INLRKRPNVQNPQSQBPVTLDFDLAELENDIKVEIRNKMIDGESGEKTPRTLVSQDER 600  
 QY 580 YIDKGNRTYTWTPVNGTDY-SLALVPTYFYIKAKIETITQARSKGKMKDSETLKP 638  
 Db 601 YIDKGNRTYTWTPVNGTDYSSALVPTYFYIKAKIETITQARY-----SETLKP 653  
 QY 639 DNFEESGYTPIADRYCNDLKIISDNTEFLNFEIDRKTNNPNSCNTDLINRVLLDAG 698  
 Db 654 DNFEESGYTFLAPDYCNDLKIISDNTEFLNFEIDRKTNNPNSCNTDLINRVLLDAG 713  
 QY 699 FTNELVQNYSKOKNIKGVKARFVVDGGITRVYPRKAGENWOENPETEYDSYKKSLDN 758  
 Db 714 FTNELVQNYSKOKNIKGVKARFVVDGGITRVYPRKAGENWOENPETEYDSYKKSLDN 773  
 QY 759 DNYVFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKSI 818  
 Db 774 DNYVFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKSI 833  
 QY 819 RDCPAGVPCDKRNSYDMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLWNIS 878  
 Db 834 RDCPAGVPCDKRNSYDMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLWNIS 893  
 QY 879 VYAFNKSYDVOSVCEPGAAPKQAGHESAVVPSIADILHIGWATAAASWILQOFLLSLT 938  
 Db 894 VYAFNKSYDVOSVCEPGAAPKQAGHESAVVPSIADILHIGWATAAASWILQOFLLSLT 953  
 QY 939 FPRLEAVEEMDDFTASLSKQSCITEQTQYFFDNDSKFSFSGVLDGNCGRIFHVEKLMN 998  
 Db 954 FPRLEAVEEMDDFTASLSKQSCITEQTQYFFDNDSKFSFSGVLDGNCGRIFHVEKLMN 1013  
 QY 999 TNLIFIMVESKGTCPDTRL 1018  
 Db 1014 TNLIFIMVESKGTCPDTRL 1033

## RESULT 4

YLJ9\_CAEEL STANDARD; PRT; 1205 AA.  
 ID YLJ9\_CAEEL  
 AC P34372;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DE 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Hypothetical protein C50C3.9 in chromosome III precursor.  
 GN C50C3.9.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.



RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,  
RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,  
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,  
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,  
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,  
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkneen R.,  
RA Sims M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden R.,  
RA Sulston J., Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K.,  
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,  
RA Wohldman P.,  
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
RT elegans.";  
RL Nature 368:32-38(1994).  
CC -1- SIMILARITY: TO CALCIUM CHANNEL ALPHA-2B SUBUNIT.  
CC -1- SIMILARITY: CONTAINS 1 VFMA DOMAIN.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
DR EMBL; L14433; AAA27969.1; -;  
DR PIR; S44617; S44617.  
DR WormPep; C50C3.11; CE00117.  
DR InterPro; IPR004010; Cache.  
DR InterPro; IPR002035; VWF\_A.  
DR Pfam; PF00092; vwa; 1.  
DR Pfam; PF02743; Cache; 1.  
DR SMART; SM00327; VWA; 1.  
DR PROSITE; PS50234; VWA; 1.  
KW Ionic channel; Ion transport; Voltage-gated channel; Calcium channel;  
KW Glycoprotein.  
FT DOMAIN 250  
FT CARBOHYD 100  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 140  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 146  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 302  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 476  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 514  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 734 AA; 85034 MW; CCFB78C8DEE4B71F CRC64;  
Query Match 11.4%; Score 611; DB 1; Length 734;  
Best Local Similarity 26.5%; Pred. No. 5.7e-29;  
Matches 179; Conservative 127; Mismatches 261; Indels 108; Gaps 19;  
QY 47 LAKTAGVQLVDYKYQDYVPEPNARQLVETAAARDIEKLLSNRSKAL--VRLALEA 104  
DB 36 MKETFSKISHETLTKONYEKLVEEQFDPAELKSKKHRIEDYLKVRFOYAKAKISLEA 95  
QY 105 EKVOAAHQWRDEFASNEVVYNAKDDLDPEK-NDSEPGSQRIKP-----VFIDDAF-G 156  
DB 96 RSRVNDSTVNDPSQSFIRFMSAKQNDGTTIYESNHLGKRLKVNKTSFNLQANFYT 155  
QY 157 QITSYQHAHVHIPTDIYEGSTIVNELNWTSLADVEYFKKNEEDPSLWQVFGSATGLAR 216  
DB 156 LPTSSVSSAVHIPTPLDYRNEOLLRRKIDW-SQIDAVYRTNREETKDLAFQLFCSBAGMY 214  
QY 217 YYPASPVV-DNSKTPNKKIDLYDVRPPWYIOGAAPKQMLILVDYSGVSGLTALKIRTS 275  
DB 215 YYPAAFWFDNQ--DEHLDLFCRNTETWINSATNSKNVILMDMSGMLGORYEVAQT 272  
QY 276 VSMLETLSDDDFVNVAFSNSNA---QDVSCFQHLVQAVNRNKKVLDKAVNITAKGTD 332  
DB 273 TEALLETLSHNDYFNIMTFSKNTFLDGCNGTNGLLQATMRNKKALRRKMDTYQSEGRAE 332  
QY 333 YKGFSEFAEQLLNYN-----VSRANCKNLIIMLFTDGGEEAQAETPAKYKDKKVRVTF 387  
DB 333 YEKALPLAFSVLLDINNNGGDDNNRGACENVILMITDGAFFNAYKKIFDYMADKKVRVTF 392

## RESULT 6

## ITH3\_MOUSE

ID ITH3\_MOUSE STANDARD; PRT; 886 AA.  
AC Q61704;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Inter-alpha-trypsin inhibitor heavy chain H3 precursor (ITI heavy  
DE chain H3).  
GN ITIH3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6N; TISSUE=Liver;  
RX MEDLINE=95194326; PubMed=7534067;  
RA Chan P., Risler J.-L., Raguenez G., Salier J.-P.;  
RT "The three heavy-chain precursors for the inter-alpha-inhibitor  
RT family in mouse: new members of the multicopper oxidase protein group  
RT with differential transcription in liver and brain.";  
RL Biochem. J. 306:505-512(1995).  
CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A  
CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,  
CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE  
CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE  
CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY  
CC SIMILARITY).  
CC -1- SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM  
CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN.  
CC BIKUNIN, INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2  
CC AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND  
CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BOTH LIVER AND BRAIN.  
CC -1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN  
CC 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY  
CC SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.  
CC -1- SIMILARITY: CONTAINS 1 VFMA DOMAIN.

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC

CC EMBL: X70393; CAA49843.1; --  
 DR MGI: 96620; Ith3.  
 DR InterPro: IPR002035; VWF\_A.  
 DR Pfam: PF00092; vwa; 1.  
 DR SMART: SM00327; VWA; 1.  
 DR PROSITE: PS0234; VWFA; 1.  
 KW Serine protease inhibitor; Repeat; Signal; Multigene family;  
 KW Glycoprotein.  
 FT SIGNAL 1 18 POTENTIAL.  
 FT PROPEP 19 30 BY SIMILARITY.  
 FT CHAIN 31 646 INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN  
 FT  
 FT PROPEP 647 886 H3.  
 FT DOMAIN 279 439 BY SIMILARITY.  
 FT CARBOHYD 88 88 VWFA.  
 FT CARBOHYD 577 577 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT BINDING 646 646 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT  
 FT BINDING 646 646 CHONDROITIN 4-SULFATE, CROSS-LINK SITE  
 FT (BY SIMILARITY).  
 SQ SEQUENCE 886 AA; 98977 MW; 15955308C7F5030A CRC64;  
 Query Match 3.7%; Score 196.5; DB 1; Length 886;  
 Best Local Similarity 20.5%; Pred. No. 0.00038;  
 Matches 189; Conservative 142; Mismatches 349; Indels 243; Gaps 46;  
 QY 45 VTLAKTASGVNQLVDIYKDYQDLYTVTPNNAQQLVEIAARDIEKLLSNRSKALVRLALEA 104  
 DB 78 VELPKAFITNFTLT-----DGVTY-PGNVKE-KEVAQKQYEKAVSQGTAGL----- 124  
 QY 105 EKQAAAHQWREDF-----ASNEVYVNAKDLDPEKNDSEPGSGORIKPVVIDDANCR 157  
 DB 125 --VKASGRKLEKTVSVNVAAGSKVTFELTYELLKRNKGKYMVLKVP-----K 173  
 QY 158 QISYQHAHVHPDIYEGSTIVLNLMTSALDVEFKKNREEDPSLLMQVFGSA-----T 212  
 DB 174 QL-VRH--FEIDAHIEPQGI-----SMLD-----ABASFTINDLLGSALTSPS 215  
 QY 213 GLARYYPASPDWNSRT-PNKTID-----LYDVRPP-----WYI-----QG- 247  
 DB 216 GKKGHSFSPSLDQQRSCPTCTDSLNGDFTIYDYNRESQNVQIVNGYFFHFAPOGL 275  
 QY 248 AASPDKLILVDVSGVSLTKLINTSVSEMLETISDDDFNVASFNASNAODVSCFO-H 306  
 DB 276 PVYPKNIVFIDVSGMSGRKIQOTREALKILDDVKEDDYINFLFST-----DVTWKDH 332  
 QY 307 LVOANVRNKKVLKADVNNITAKITDYKGFSAFQOLLNLYNVRAN-----CNKIIML 360  
 DB 333 LVQATPANLKEARTFVKNIHQDSMTNINDGLKGTEML---NKAREDTVPERSSTIIM 389  
 QY 361 FTDG-----GEERAQETFAKYN--DKKVRVFTFSVGOHNDYRGPTQWMAENKGYEYELP 414  
 DB 390 LTDGDANTGESRPEKTOENVRNAIGGKFLYNLGFG--NNLNTNFLTALENHGLARRIY 448  
 QY 415 SIGAIRINTQEVLDVLRPMVLGAKAKOVQNTVYLDALGLVITGLPVENITGONE 474  
 DB 449 EDSANDLQLQGGVEEVANPL-----TNYEVEYENA-----ILDITRNSY 489  
 QY 475 NKTNLKNQILGMVGVDVSLDIEKRLTPRTLCPNGYFAIDPNQYVLLHLPNLPKNPKS 534  
 DB 490 PHFYDGSVEIVAGRLDRNMN-----FKADVKHGALN-----DLTF 527  
 QY 535 QEPVTLDFDALENDIKVEIRNKMIDGSGEK--TFRTLVKSQDERYIDKGNRYTWTTP 592  
 DB 528 TEVDMEEMDAALK-----EGYIFGDYIERLWAYLTIEOLLKRNKNAKDEKENIT- 579  
 QY 593 VNGDYSLA--LVLPITYSPYIKAKIEETITQARSKKGMKMDSET-----LKPDPNEESG 645  
 DB 580 AEALDLSLAYHFVPLTSMVVTKPEDNEQTSIADNAGEAFATYTSFLTTQOSSGP 639  
 QY 646 YTFIAPRDYCNLDKISDNNTEFLNFEIDRKTPNPNSCNTDLINRVLLDAGFTNELVQ 705  
 DB 640 YYYV-----DGPDPHTIQI-----PGKNDISICFNIDEKPGCTVLRLIQ 676

## RESULT 7

ITH3\_HUMAN  
 ID ITH3\_HUMAN STANDARD; PRT; 885 AA.  
 AC Q06033; Q99085;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Inter-alpha-trypsin inhibitor heavy chain H3 precursor (ITI heavy  
 chain H3) (Serum-derived hyaluronan-associated protein) (SHAP).  
 GN ITH3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=93215656; PubMed=7681778;  
 RA Bourguignon J., Diarra-Mehrpour M., Thiberville L., Bost F.,  
 Sesboue R., Martin J.P.;  
 RT "Human pre-alpha-trypsin inhibitor-precursor heavy chain. cDNA and  
 deduced amino-acid sequence.";  
 RL Eur. J. Biochem. 212:771-776(1993).  
 RN [2]  
 RP SEQUENCE OF 341-885 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=89137072; PubMed=2465147;  
 RA Diarra-Mehrpour M., Bourguignon J., Sesboue R., Mattei M.-G.,  
 Passage E., Sallier J.P., Martin J.P.;  
 RT "Human plasma inter-alpha-trypsin inhibitor is encoded by four genes  
 on three chromosomes.";  
 RL Eur. J. Biochem. 179:147-154(1989).  
 RN [3]  
 RP SEQUENCE OF 30-49; 463-477 AND 497-515.  
 RX MEDLINE=89380192; PubMed=2476436;  
 RA Engchild J.J., Thøgersen I.B., Pizzo S.V., Salvesen G.;  
 RT "Analysis of inter-alpha-trypsin inhibitor and a novel trypsin  
 inhibitor, pre-alpha-trypsin inhibitor, from human plasma.";  
 RL J. Biol. Chem. 264:15975-15981(1989).  
 RN [4]  
 RP SEQUENCE OF 631-647, AND CROSS-LINKAGE SITE TO BIKUNIN.  
 RX MEDLINE=91093267; PubMed=1898736;  
 RA Engchild J.J., Salvesen G., Hefta S.A., Thøgersen I.B.,  
 Rutherford S., Pizzo S.V.;  
 RT "Chondroitin 4-sulfate covalently cross-links the chains of the  
 human blood protein pre-alpha-inhibitor.";  
 RL J. Biol. Chem. 266:747-751(1991).  
 CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A  
 BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,  
 INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE  
 LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE  
 ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES.  
 CC -1- SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM  
 ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,  
 BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2  
 AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND

QY 706 NYWSKOKNIKVKARFVVTDGITRVYPKEAGENQENPETEYDSFYKRSLDNDNYVETA 765  
 DB 677 D-----PVT--GIT-VTGIIIGD-----KRS--NASSRTGK 702  
 QY 766 PYFNKSGPGAYESGIMVSKAVEIYIQGLKLLPAPVGVKIDVNSWIENTTKTSIRDPCAGP 825  
 DB 703 TYFGLGLGITNAMDPRVEVTEKIILG-----TGABELSTFSWLDITVTVTQ-----TGL 750  
 QY 826 VDCCKRNSDVMDCVILDDG-GFLLMAN-----HDDYTNQIGRFFGEIDPSLMRLHVN 876  
 DB 751 SVTINRKNMV--VSFGDGISFVILHQVWKHPVHQDFLG-----FYVDSHRMSAOTH 803  
 QY 877 ISVYAFNKSYDQSV-CEPGAAP 898  
 DB 804 GLLGQFFQPFDFKVFGRPGSDP 826



BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.  
 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE.  
 -1- SIMILARITY: BELONGS TO THE ITH FAMILY.  
 -1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.

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EMBL; X67055; CAA47439.1; -  
 EMBL; X14690; CAA32821.1; -  
 GenBank; HGNC:6168; ITH3.  
 MIM; 146650;  
 InterPro; IPR002035; VWF\_A.  
 Pfam; PF00092; vwa; 1.  
 SMART; SM00327; VWFA; 1.  
 PROSITE; PS0234; VWFA; 1.  
 Serine protease inhibitor; Repeat; Signal; Multigene family;  
 Glycoprotein. 1 17 POTENTIAL.  
 SIGNAL 18 30  
 PROPEP 18 30  
 CHAIN 31 647  
 INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3.  
 PROPEP 648 885  
 DOMAIN 278 438  
 CARBOHYD 87 87  
 BINDING 576 576  
 CONFLICT 647 647  
 CONFLICT 344 344  
 CONFLICT 357 357  
 CONFLICT 846 846  
 SEQUENCE 885 AA; 99131 MW; BC63856F8F54A1B CRC64;

Query Match 3.5%; Score 185; DB 1; Length 885;  
 Best Local Similarity 21.3%; Pred. No. 0.0019;  
 Matches 137; Conservative 113; Mismatches 243; Indels 150; Gaps 36;

QY 45 VTLAKTASGVNQLDIYKQYQDIYVPEPNNARQVLEIARDTEKLLSNRKAIVRLALEA 104  
 DB 77 VELPKTAFITFTLTIT-----DGVTY-PGNVKE-KVAKQYKAVSGKTAGL----- 123  
 QY 105 EKVOAAHWRDEF-----ASNEVYVNAKDDLPKNDSEPGSQRIKPVFIDDANFGR 157  
 DB 124 --VKASGRKLEFTSVNVAAGSKVTFELTYEELLKRHKGYEMLYKVP-----K 172  
 QY 158 QISYQHAHVHPTDIYEGSTIVLNLNMTSALDEVFKKNREEDPSLLWQVFGSA-----T 212  
 DB 173 QL-VKHFIEV--DIPEQGI-----SMLD-----AEASFTINDLLGSALTCKFS 214  
 QY 213 GLARYYPASPWDNST-PNKKID-----LYDVRRP-----WYT-----QG- 247  
 DB 215 GKRGHVSFPKSLDQQRSCFTDLSLNGDFTITYDVNRESPGNVQIVNGYFHFPAQGL 274  
 QY 248 AASPDKMLILVDVSGSVGLTLKIRTSVSEMLTSDDDFVNVAFSNADVSCF-OH 306  
 DB 275 PVVPKVNVAVIDISGSMAGRKLEQTKALLRILEDKMEEDYLNFLFSG---DVTWKEH 331  
 QY 307 LVOANVRNKKVLKADVNTTAKGIDYKKGFSFAFQLNLYNVR-----ANCNKIIML 360  
 DB 332 LVQATPENLQEARFTFKSKMEDKGMTINDGLLRGISML---NKAREHRIPERSTSIIV 388  
 QY 361 FTDG-----GEERAQEIFAKYN--DKKVRVFTFSQOHNYDRGPQIOWACENKGYEYIP 414  
 DB 389 LTDGDGAVNGESPEKIQENVRNAIGKGFPLYNLGFG--NNLNTNFLENMALENHGFARIY 447  
 QY 415 SIGAIRINTQEVLDVIGRPWLAGAKAKOVMTNIVYLDAL-----LGLVITGTL 465  
 DB 448 EDSADADLQGGVEEVANPL-LTGVEMEYPE--NAILDLTQNTYOHFYDGSIVVAGRLV 504

QY 466 VFNITGQENKTNLK-----NQLILGVMGVDSLEIKRLTPRFTLCPNGYYPADPN-- 518  
 DB 505 DEDM--NSFKADVKGHGATNDL---TFTTEVDKMEK-----ALQERYIFG---NYI 550  
 QY 519 ----GYVLLHPNLOPK---NPKSQEPVTLDFLDAELENKIKVEIRKNKMDGSEKFTFT 571  
 DB 551 ERLWAYITIPQLLEKKRNAHGEKENITARALDLSIKYHFVTLTSMVTKPE----- 603  
 QY 572 LVKSQDERYI-DKGNRTYTTPVN-GTDSYLSALVLPYSPYI 612  
 DB 604 --DNEDEIRAADKPGDAEATPVSPMSYLTSTYQPPONPIYV 644

RESULT 8  
 ITH3\_RAT  
 ID ITH3\_RAT STANDARD; PRT; 887 AA.  
 AC Q63416;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Inter-alpha-trypsin inhibitor heavy chain H3 precursor (ITI heavy chain H3).  
 DE ITH3.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=101116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;  
 RA Blom A., Fries E.;  
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY SIMILARITY).  
 CC -1- SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN.  
 CC BIKUNIN, INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2 AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.  
 CC -1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE ITH FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.

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EMBL; X83231; CAA58233.1; -  
 InterPro; IPR002035; VWF\_A.  
 Pfam; PF00092; vwa; 1.  
 SMART; SM00327; VWFA; 1.  
 PROSITE; PS0234; VWFA; 1.  
 Serine protease inhibitor; Repeat; Signal; Multigene family;  
 Glycoprotein.  
 SIGNAL 1 21 POTENTIAL.  
 PROPEP 22 33 BY SIMILARITY.  
 CHAIN 34 647 INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3.  
 PROPEP 648 887 BY SIMILARITY.  
 DOMAIN 282 442 VWFA.  
 FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 580 580 N-LINKED (GLCNAC. . .) (POTENTIAL).



RESULT	9
ID	YFBK_ECOLI
IID	YFBK_ECOLI
AC	P76481;
PROT	STANDARD; PRRT; 575 AA.
REL	01-NOV-1997 (Rel. 35, Created)
DT	01-NOV-1997 (Rel. 35, Last sequence update)
DE	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Hypothetical protein yfbk.
OS	yfbk OR B2270.
OS	Escherichia coli.
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC	Escherichia.
NCBI_TaxID=562;	
[1]	SEQUENCE FROM N.A.
RP	STRAIN-K12 / MG1655;
RC	MEDLINE=97426617; PubMed=9278503;
RRX	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RRA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RRR	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RRR	Mau B., Shao Y.;
RRT	"The complete genome sequence of Escherichia coli K-12.";
RPT	Science 277:1453-1474(1997).
CCC	-!- SIMILARITY: TO SYNECHOCYSTIS PCC 6803 SLL0103.
CCC	-!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
CCC	-----
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CCC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CCC	or send an email to license@isb-sib.ch)
CCC	-----
EMBL:	AE000317; AAC75330.1; -
ECOGene:	EG14095; yfbk.
InterPro:	IIPR002035; VWF_A.
Pfam:	PF00092; vwa; 1.
SMART:	SM00327; VWFA; 1.
PROSITE:	PS50234; VWFA; 1.
Hypothetical protein; Complete proteome.	
DOMAIN	216 394 VWFA
SEQUENCE	575 AA; 63634 MW; 7BB6A1A77A2BE111 CRC64;
Query Match	3.2%; Score 168.5; DB 1; Length 575;
Best Local Similarity	21.6%; Pred. No. 0.0095;
Matches	111; Conservative 94; Mismatches 205; Indels 105; Gaps 24;
71	EPNNARQLVEITAARDIEKLNSRKALVRLALEAKVQAQHWREDFASNEWVYNAKDD 130
22	OPEKNESQQQPSPTEQQVLAAQQAATK---EAPQSAAA---AKALAQQEQVQSDKQA 75
131	LDPKND-----SEFGSQRIRKPVETDIDANFRGLSIYQHAA---VHIPIDI 172
76	LQGRLOEAPTFAAAKAKATHIANPGTARYQQF---DDNPVKQVAQNPLAFSLDVDGFS 132
173	YEGSTIVLE-----LNWTSALDEVFKNREEDPSLLWQVFGSATGLARY 218
133	YANYVRFLNQGLPPPDPAVRVEELVFNPPSDWDI--KDKQISPKPIPFAMRYELA--- 187
219	PASPWDNSRTPNKRIDLYDVRRRWPIQGAASPKMDLLILDVDVSGS-VSGLTLKLTITSVS 277
188	PA-PW-NEQRTLKAVDILLAKDRKSEULPAS----NLVFLIDTSGSMISDERLPFIQSSLK 241
278	EMLETLSDDDFVNVAASNADVCSCFOHLVOANVRNKKYLKDVAWNNTAKGITDYKKGFF 337
242	LLVKLEREQDNIAIVTAGDSRIA-----LPSISGSKHAEINAAIDSLDAGSTNGGAGL 296
338	SFAPEQLLNLYNVSRANCNKIIIMLFTDG-----GEERAQEITFAKNKDKKRVTFPSVGQ 391
297	ELAYQQOATK-GFIKGGINR-ILLATDGFNFVIDDPKSIESWKVKRGSGVTLSFTFGVN 354
392	HNYDRGPIONMACENKGYEYIPEISGAIRINTQBYDLVLRPMVL--AGDKAKGVQ --- 445

DB 355 SNYNEAMVRIADVGNVSYIDTSL-----BAQKVLNSEMRLITVAKDVKQAQLEFNPA 410  
QY 446 WTNVYLDALGLVGLVTLGVNITGNENKTNLKNQILGVGMVD-VSLEDI---KELT 501  
DB 411 WYTEY---RQIGYE-----KRQLRVEHFNNNDVNDAGDIGAGRHIT 447  
QY 502 PRTFLPCNGYFAIDPBGVLLHPLNLPKNPKSQE 536  
DB 448 LFLFELTNGQKASIDKLRYA--PDNKLAKSDTKYE 480  
RESULT 10  
ID ITH3\_MESAU STANDARD; PRT; 886 AA.  
AC P97280;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Inter-alpha-trypsin inhibitor heavy chain H3 precursor (ITI heavy  
chain H3) (H33).  
GN ITH3.  
OS Mesocricetus auratus (Golden hamster).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
OC Mesocricetus.  
OX NCBI\_TaxID=10036;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=97420688; PubMed=9276673;  
RA Nakatani T., Suzuki Y., Yamamoto T., Sinohara H.;  
RT "Molecular cloning and sequencing of cDNAs encoding three heavy-chain  
RT precursors of the inter-alpha-trypsin inhibitor in Syrian hamster:  
RT implications for the evolution of the inter-alpha-trypsin inhibitor  
RT heavy chain family.";  
RL J. Biochem. 122:71-82(1997).  
RN [2]  
RP SEQUENCE OF 31-50; 446-472 AND 504-523, AND SUBUNITS.  
RC TISSUE=Plasma;  
RX MEDLINE=97018241; PubMed=8864857;  
RA Yamamoto T., Yamamoto K., Sinohara H.;  
RT "Inter-alpha-trypsin inhibitor and its related proteins in Syrian  
RT hamster urine and plasma.";  
RL J. Biochem. 120:145-152(1996).  
CC -!- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A  
CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,  
CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE  
CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE  
CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY  
CC SIMILARITY).  
CC -!- SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM  
CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,  
CC BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2  
CC AND BIKUNIN. INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND  
CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.  
CC -!- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN  
CC 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY  
CC SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE ITH3 FAMILY.  
CC -!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.  
CC -----  
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CC -----  
CC EMBL; D89287; BAA13940.1; -  
CC InterPro; IPR002035; VWF\_A.  
CC Pfam; PF00092; vwa; 1.  
CC

DR SMART; SM00327; VWA; 1.  
DR PROSITE; PS0234; VWFA; 1.  
KW Serine protease inhibitor; Repeat; signal; Multigene family;  
KW Glycoprotein. 1 18 POTENTIAL.  
FT SIGNAL 19 30 BY SIMILARITY.  
FT PROPEP 31 646 INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN  
FT CHAIN H3.  
FT PROPEP 647 886 BY SIMILARITY.  
FT DOMAIN 279 439 VWFA.  
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 577 577 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT BINDING 646 646 CHONDROITIN 4-SULFATE, CROSS-LINK SITE  
FT (BY SIMILARITY).  
SQ SEQUENCE 886 AA; 99018 MW; AC0594CG65276B8 CRC64;  
Query Match 3.1%; Score 166; DB 1; Length 886;  
Best Local Similarity 23.2%; Pred. No. 0.025;  
Matches 66; Conservative 57; Mismatches 111; Indels 51; Gaps 11;  
QY 202 SLLMQVFGSATGLARYYPASPVDNSRT-PNKID-----LYDVRRL-PWYIOGA-- 248  
DB 208 SALTKEFSFGKKGHVSPKPS---LDQQRSCPTCTDSLNGDFTIVDVNRESPGNVQVWG 264  
QY 249 -----ASPKDMLILVDVSGSVGLTLKLTISYSEMLETLSDDDFNVASFNS 296  
DB 265 YFVHFFAPOGLPVVYKNIIVFIDISSMAGRKIQOTRVALKILDMMKQDDYLNFLFST 324  
QY 297 NAQDVSCFQHLVQANVRNKKVLDVNNITAKGITDYKKGFSFAFEOLLN---YVVSRA 352  
DB 325 GV--TTWKDSLVOATPANLEARTFVSISDOGMTINDGLRGIMLTDAREQHIVPER 382  
QY 353 NCNKIIMFTDG-----GEERAQEIFAKYKDKKVKRVFTSVG-OHNVDRGPIDQWACENK 407  
DB 383 STSIIML-TGDANTGESRPEKIQENVRKAIEGRFPLNLFNGFNGLNYNFMLETMALENH 441  
QY 408 GYVEIPESIGAIRINTQYLDVLGRPMVLACDRKAKQVQWTVNYLD 452  
DB 442 GVARRIYEDSDANLQLOGFVEEVANPLL-----TNVEVE 475  
RESULT 11  
ID DPOL\_THEST STANDARD; PRT; 1829 AA.  
AC O33845;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE DNA polymerase (EC 2.7.7.7).  
GN POL..  
OS Thermococcus sp. (strain TY).  
OC Archaea; Euryarchaeota; Thermococci; Thermococcaceae;  
OC Thermococcus.  
OX NCBI\_TaxID=110163;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=98094267; PubMed=9434178;  
RA Niehaus F., Frey B., Antranikian G.;  
RT "Cloning and characterisation of a thermostable alpha-DNA polymerase  
RT from the hyperthermophilic archaeon Thermococcus sp. TY.";  
RL Gene 204:153-158(1997).  
CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate  
CC + [DNA] (N).  
CC -!- PTM: THIS PROTEIN UNDERGOES A PROTEIN SELF SPLICING THAT INVOLVES  
CC A POST-TRANSLATIONAL EXCISION OF THE THREE INTERVENING REGION  
CC (INTEINS) FOLLOWED BY PEPTIDE LIGATION.  
CC -!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; D89287; BAA13940.1; -  
CC InterPro; IPR002035; VWF\_A.  
CC Pfam; PF00092; vwa; 1.  
CC

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CC  EMBL: Y13030; CAA73475.1; -.
CC  HSSP; P56889; IYGO.
DR  InterPro; IPR002064; DNA_pol_B.
DR  InterPro; IPR003586; Hedgehog_hintC.
DR  InterPro; IPR003587; Hedgehog_hintN.
DR  InterPro; IPR002203; Intein.
DR  InterPro; IPR004042; Intein_endonuc.
DR  InterPro; IPR004578; Pol2.
DR  Pfam; PF00136; DNA_pol_B; 4.
DR  Pfam; PF03104; DNA_pol_B_exo; 1.
DR  PRINTS; PR00379; INTEIN.
DR  SMART; SM00305; HintC; 3.
DR  SMART; SM00306; Hintn; 3.
DR  SMART; SM00486; POLBc; 1.
DR  TIGRFAMs; TIGR00592; pol2; 2.
DR  PROSITE; PS00116; DNA_POLYMERASE_B; FALSE_NEG.
DR  PROSITE; PS00818; INTEIN_C_TER; 3.
DR  PROSITE; PS00819; INTEIN_ENDONUCLEASE; 2.
DR  PROSITE; PS00817; INTEIN_N_TER; 3.
KW  Transferase; DNA-directed DNA polymerase; DNA replication;
KW  DNA-binding; Hydrolase; Endonuclease; Autocatalytic cleavage;
KW  Protein splicing.
FT  CHAIN 1 409 DNA POLYMERASE, 1ST PART (POTENTIAL).
FT  CHAIN 410 769 INTEIN I.
FT  CHAIN 770 855 DNA POLYMERASE, 2ND PART (POTENTIAL).
FT  CHAIN 856 1392 INTEIN II.
FT  CHAIN 1393 1441 DNA POLYMERASE, 3RD PART (POTENTIAL).
FT  CHAIN 1442 1598 INTEIN III.
FT  CHAIN 1599 1829 DNA POLYMERASE, 4TH PART (POTENTIAL).
SQ  SEQUENCE 1829 AA; 211875 MW; A113A8BC57EB9CB3 CRC64;

Query Match 3.08; Score 162; DB 1; Length 1829;
Best Local Similarity 20.88; Pred. No. 0.13; 294; Indels 284; Gaps 42;
Matches 178; Conservative 101; Mismatches 86;

QY 16 SLLIGSSQEPFPS-----AVTIKSW-----DKMQEDLVTLA 48
DB 229 TLLGRDKEHPKTHRMGDSFAVEIKGRIHDFLPVVRRTINLTYTLEAVEAVLGKT 288
QY 49 KTASGVNOLVDIEYKQDL-----YVPEPNARQLVETAAKDIEKLSNRKALVRLALE 103
DB 289 KSKLGAETIAATWETESMKLAQSM-----DARATYEL-----GKEFPPEAE 334
QY 104 AEKVQAQHQRDFAS--NEVYY-----NAKDDLPKNDSEPGSQRIKPVFI----- 150
DB 335 LAKLIGQSVMSRSTGNLVEWYLLRVAYERNELAPNKPDEEYRRRLRTTYLGGVYKE 394
QY 151 DDANFGROISYQAAVHIPTD---IYEGSTIV---LNLNWTSAIDVFKKNEEDPSL 203
DB 395 PERGLWENLAYLDFRCH-PADTKVIVKGKGVINSDVKEGYILGIDG----- 441
QY 204 LMQVFGSATGLARYYPASPDVNSR---TPN-KIDLYDVRRPVWYIQGAAPKMDLILVD 259
DB 442 -WQ--RVKVKWKYHIEGKLINGLKCTPNHKVPVVTENDRQTRI-----RDSLAKSF 491
QY 260 VGSVSGLTALKIRTSVSEMLETSLDDDFVNVASFNSN----- 297
DB 492 LSGKVKG---KIITTKL-----FEKIAFEKKNPSEETLKGELSGIILAEQTL 537
QY 298 -AQDVSCF-----QHLVQANV-RNKKVLKDAV-----NNITAKG----- 329
DB 538 LRKDIETFDSSRGKRKRISHOYRVEITIGENEKELLERYIFDKLFGIRPSVKKKGDFNA 597
QY 330 ---ITDYKKGFSFAPFOLLNYSNRANCKIIMLFTDGGEEAQAETFAKYNKDKKVRVTF 387
DB 598 LKITTAKKAVYLIQIEELAK-NIESLYAPAVLGRGF-----ERDAVNRKIRSTIVYT- 647
QY 388 SVQHNVDGRGPIQWACENKGY---YYEIPSGAIRINTQEVLDVLGRPMVLGADKQKV 444
DB 648 -QCTNNKWKIDIVAKLLDLSLGIPIYSRYKYIENGKELTKHITETGRD----- 695

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QY 445 QWTVNYDLALELGLVITGTLPVFNITQNE-----NKTNLKNQLILGVMGVDVSLE 495
DB 696 -----GLILFQTLVGFISSEKNEALEKLEVRMNRKKNNSFYNLSTFVSSE 743
QY 496 DIRRLTPRFTLCPNGYFAIDPNGYVLLHPNLOPKPKPSOEPTVTLDFDAELENDIKVEI 555
DB 744 YKGEVYDLTLEGNYYFA---NG-ILTHNSLYPSLIIVTHN-VSPDTLRE----- 789
QY 556 RNKWDGSEGEKTFRTLKVSQDERYIDKGNRTVTWTPVNGTDYSLALVLTPTSYFYVIKAK 615
DB 790 -----CKNVDVAPIVG--YKCKDFPG-----FIPSI 815
QY 616 IETITQARSKKGMKMDSETLKPDNFEESY-----TFIAPRDYCNLDKISDNTE 666
DB 816 LGEIITMRQEKIKKMK--ATIDPIEKMLDYRQRAVKVLLANSILPNW---LPIIENGVE 870
QY 667 FLINFEFDR-----KTPNPNPCNTDLINRVLLDAGFTNVLVONTWSKOKNKGKARF 721
DB 871 KFKVIGEFIDRYMEEQDKVRYTVDNTEVLF---VDNIFAFSL--NKESKKSEIKKYKAL- 924
QY 722 VVTDGGITRVYPKEAGE 738
DB 925 -----IRHKYGEAYE 935

RESULT 12
Y103_SYNY3
ID Y103_SYNY3 STANDARD; PRT; 420 AA.
AC Q55874;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein sl10103.
GN SL10103
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96127529; PubMed=8590279;
RA Kaneko T., Tanaka A., Sato S., Kotani H., Suzuki T., Miyajima N.,
RA Sugiyura M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT region from map positions 64% to 92% of the genome.";
RL DNA Res. 2:153-166(1995)
CC -!- SIMILARITY: TO E.COLI YF8K.
CC -!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
CC -----
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DR EMBL: D64004; BAA10635.1; -.
DR InterPro: IPR002035; VWF_A.
DR Pfam; PF00092; vwa; 1.
DR SMART; SM00327; VWFA; 1.
DR PROSITE; PS0234; VWFA; 1.
KW Hypothetical protein; Complete proteome.
FT DOMAIN 43 215 VWFA.
SQ SEQUENCE 420 AA; 45849 MW; E7111B51478E74F3 CRC64;

Query Match 3.08; Score 160.5; DB 1; Length 420;
Best Local Similarity 21.1%; Pred. No. 0.018;
Matches 86; Conservative 86; Mismatches 181; Indels 55; Gaps 16;

QY 251 PKDMLILVDYSGVSGLTALKIRTSVSEMLETSLDDDFVNVASFNSNAQDVSCFQHLVQA 310
DB 648 -QCTNNKWKIDIVAKLLDLSLGIPIYSRYKYIENGKELTKHITETGRD----- 695

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Db 41 PLNCLVLDHSGMDQPLETVKSAALGLIDRLIEDRLSLVIAFDHRAKIV-----IENQ 95  
 QY 311 NVNKKVLDKANNITAKITDYKKGFSFAFQQLNLYNVNVRANCKIIMLFDDGGEAAQ 370  
 Db 96 QVNGAAIAIAERKAEGGTADICGLIGIQEAARKGREDVRS---HIFLLTDGENEHGD 152  
 QY 371 E-----IFAKYNDKKVRVFTSFVSGHNYDRGPIONMACENKG---YYEIPSGAIRINTQ 424  
 Db 153 NDRCLKLGTVASDYKLVITLFGDGH-WNODVLEIAASAQGSLSYIENPS-EALHTFRQ 210  
 QY 425 EYLDVLGRPMVLADGKAKOVONTNVLDALELG-----LVITGLPVPFNITGONENKTNLK 480  
 Db 211 LF-----QRMSNVGLTNAHL-LLELAPOAHLAI--VKPVAQVSPETMDLT-VQ 254  
 QY 481 NQLILGVMGVDVSLDIKRLTFRFPCNPYFAIDPNQYVLLHNPLOPKPKSOE----- 536  
 Db 255 NQGAIEEVLGLMDLTDQERV-----LLNLXLDQLLPQGHVIGQVQIIRYDDPASQTNLL 309  
 QY 537 ----PVTLDFAELNDIKVIRNMKIDGESGKT--FRLVKSQDERYIDKGNRTYTW 590  
 Db 310 SDPLPLTIQ-VQTQYQPTDQVQVQSILTLAKYRQTQIAETKLRAGDQGAATMLQTAAK 368  
 QY 591 TPVNGTDVSLALVLTPTSPFYIKAKIETITQARSKKGKMDSEFLKP 638  
 Db 369 TALQMGDKNGATILQTN-----TRLQSGEDLSGDRKTRMVSKTTLQ 413

RESULT 13  
 ITH2\_HUMAN  
 ID ITH2\_HUMAN STANDARD; PRT; 946 AA.  
 AC P19823; Q15484; Q14659;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DE 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy  
 DE chain H2) (Inter-alpha-trypsin inhibitor complex component II)  
 DE (Serum-derived hyaluronan-associated protein) (SHAP).  
 GN ITH2 OR IGHEP2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE=8815237; PubMed=2450046;  
 RA Gebhard W., Schreitmuller T., Hochstrasser K., Wachter E.;  
 RT "Complementary DNA and derived amino acid sequence of the precursor  
 RT of one of the three protein components of the inter-alpha-trypsin  
 RT inhibitor complex.";  
 RL FEBS Lett. 229:63-67(1988).  
 RN [2]  
 RP SEQUENCE OF 384-865 FROM N.A.  
 RX MEDLINE=88068576; PubMed=2446322;  
 RA Salier J.P., Diarra-Mehrpour M., Sesboue R., Bourguignon J.,  
 RA Benarous R., Okubo I., Kurachi S., Kurachi K., Martin J.P.;  
 RT "Isolation and characterization of cDNAs encoding the heavy chain of  
 RT human inter-alpha-trypsin inhibitor (I alpha TI): unambiguous  
 RT evidence for multipolypeptide chain structure of I alpha TI";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:8272-8276(1987).  
 RN [3]  
 RP SEQUENCE OF 384-766 FROM N.A.  
 RX MEDLINE=89076497; PubMed=2462430;  
 RA Salier J.P., Diarra-Mehrpour M., Sesboue R., Bourguignon J.,  
 RA Martin J.P.;  
 RT "Human inter-alpha-trypsin inhibitor. Isolation and characterization  
 RT of heavy (H) chain cDNA clones coding for a 383 amino-acid sequence  
 RT of the H chain.";  
 RL Biol. Chem. Hoppe-Seyler 369:15-18(1988).  
 RN [4]  
 RP PARTIAL SEQUENCE FROM N.A.  
 RX TISSUP=Liver;  
 FC MEDLINE=88024442; PubMed=3663330;  
 RA Schreitmuller T., Hochstrasser K., Resinger P.W.M., Wachter E.,

RA Gebhard W.;  
 RT "cDNA cloning of human inter-alpha-trypsin inhibitor discloses three  
 RT different proteins.";  
 RL Biol. Chem. Hoppe-Seyler 368:963-970(1987).  
 RN [5]  
 RP SEQUENCE OF 55-74; 116-127; 224-246; 295-307 AND 365-385.  
 RX MEDLINE=89380192; PubMed=2476436;  
 RA Enghild J.J., Thøgersen I.B., Pizzo S.V., Salvesen G.;  
 RT "Analysis of inter-alpha-trypsin inhibitor and a novel trypsin  
 RT inhibitor, pre-alpha-trypsin inhibitor, from human plasma.  
 RT Polypeptide chain stoichiometry and assembly by glycan.";  
 RL J. Biol. Chem. 264:15975-15981(1989).  
 RN [6]  
 RP SEQUENCE OF 55-64.  
 RC TISSUE=Plasma;  
 RX MEDLINE=93039735; PubMed=1384548;  
 RA Malki N., Balduyck M., Maes P., Capon C., Mizon C., Han K.K.,  
 RA Tartar A., Fournet B., Mizon J.;  
 RT "The heavy chains of human plasma inter-alpha-trypsin inhibitor: their  
 RT isolation, their identification by electrophoresis and partial  
 RT sequencing. Differential reactivity with concanavalin A.";  
 RL Biol. Chem. Hoppe-Seyler 373:1009-1018(1992).  
 RN [7]  
 RP SEQUENCE OF 55-64 AND 681-702, CROSS-LINK STRUCTURE, AND  
 RC CARBOHYDRATE-LINKAGE SITES T-691.  
 RX MEDLINE=93232026; PubMed=7682553;  
 RA Enghild J.J., Salvesen G., Thøgersen I.B., Valnickova Z.,  
 RA Pizzo S.V., Hefta S.A.;  
 RT "Presence of the protein-glycosaminoglycan-protein covalent cross-link  
 RT in the inter-alpha-inhibitor-related proteinase inhibitor heavy chain  
 RT 2/bikunin.";  
 RL J. Biol. Chem. 268:8711-8716(1993).  
 RN [8]  
 RP SEQUENCE OF 67-101, AND HYALURONAN BINDING.  
 RC TISSUE=Serum;  
 RX MEDLINE=94075371; PubMed=7504674;  
 RA Huang L., Yoneda M., Kimata K.;  
 RT "A serum-derived hyaluronan-associated protein (SHAP) is the heavy  
 RT chain of the inter-alpha-trypsin inhibitor.";  
 RL J. Biol. Chem. 268:26725-26730(1993).  
 RN [9]  
 RP SEQUENCE OF 699-702, AND COVALENT LINKAGE WITH CHONDROITIN SULFATE.  
 RC TISSUE=Plasma;  
 RX MEDLINE=94229087; PubMed=7513643;  
 RA Morelle W., Capon C., Balduyck M., Sautiere P., Kouach M.,  
 RA Michalski C., Fournet B., Mizon J.;  
 RT "Chondroitin sulphate covalently cross-links the three polypeptide  
 RT chains of inter-alpha-trypsin inhibitor.";  
 RL Eur. J. Biochem. 221:881-888(1994).  
 RN [10]  
 RP CARBOHYDRATE-LINKAGE SITES, AND MASS SPECTROMETRY.  
 RX MEDLINE=98343966; PubMed=9677337;  
 RA Flahaut C., Capon C., Balduyck M., Ricart G., Sautiere P., Mizon J.;  
 RT "Glycosylation pattern of human inter-alpha-inhibitor heavy chains.";  
 RN [11]  
 RP CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.  
 RX MEDLINE=98087700; PubMed=9425062;  
 RA Olsen E.H.N., Rahbek-Nielsen H., Thøgersen I.B., Roepstorff P.,  
 RA Enghild J.J.;  
 RT "Posttranslational modifications of human inter-alpha-inhibitor:  
 RT identification of glycans and disulfide bridges in heavy chains 1 and  
 RT 2.";  
 RL Biochemistry 37:408-416(1998).  
 CC -!- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A  
 CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,  
 CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE  
 CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE  
 CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES.  
 CC -!- SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM  
 CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,  
 CC BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2  
 CC AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND

159	QY	ISYQH-----AAVHPITDIYEGSTIVLNELWTSALD-----EYFKKNREE-----	199
192	Db	GSYEHRIYQLQGRLAKHLIEDVVVIEPOGLRFLHPYDFTFEGHFGCVPIVSKGQOKAHVSF	251
200	QY	DFSLLWQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVRRRP-----WYIOGAA	249
252	Db	KPTVAQQ-----RICPSCR--ETAVDGELVLYDYKREEKAGELEVNGYFVHFFA	300
250	QY	S-----PKDMLILVDVSGSVSGLTLKLIRTSVSEMLETLSDDDPVNVASPNNAQDVSC	303
301	Db	PNLDPPIPKNILLFIDVSGMWGVKMKQTVKAMKTLDDLRAEDHFSIDFNQNIIR--TW	358
304	QY	FQHLVQANVRNKVYLKDAYNNITAKGITDYKKGFE--SPAFQQLNLYNVRANCKNIIML	360
359	Db	RNDLISATKTQAVADAKRYTEKTOPSGGTNINALLRAIFILNEANNLGLDPSVSLIIL	418
361	QY	FTDG-----GEERAQEIFAKYNDKKVRVFTFSGVQ--HNYDRGPIDWMAACENKG--	408
419	Db	VSDGDPFVGELEKLSKTQKNVKNIQDNIISLSLGMGFDVDYDFLKRSLNSHENHIAQRIYV	478
409	QY	-----YYVEI--PSIGAIRIN--TOEYLDVL-----GRPMVLAG--DKAKQ	443
479	Db	NODTSSOLKKFYNOVSTPLLRNVQFNPHTSVTDVTQNNFHYFGGSEIIVVAGKFDPAK-	537
444	QY	VQNTNYLDALEGLGIVTGLPFVNITGQNKNTLKNOLILGVMGVDVSLEDI-----	499
538	Db	LOGIE--SWITA-----TSANTQLVLETLQAMDLDQDFLSKDKH	574
500	QY	LTPRFILCPNGYYFAIDPNGYVILLHPNLQPNKPKQSEPTVTLDFDLAELENDIKVEIRNM	559
575	Db	ADPQFTR-KLWAYLTIN--QLLAERSLAP-TAAAKRRITRSILOMSLDHIVTPTLSLV	629
560	QY	IDGSGEKTPTRTLVKSQD	577
630	Db	IENEGDERMLADAPPQD	647
RESULT 14			
ATX1_PLAFA			
ID	ATX1_PLAFA	STANDARD;	PRT; 1956 AA.
AC	Q04956;		
DT	30-MAY-2000 (Rel. 39, Created)		
DT	30-MAY-2000 (Rel. 39, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
OS	Probable cation-transporting ATPase 1 (EC 3.6.3.-).		
OS	Plasmodium falciparum.		
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.		
NCBI_TaxID	=5833;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=T9/96;		
RX	MEDLINE=93132070; PubMed=8421054;		
RA	Krishna S., Cowan G., Meade J.C., Wells R.A., Stringer J.R.,		
RA	Robson K.J.;		
RT	"A family of cation ATPase-like molecules from Plasmodium		
RT	falciparum.";		
RL	J. Cell Biol. 120:385-398(1993).		
CC	- - CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.		
CC	- - SUBCELLULAR LOCATION: Integral membrane protein.		
CC	- - SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2		
CC	ATPASES). SUBFAMILY V.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
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CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>		
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).		
CC	-----		
DR	EMBL; X65738; CAA46646.1; -		
DR	InterPro; IPR001757; ATPase_E1-E2.		

[illegible]

DB	517	KNKNWLS--DFTHIK--	-----EMNTSEYIHSKDDNIHKN-----	549
QY	593	VNGDYSLALVLPYTFYFYKAKIEETIQA	RSKSGKMKMD-----SETLKPDNFE	642
DB	550	-----STISEYIKDNKNLHFTSSK--K	KSITERSNFWLQVTKSCLLKDHYIK	596
QY	643	ESGYFTIAPRDYCNDLKISDNN--TEFLN	-----FNEF--IDRKTNNPSCNTDLINRV	693
DB	597	EKKKEYTNNYTCNDLHINDSTCSSYLLNS	ETKDAYCEYYNIDH-----LCD---INKK	647
QY	694	LLDAGFTNVLQVYWSKQKNIKGVKARFV	VDGGITRVYPKEAGENWQENPETYEDSYK	753
DB	648	NMDINSKNELMGKYSKNELMGKTIKNE	M-----GKYSK	681
QY	754	RLSDNDNVYTABYFNKSGPGAYESGIMV	SKAVEIYIIGKLLKPAVVG-----IKIDVN	807
DB	682	NEL-----MGYSKNELMGKYSKNELMG	KYSKNELMGKYSKNELMGKTIKNQGVDTN	734
QY	808	SWTENFTKTSIRD--PCAGPVCDCRNSV	MDCV-----ILDGGFLLMANHDDYTNQIGRF	862
DB	735	IYHMCNCDNYDYPCD---YNCNCCNDYH	HRLEYHNKONSFNIPPEKKNYSNISEH	791
QY	863	-----FGEIDPPLMRHLVNIYSYAF	-----NKS	886
DB	792	IKINYILLFEALACCHTLSKVNNKMGD	VLEITMFNTCDMLNNNSFIKEKKKNC	851
QY	887	DYQSVCEPGAAPKQAGHRSAYVPSIAD	ILHIGWATAAAWSIIQQFLLSLTFPRLL	946
DB	852	DFOKI--DGDKNIGANDERCHLN-----	NIVSYNILKRF-----	884
QY	947	EMEDDDFTASLSKQSCITBQTYFFDND	SKS 977	
DB	885	-----EFQSRQLRMSVIVKST--YGN	NDDNN 909	
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AC	P97279;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy			
DE	chain H2) (HC2).			
GN	ITI2.			
OS	Mesocricetus auratus (Golden hamster).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;			
OC	Mesocricetus			
OX	NCBI_TaxID=10036;			
RP	[1]			
RN	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RC	MEDLINE=97420686; PubMed=9276673;			
RA	Nakatani T., Suzuki Y., Yamamoto T., Sinohara H.;			
RA	"Molecular cloning and sequencing of cDNAs encoding three heavy-chain			
RT	precursors of the inter-alpha-trypsin inhibitor in Syrian hamster:			
RT	implications for the evolution of the inter-alpha-trypsin inhibitor			
RT	heavy chain family.";			
RT	J. Biol. Chem. 267:1241-1245 (1992).			
RT	J. Biochem. 122:71-82(1997).			
RN	[2]			
RN	SEQUENCE OF 55-64; 140-146; 151-156; 424-447; 500-528 AND 577-605,			
RP	AND SUBUNIT8			
RC	TISSUE=Plasma;			
RC	MEDLINE=97018241; PubMed=8864857;			
RA	Yamamoto T., Yamamoto K., Sinohara H.;			
RT	"Inter-alpha-trypsin inhibitor and its related proteins in Syrian			
RT	hamster urine and plasma.";			
RT	J. Biochem. 120:145-152(1996).			
CC	!- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A			
CC	BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,			
CC	INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE			
CC	LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE			

CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY  
CC SIMILARITY).  
CC -1- SUBUNIT: 1-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM  
CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,  
CC BIKUNIN. INTER-ALPHA-INHIBITOR (1-ALPHA-1) IS COMPOSED OF H1, H2  
CC AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (1-ALPHA-LI) OF H2 AND  
CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.  
CC -1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN  
CC 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY  
CC SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.  
CC -1- SIMILARITY: CONTAINS 1 WFA DOMAIN.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: D89286; BAA13939.1; -  
CC InterPro: IPR002035; WVF\_A.  
CC Pfam: PF00092; wva; 1.  
CC SMART: SM00327; WVA; 1.  
CC PROSITE: PS02234; WFA: 1.  
CC Glycoprotein.  
CC Serine protease inhibitor; Repeat; Signal; Multigene family;  
CC  
CC SIGNAL 1 18 POTENTIAL.  
CC PROPEP 19 54 BY SIMILARITY.  
CC CHAIN 55 702 INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN  
CC H2.  
CC  
CC PROPEP 703 946 BY SIMILARITY.  
CC DOMAIN 308 468 WFA.  
CC CARBOHYD 118 118 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC CARBOHYD 578 578 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC BINDING 702 702 CHONDROITIN 4-SULFATE, CROSS-LINK SITE  
CC (BY SIMILARITY).  
CC  
CC CONFLICT 510 510 V -> Y (IN REF. 2).  
CC CONFLICT 595 595 E -> I (IN REF. 2).  
CC SEQUENCE 946 AA; 106580 MW; CABF565458E7B2E CRC64;

Query Match 2.9%; Score 153; DB 1; Length 946;  
Best Local Similarity 19.9%; Pred. No. 0.16;  
Matches 128; Conservative 97; Mismatches 256; Indels 162; Gaps 31;

Db 604 IKRKITKTILOMSLDHIVTPTAMVNIENAGDE--RMLADSPQDHSKCCSGALYYGTV 661  
QY 594 NGTDYSLALVLPYTFYFYKAKIESTITQARSKKGMKDSSETLKPDPNE-ESGYTFI--- 649  
Db 662 ASAS-----IPSW-----ASPSPTPVNAMLAVGANRLESTPPPHVIRVENDPHFIYL 709  
QY 650 --APRDYCNDLK-----ISDNNTEFLNFEFIDRKTNNPNSCNT----- 687  
Db 710 PKSQKNKICFNIDSEPCIKLSLVSDEPESGILVN-GOLIGAKKAENGKLRITYEKLGFYFQK 768  
QY 688 -----DLINRVLLDAGFTNELVQVNSKQKNIGVKARFVWTDG-GITRVYPKE---- 735  
Db 769 EDMKIEISTENITLINGSSTTSL---FWSDTAHLGNQRVLISVKKGKSVTLTLNKEMFFS 825  
QY 736 --AGENWQENPEYEDSFYKRSKLDNDNVYFTAPYFNKSGPGAY 776  
Db 826 VLLHHVWKHP-----VNVDFLGILYLPPTNKFSPSAH 857

Search completed: February 10, 2003, 14:19:17  
Job time : 16.3394 secs

QY 235 LYDVRRRP-----WYTOGAAS-----PKDMLILVDVSGSVGLTLKLIRTSVSE 278  
Db 276 MYDVNREEKVGLEVFYVHFHAFAPENLDIPKNIILFVIDVSGMWGKMKQTVAMKT 335  
QY 279 MLETLSDDDFVNVASFNSAQDVSCFOHLVOANVRNKKVLKDAVNNTAKGITDYKKGF- 337  
Db 336 ILDDLRTEDQFSVDVFNHVR--TWNRDLVSATKTQITDAKRYIEKTOPSGGTNINEALL 393  
QY 338 --SFAPEQLLNVRNCRANKIIMLFDTG-----GEERAQEI--PAKYNKKKKRVFTFSV 389  
Db 394 RAIFILNEASNLGMLNPDOSVSLVLVSDGPTVGEGLSKIKQKNVQNIQDNISLFLGI 453  
QY 390 GQHYDRGPQIWMACENKG-----YYEYI--PSIGAIRINTOE--YLD 428  
Db 454 G-PDVDYDFLKLRLSNENRGIAQRYGNRDTSSQLKKFYNQVSTPLLRNVQFNPQASVTD 512  
QY 429 VL-----GRPMVLG--DKAKOVQWTVNYLDALEGLIVITGTLVPVFNITGQENKNT 477  
Db 513 VTQNSFHNFGSGEIVVACKYDPSK-----LAEQSIITAT-----ST 550  
QY 478 NLKNQLILGVNGYDVSLEDI----KRLTPRFTLCPNGYYFAIDPNGYVLLHPNLPKNPK 533  
Db 551 N--TELVLLETLSQMDLEDLFSLDKHADPNFTK-KLWAVLTIN---QLLAERSLAP-TAA 603  
QY 534 SQEPVTLDFLDALENDIKVEIRNKMIDGESGEKFTFLVKSQDERYIDKGNRTYTWTPV 593

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 10, 2003, 14:13:50 ; Search time 33.6207 Seconds  
(without alignments)  
4106.031 Million cell updates/sec

Title: US-10-090-827-7

Perfect score: 5446

Sequence: 1 MAAGCLLALTLTFLQSLIG.....RLLIQAQSTGDPDCDMVK 1036

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 13250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5446	100.0	1036	22 AAU01029	Pig secreted solub
2	5446	100.0	1036	22 AAB62253	Porcine calcium ch
3	5446	100.0	1063	22 AAU01030	Pig secreted solub
4	5446	100.0	1063	22 AAB62254	Porcine calcium ch
5	5446	100.0	1069	22 AAU01031	Pig secreted solub
6	5446	100.0	1069	22 AAB62255	Porcine calcium ch
7	5446	100.0	1091	22 AAU01027	Pig secreted solub
8	5446	100.0	1091	22 AAB62251	Porcine calcium ch
9	5380	98.8	1036	22 AAU01033	Human secreted sol
10	5380	98.8	1036	22 AAB62257	Porcine calcium ch

11	5380	98.8	1063	22 AAU01034	Human secreted sol
12	5380	98.8	1063	22 AAB62258	Porcine calcium ch
13	5380	98.8	1091	16 AAR71011	Human neuronal cal
14	5380	98.8	1091	19 AAW63145	Human calcium chan
15	5380	98.8	1091	21 AAB10576	Human calcium chan
16	5380	98.8	1091	22 AAU01035	Human secreted sol
17	5380	98.8	1091	22 AAB62259	Porcine calcium ch
18	5376	98.7	1091	19 AAW37879	Human calcium chan
19	5374	98.7	1091	14 AAR33553	Sequence of the al
20	5360.5	98.4	1110	19 AAW63148	Human calcium chan
21	5349	98.2	1018	22 AAU01028	Pig secreted solub
22	5349	98.2	1018	22 AAB62252	Porcine calcium ch
23	5340.5	98.1	1086	16 AAR71013	Human neuronal cal
24	5340.5	98.1	1086	19 AAW63153	Human calcium chan
25	5340.5	98.1	1086	21 AAB10587	Human calcium chan
26	5323.5	97.8	1084	16 AAR71015	Human neuronal cal
27	5323.5	97.8	1084	19 AAW63155	Human calcium chan
28	5323.5	97.8	1084	21 AAB10589	Human neuronal cal
29	5304	97.4	1103	16 AAR71012	Human calcium chan
30	5304	97.4	1103	19 AAW63151	Human neuronal cal
31	5304	97.4	1103	21 AAB10586	Human calcium chan
32	5288	97.1	1018	22 AAU01032	Human calcium chan
33	5288	97.1	1018	22 AAB62256	Porcine secreted sol
34	5284	97.0	1079	19 AAB63154	Porcine calcium ch
35	5284	97.0	1079	21 AAB10588	Human calcium chan
36	5278	96.9	1079	16 AAR71014	Human neuronal cal
37	5258.5	96.6	1106	18 AAW37712	Rabbit skeletal ca
38	5258.5	96.6	1106	18 AAW18389	Rabbit calcium cha
39	5258.5	96.6	1106	21 AAR77545	Rabbit skeletal ca
40	5237.5	96.2	1106	16 AAR73056	Rabbit skeletal ca
41	5130.5	94.2	1100	10 AAF95644	Rabbit skeletal mus
42	2924.5	53.7	1082	22 AAU01015	Human secreted sol
43	2924.5	53.7	1082	22 AAB62239	Human calcium chan
44	2924.5	53.7	1109	22 AAU01016	Human secreted sol
45	2924.5	53.7	1109	22 AAB62240	Human calcium chan

#### ALIGNMENTS

#### RESULT 1

AAU01029  
ID AAU01029 standard; Protein; 1036 AA.

XX AAU01029;

XX AC AAU01029;

XX DT 04-JUL-2001 (first entry)

XX DE Pig secreted soluble alpha2delta calcium channel subunit #3 protein.

XX KW Pig; secreted calcium channel alpha2delta subunit; alpha2delta-2;

XX KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;

XX KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;

XX KW filter binding assay; wheat germ lectin flashplate assay; porcine.

XX OS Sus scrofa.

XX PN WO200119870-A2.

XX PD 22-MAR-2001.

XX PF 18-SEP-2000; 2000WO-EP09137.

XX PR 16-SEP-1999; 99US-0397550.

XX PA (WARN ) WARNER LAMBERT CO.

XX PI Brown JP, Bertelli F;

XX XX WPI: 2001-235262/24.

XX DR N-PSDB; AAS01421.

XX .PT

Calcium channel alpha2delta subunits, useful in e.g. SPA assays,

Flashplate assays, Nickel Flashplate assays, Filter binding assays or Wheat Germ Lectin Flashplate assays - Claim 31; Page 117-120; 160pp; English.

The present sequence represents pig secreted calcium channel alpha2delta subunit #3 which is soluble and retains the functional characteristics of the full length or wild type alpha2delta subunit from which it is derived. The invention relates to truncated alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit proteins which retain their affinity for radioactively labelled gabapentin. The alpha2delta subunit is 1 of the components of the heteromultimeric voltage-dependent calcium channel (VDC) complexes present in neuronal and non-neuronal tissues including heart and skeletal muscle. Numerous soluble forms of the human calcium channel alpha2delta subunits (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the porcine calcium channel alpha2delta subunits (AAU01027-AAU01031) are described. The secreted soluble alpha2delta subunit may be used in assays e.g. scintillation proximity assay (SPA), flashplate, nickel flashplate, filter binding or wheat germ lectin flashplate assays to detect or measure the binding or interaction of a ligand (e.g. gabapentin, L-Norleucine, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Isoleucine, L-Valine, Spermine and/or L-Phenylalanine) of a calcium channel alpha2delta subunit.

Sequence 1036 AA;

Query Match 100.0%; Score 5446; DB 22; Length 1036;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLFOSLLIGPSSOPFPFSAVTIKSWDKQEDLVTLAKTAGSYNQLVDI 60  
DB 1 MAAGCLLALTTLFOSLLIGPSSOPFPFSAVTIKSWDKQEDLVTLAKTAGSYNQLVDI 60  
QY 61 YEKYODLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVRLALEAEKVOAAHQWREDFASN 120  
DB 61 YEKYODLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVRLALEAEKVOAAHQWREDFASN 120  
QY 121 EYVYNAKDDLDPEKNDSEPSQRIKPVFIDANFGROIYSOHAHVHPTDIYEGSTIVL 180  
DB 121 EYVYNAKDDLDPEKNDSEPSQRIKPVFIDANFGROIYSOHAHVHPTDIYEGSTIVL 180  
QY 181 NELNWTSAIDVFKKREDESLMQVFGSATGLARYYPASPDVNSRTPNKIDLYDVR 240  
DB 181 NELNWTSAIDVFKKREDESLMQVFGSATGLARYYPASPDVNSRTPNKIDLYDVR 240  
QY 241 RPWYIQAASPKDMLILVDVSGVSGLTFLKIRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
DB 241 RPWYIQAASPKDMLILVDVSGVSGLTFLKIRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
QY 301 VSCFQHLVQANVRNKKVLKDAVNNTAKGIDTDYKGFSAFQELLNLYNVRANCNKIIML 360  
DB 301 VSCFQHLVQANVRNKKVLKDAVNNTAKGIDTDYKGFSAFQELLNLYNVRANCNKIIML 360  
QY 361 FTDGGEERAQEIFAKYKNDKKVRVFTFSVGQHNDRGPIQMACENKGYIIEISGAIR 420  
DB 361 FTDGGEERAQEIFAKYKNDKKVRVFTFSVGQHNDRGPIQMACENKGYIIEISGAIR 420  
QY 421 INTQEYLDVLRGPMVLADKAKQVQWTVNYLDALGLVITGTLVPFNITQONENKTNLK 480  
DB 421 INTQEYLDVLRGPMVLADKAKQVQWTVNYLDALGLVITGTLVPFNITQONENKTNLK 480  
QY 481 NQLILGVNGVDVSLIEDIKRLTPRTLCNGYFFAIDPNGYVLLHPNLPKNPKSQEPVTL 540  
DB 481 NQLILGVNGVDVSLIEDIKRLTPRTLCNGYFFAIDPNGYVLLHPNLPKNPKSQEPVTL 540  
QY 541 DFLDALENDIKVEIRNMKIDGSEKTRFLVKSQDERYIDKGNRTVWTPVNGTDYSL 600  
DB 541 DFLDALENDIKVEIRNMKIDGSEKTRFLVKSQDERYIDKGNRTVWTPVNGTDYSL 600  
QY 601 ALVLPYTSFYIYKAKIETITQARKSKGKMDSETLKPDPNFEEGYTFIAPRDCNDLKI 660  
DB 601 ALVLPYTSFYIYKAKIETITQARKSKGKMDSETLKPDPNFEEGYTFIAPRDCNDLKI 660

QY 661 SDNTEFLNFNNEFIDRKTPNPNPSCNTDLINRVLLDAGFTNELVQVWSKQKNIKGVKAR 720  
DB 661 SDNTEFLNFNNEFIDRKTPNPNPSCNTDLINRVLLDAGFTNELVQVWSKQKNIKGVKAR 720  
QY 721 FVYTDGGITRVYPKEAGENQWENPETIYEDSFYKRSLDNDNYVFTADYFNKSGPGAYESGI 780  
DB 721 FVYTDGGITRVYPKEAGENQWENPETIYEDSFYKRSLDNDNYVFTADYFNKSGPGAYESGI 780  
QY 781 MVSKAVEIYIQGLLPAVVGKIDVNSWENFTKTSIRDPGAGPVCDCKRNSDVMDCVI 840  
DB 781 MVSKAVEIYIQGLLPAVVGKIDVNSWENFTKTSIRDPGAGPVCDCKRNSDVMDCVI 840  
QY 841 LDDGGFLLMANHDDYTNOIGRFFGEIDPISLRHLVNIISVYAFNKSVDYQSVCEPGAAPKQ 900  
DB 841 LDDGGFLLMANHDDYTNOIGRFFGEIDPISLRHLVNIISVYAFNKSVDYQSVCEPGAAPKQ 900  
QY 901 GAGHRSAVYPSIADILHIGWATAAASWILQOFLLSLTPRLLLEAVEMEDDDFTASLSKQ 960  
DB 901 GAGHRSAVYPSIADILHIGWATAAASWILQOFLLSLTPRLLLEAVEMEDDDFTASLSKQ 960  
QY 961 SCITEQTYFFDNDKSFSGVLDCGNCSTRIFHVEKLMNTNLIFIMVESKGTCPCDTRLLI 1020  
DB 961 SCITEQTYFFDNDKSFSGVLDCGNCSTRIFHVEKLMNTNLIFIMVESKGTCPCDTRLLI 1020  
QY 1021 QAEQTSDDGPDPCDMVK 1036  
DB 1021 QAEQTSDDGPDPCDMVK 1036  
RESULT 2  
AAB62253  
ID AAB62253 standard; Protein: 1036 AA.  
XX  
AC AAB62253;  
XX  
DT 11-JUN-2001 (first entry)  
XX  
DE Porcine calcium channel subunit alpha2delta-3.  
XX  
KW Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;  
KW nervous system disorder; pain; epilepsy; anxiety; pig.  
XX  
OS Sus scrofa.  
XX  
PN W0200120336-A2.  
XX  
PD 22-MAR-2001.  
XX  
PF 18-SEP-2000; 2000WO-EP09136.  
XX  
PR 16-SEP-1999; 99US-0397549.  
XX  
PA (WARN ) WARNER LAMBERT CO.  
PI  
PI Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;  
XX WPI; 2001-257902/26.  
DR N-PSDB; AAF57558.  
XX  
PT Competitive binding assay for screening ligands which bind a cerebral  
PT cortical voltage-dependent calcium channel alpha2delta-1 subunit,  
PT where the ligands identified are useful for treating disorders of the  
PT nervous system, including pain -  
XX  
PS Claim 8; Page 116-119; 158pp; English.  
XX  
CC The invention relates to a new method for screening ligands which bind a  
CC cerebral cortical voltage-dependent calcium channel alpha2delta subunit,  
CC preferably alpha2delta-1 subunit. The method comprises contacting a  
CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of  
CC interest and a labelled compound which binds the subunit, followed by  
CC measuring the level of binding of the labelled compound to alpha2delta-1

CC subunit. The method is useful for screening ligands, preferably  
 CC biologically active products that modulate a nervous system function,  
 CC which bind a cerebral cortical voltage-dependent calcium channel  
 CC alpha2delta-1 subunit. The ligands identified by the method are useful  
 CC for treating disorders of the nervous system, including pain, epilepsy  
 CC and anxiety. The present sequence represents a porcine calcium channel  
 CC subunit alpha2delta-3.  
 XX

SQ Sequence 1036 AA;

Query Match 100.0%; Score 5446; DB 22; Length 1036;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLTQSLILGPSQEPFPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
 DB 1 MAAGCLLALTTLTQSLILGPSQEPFPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
 QY 61 YEKYQDLYTVEPNARQLVEIARDEKLLSNRSKALVRLALEAEKVQAAHQWREDFASN 120  
 DB 61 YEKYQDLYTVEPNARQLVEIARDEKLLSNRSKALVRLALEAEKVQAAHQWREDFASN 120  
 QY 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFIDDANFGROIYSQHAHVHPTDIYEGSTIVL 180  
 DB 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFIDDANFGROIYSQHAHVHPTDIYEGSTIVL 180  
 QY 181 NELNWTLSALDEVFKKNEEDPSLLMQVFGSATGLARYYPASPWVNSRTPNPKIDLYDVR 240  
 DB 181 NELNWTLSALDEVFKKNEEDPSLLMQVFGSATGLARYYPASPWVNSRTPNPKIDLYDVR 240  
 QY 241 RPWYIOGAASPKDMLILVDYSSVSGLTLLKLRITSVSEMLETLSDDDFVNVASFNSNAOD 300  
 DB 241 RPWYIOGAASPKDMLILVDYSSVSGLTLLKLRITSVSEMLETLSDDDFVNVASFNSNAOD 300  
 QY 301 VSCFQHLVQANVRNKKVLDAVNNTAKGIDYKKGFSFAFQOLLNYSVRANCKNIML 360  
 DB 301 VSCFQHLVQANVRNKKVLDAVNNTAKGIDYKKGFSFAFQOLLNYSVRANCKNIML 360  
 QY 361 FTDGGEARAEIFAKYKNDKVRVFTFSVGQHNDRGPIQWACENKGYIYIPISGAIR 420  
 DB 361 FTDGGEARAEIFAKYKNDKVRVFTFSVGQHNDRGPIQWACENKGYIYIPISGAIR 420  
 QY 421 INTQEVLDVLRPMVLGAKAKQVQWNTNYLDALGLVITGTLPVFNITGQENKTNLK 480  
 DB 421 INTQEVLDVLRPMVLGAKAKQVQWNTNYLDALGLVITGTLPVFNITGQENKTNLK 480  
 QY 481 NQILGVMGVDSLEDIKRLTPRFTLCPNGYVFAIDPNGYVLLHPLQPKNPKSEPVTL 540  
 DB 481 NQILGVMGVDSLEDIKRLTPRFTLCPNGYVFAIDPNGYVLLHPLQPKNPKSEPVTL 540  
 QY 541 DFLDAELENDIKVEIRKMKIDGESGKFTTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
 DB 541 DFLDAELENDIKVEIRKMKIDGESGKFTTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
 QY 601 ALVLPYSFYIAKATEETITQARSKKGMKQSETLKPONFESGYTFIAPRDYCNLDKI 660  
 DB 601 ALVLPYSFYIAKATEETITQARSKKGMKQSETLKPONFESGYTFIAPRDYCNLDKI 660  
 QY 661 SDNNTFLLNFNEIDRKTNNPNSCNTDLINRVLLDAGFTNELVQNSKQKNIKVAKR 720  
 DB 661 SDNNTFLLNFNEIDRKTNNPNSCNTDLINRVLLDAGFTNELVQNSKQKNIKVAKR 720  
 QY 721 FVYTDGGITRVYKPEAGENQWENPETYEDSFYKRSILDNDNYVFTAPYFNKSGPGAYESGI 780  
 DB 721 FVYTDGGITRVYKPEAGENQWENPETYEDSFYKRSILDNDNYVFTAPYFNKSGPGAYESGI 780  
 QY 781 MVSQKVEIYIQGLKLLPAVVGKIDVNSWENFTKTSIRDPACGVPCCDKRNSDVMDCVI 840  
 DB 781 MVSQKVEIYIQGLKLLPAVVGKIDVNSWENFTKTSIRDPACGVPCCDKRNSDVMDCVI 840  
 QY 841 LDDGGFLLMANHDDYTNQIGRFGEIDPSLMRHLVNIYSYAFNKSVDYQSVCEPNAAPQ 900  
 DB 841 LDDGGFLLMANHDDYTNQIGRFGEIDPSLMRHLVNIYSYAFNKSVDYQSVCEPNAAPQ 900

QY 901 GAGHSAYVPSIADILHIGWATAAAWSILOQFLSLTFFPRLLEAVEMEDDDFTASLSQ 960  
 DB 901 GAGHSAYVPSIADILHIGWATAAAWSILOQFLSLTFFPRLLEAVEMEDDDFTASLSQ 960  
 QY 961 SCITEQTOYFFDNDKSPSGVLDGNCNRSRIFHVEKLMNTNLIIFIMVSKGTCPCDTRLLI 1020  
 DB 961 SCITEQTOYFFDNDKSPSGVLDGNCNRSRIFHVEKLMNTNLIIFIMVSKGTCPCDTRLLI 1020  
 QY 1021 QAEQTSDDGPDPCDMVK 1036  
 DB 1021 QAEQTSDDGPDPCDMVK 1036  
 RESULT 3  
 AAU01030  
 ID AAU01030 standard; Protein; 1063 AA.  
 XX AAU01030;  
 AC AAU01030;  
 XX DT 04-JUL-2001 (first entry)  
 XX Pig secreted soluble alpha2delta calcium channel subunit #4 protein.  
 DE Pig; secreted calcium channel alpha2delta subunit; alpha2delta-2;  
 XX alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;  
 KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;  
 KW filter binding assay; wheat germ lectin flashplate assay; porcine.  
 XX Sus scrofa.  
 OS WO200119870-A2.  
 XX PN 22-MAR-2001.  
 PD 18-SEP-2000; 2000WO-EP09137.  
 XX PF 16-SEP-1999; 99US-0397550.  
 PR (WARN ) WARNER LAMBERT CO.  
 XX PI Brown JP, Bertelli F;  
 XX WPI; 2001-235262/24.  
 DR N-PSDB; AAS01422.  
 XX Calcium channel alpha2delta subunits, useful in e.g. SPA assays,  
 PT Flashplate assays, Nickel Flashplate assays, Filter binding assays or  
 PT Wheat Germ Lectin Flashplate assays -  
 XX Claim 31; Page 120-124; 160pp; English.  
 PS The present sequence represents pig secreted calcium channel alpha2delta  
 CC subunit #4 which is soluble and retains the functional characteristics  
 CC of the full length or wild type alpha2delta subunit from which it is  
 CC derived. The invention relates to truncated alpha2delta-2, alpha2delta-3  
 CC or alpha2delta-4 subunit soluble proteins which retain their affinity for  
 CC radioactively labelled gabapentin. The alpha2delta subunit is 1 of the  
 CC components of the heteromultimeric voltage-dependent calcium channel  
 CC (VDCC) complexes present in neuronal and non-neuronal tissues including  
 CC heart and skeletal muscle. Numerous soluble forms of the human calcium  
 CC channel alpha2delta subunits (AAU01014-AAU01024 and AAU01032-AAU01038)  
 CC and 5 soluble forms of the porcine calcium channel alpha2delta subunits  
 CC (AAU01027-AAU01031) are described. The secreted soluble alpha2delta  
 CC subunit may be used in assays e.g. scintillation proximity assay (SPA),  
 CC flashplate, nickel flashplate, filter binding or wheat germ lectin  
 CC flashplate assays to detect or measure the binding or interaction of a  
 CC ligand (e.g. gabapentin, L-Norleucine, L-Allo-Isoleucine, L-methionine,  
 CC L-Leucine, L-Isoleucine, L-Valine, Spermine and/or L-Phenylalanine) of  
 CC a calcium channel alpha2delta subunit.  
 XX Sequence 1063 AA;

Query Match 100.0%; Score 5446; DB 22; Length 1063;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLTQSLIGPSSQEPFPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
Db 1 MAAGCLLALTLTQSLIGPSSQEPFPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

QY 61 YEKYQDLYTVEPNARQOLVEIARDIEKLLSNRSKALVRLALEAEKVQAAHQRDEFASN 120  
Db 61 YEKYQDLYTVEPNARQOLVEIARDIEKLLSNRSKALVRLALEAEKVQAAHQRDEFASN 120

QY 121 EVVYYNAKDDLDPEKNDSEPGSQRIKPVFIDANFRQISYQHAHVHIPTDIYEGSTIVL 180  
Db 121 EVVYYNAKDDLDPEKNDSEPGSQRIKPVFIDANFRQISYQHAHVHIPTDIYEGSTIVL 180

QY 181 NELNWTSALEDEVKKNREEDPSLLWVFGSATGLARYYPASVPWDSRTPNKIDLYDVR 240  
Db 181 NELNWTSALEDEVKKNREEDPSLLWVFGSATGLARYYPASVPWDSRTPNKIDLYDVR 240

QY 241 RPWYIOGAASPKDMLTLVDVSGVSLTKLRTSVSEMLETSLDSDDFVNVASFNSAQD 300  
Db 241 RPWYIOGAASPKDMLTLVDVSGVSLTKLRTSVSEMLETSLDSDDFVNVASFNSAQD 300

QY 301 VSCFQHLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFQOLLNINVRANCNKIIML 360  
Db 301 VSCFQHLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFQOLLNINVRANCNKIIML 360

QY 361 FTDGGERAQEIPAKYNNKDKVRVTFSSVQGHNYDRGPIQWMACENKGYEIPISGAIR 420  
Db 361 FTDGGERAQEIPAKYNNKDKVRVTFSSVQGHNYDRGPIQWMACENKGYEIPISGAIR 420

QY 421 INTQEYLDVLGRPWLKAGKQVQWNTVLDALGLVITGLTPVFNITGQENKNTLK 480  
Db 421 INTQEYLDVLGRPWLKAGKQVQWNTVLDALGLVITGLTPVFNITGQENKNTLK 480

QY 481 NQILGVMGVDVSLDIKRLTPFTLCPNGYYFAIDPNGYVLLHPNLPKPKSQEPVTL 540  
Db 481 NQILGVMGVDVSLDIKRLTPFTLCPNGYYFAIDPNGYVLLHPNLPKPKSQEPVTL 540

QY 541 DFLDAELENDIKVEIRNKMIDSEKFTRTLVKSQDERYIDKGNRTYTPVNGTDSL 600  
Db 541 DFLDAELENDIKVEIRNKMIDSEKFTRTLVKSQDERYIDKGNRTYTPVNGTDSL 600

QY 601 ALVLPYSYIYKAKTEETITQARKKGMKDSITLKPDPNFEESGYTFTAPDYCNDLKI 660  
Db 601 ALVLPYSYIYKAKTEETITQARKKGMKDSITLKPDPNFEESGYTFTAPDYCNDLKI 660

QY 661 SDNNTFLLNFEFIDRKTTPNPNPSCNTDLINRVLLDAGFTNELVQYWSKQKNIKGVKAR 720  
Db 661 SDNNTFLLNFEFIDRKTTPNPNPSCNTDLINRVLLDAGFTNELVQYWSKQKNIKGVKAR 720

QY 721 FVYTDGGITRVYPKEAGENWQENPETYEDSFYKRSILDNDNYVFTAPYTNKSGPGAYESGI 780  
Db 721 FVYTDGGITRVYPKEAGENWQENPETYEDSFYKRSILDNDNYVFTAPYTNKSGPGAYESGI 780

QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTKTSIRDCPAGVPCDKRNSDVMDCVI 840  
Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTKTSIRDCPAGVPCDKRNSDVMDCVI 840

QY 841 LDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLNINISVYAFNKSYSYQSVCEPGAAPKQ 900  
Db 841 LDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLNINISVYAFNKSYSYQSVCEPGAAPKQ 900

QY 901 GAGHSAYVPSIADILHIGWATAAANSILOQFLSLTFPRLLEAVEMDDDFASLSKQ 960  
Db 901 GAGHSAYVPSIADILHIGWATAAANSILOQFLSLTFPRLLEAVEMDDDFASLSKQ 960

QY 961 SCITEQTQYFFNDKSKFSGLVDCGNCRSIRFHEVKLMTNLIIFTWESKGTCPDTRLLI 1020  
Db 961 SCITEQTQYFFNDKSKFSGLVDCGNCRSIRFHEVKLMTNLIIFTWESKGTCPDTRLLI 1020

QY 1021 QAEQTSDDGPDPCDMVK 1036

Db 1021 QAEQTSDDGPDPCDMVK 1036

RESULT 4  
AAB62254  
ID AAB62254 standard; Protein; 1063 AA.  
XX AAB62254;  
AC AAB62254;  
XX 11-JUN-2001 (first entry)  
XX Porcine calcium channel subunit alpha2delta-4.  
XX Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;  
XX nervous system disorder; pain; epilepsy; anxiety; pig.  
XX Sus scrofa.  
XX WO200120336-A2.  
XX 22-MAR-2001.  
XX 18-SEP-2000; 2000WO-EP09136.  
XX 16-SEP-1999; 99US-0397549.  
XX (WARN ) WARNER LAMBERT CO.  
XX Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;  
XX WPI; 2001-257902/26.  
XX N-PSDB; AAF57559.  
XX Competitive binding assay for screening ligands which bind a cerebral  
XX cortical voltage-dependent calcium channel alpha2delta-1 subunit,  
XX where the ligands identified are useful for treating disorders of the  
XX nervous system, including pain -  
PS Claim 8; Page 119-122; 158pp; English.  
XX The invention relates to a new method for screening ligands which bind a  
XX cerebral cortical voltage-dependent calcium channel alpha2delta subunit,  
XX preferably alpha2delta-1 subunit. The method comprises contacting a  
XX secreted soluble recombinant alpha2delta-1 subunit with a ligand of  
XX interest and a labelled compound which binds the subunit, followed by  
XX measuring the level of binding of the labelled compound to alpha2delta-1  
XX subunit. The method is useful for screening ligands, preferably  
XX biologically active products that modulate a nervous system function,  
XX which bind a cerebral cortical voltage-dependent calcium channel  
XX alpha2delta-1 subunit. The ligands identified by the method are useful  
XX for treating disorders of the nervous system, including pain, epilepsy  
XX and anxiety. The present sequence represents a porcine calcium channel  
XX subunit alpha2delta-4.  
SQ Sequence 1063 AA;  
Query Match 100.0%; Score 5446; DB 22; Length 1063;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLTQSLIGPSSQEPFPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
Db 1 MAAGCLLALTLTQSLIGPSSQEPFPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

QY 61 YEKYQDLYTVEPNARQOLVEIARDIEKLLSNRSKALVRLALEAEKVQAAHQRDEFASN 120  
Db 61 YEKYQDLYTVEPNARQOLVEIARDIEKLLSNRSKALVRLALEAEKVQAAHQRDEFASN 120

QY 121 EVVYYNAKDDLDPEKNDSEPGSQRIKPVFIDANFRQISYQHAHVHIPTDIYEGSTIVL 180  
Db 121 EVVYYNAKDDLDPEKNDSEPGSQRIKPVFIDANFRQISYQHAHVHIPTDIYEGSTIVL 180

QY 181 NELNWTSALEDEVEFKKREEDPSLLWQVFGSATGLARYYPASPWVNSRTPNKIDYDVRR 240  
 Db 181 NELNWTSALEDEVEFKKREEDPSLLWQVFGSATGLARYYPASPWVNSRTPNKIDYDVRR 240  
 QY 241 RPWYIOGAASPKDMLILVDVSGVSGTLKLLRTSVSEMLETSLDDDFVNVASFNSNAQ 300  
 Db 241 RPWYIOGAASPKDMLILVDVSGVSGTLKLLRTSVSEMLETSLDDDFVNVASFNSNAQ 300  
 QY 301 VSCFQHLVQANVRNKKVLDKAVNNITPAKGTIDYKKGFSFAFPELLNLYNVRANCNKIIML 360  
 Db 301 VSCFQHLVQANVRNKKVLDKAVNNITPAKGTIDYKKGFSFAFPELLNLYNVRANCNKIIML 360  
 QY 361 FTDGGERAQEIFAQYKKNOKKRVFTFVSGQHNDRGPIQWACENKGYEIPISGAI 420  
 Db 361 FTDGGERAQEIFAQYKKNOKKRVFTFVSGQHNDRGPIQWACENKGYEIPISGAI 420  
 QY 421 INTQEVLDVLRPMVLGDKAKOVQWTVNYLDALGLVITGTLVPFNITGONENKTNL 480  
 Db 421 INTQEVLDVLRPMVLGDKAKOVQWTVNYLDALGLVITGTLVPFNITGONENKTNL 480  
 QY 481 NQILILGVMGVDSLEDIKRLTFRFTLCPNGYYFAIDPNGYVLLHPNLOPKNPKSEPVTL 540  
 Db 481 NQILILGVMGVDSLEDIKRLTFRFTLCPNGYYFAIDPNGYVLLHPNLOPKNPKSEPVTL 540  
 QY 541 DFLDAELENDIKVEIRNKMIDGESKEPTRTLVKSDQERYIDKGNRTYTWTPVNGTDYSL 600  
 Db 541 DFLDAELENDIKVEIRNKMIDGESKEPTRTLVKSDQERYIDKGNRTYTWTPVNGTDYSL 600  
 QY 601 ALVLPYFYIYAKAIEETITQARSKKGMKDSITLKPDPNFESEGYTFIAPRDYCNLDKI 660  
 Db 601 ALVLPYFYIYAKAIEETITQARSKKGMKDSITLKPDPNFESEGYTFIAPRDYCNLDKI 660  
 QY 661 SONNTEFLNFEFIDRKTTPNPNPSCNTDLINRVLLDAGFTNBLVQYNSKQNKIKGVKAR 720  
 Db 661 SONNTEFLNFEFIDRKTTPNPNPSCNTDLINRVLLDAGFTNBLVQYNSKQNKIKGVKAR 720  
 QY 721 FVYTDGGITRVYPKAGENWQENPETEYDSFYKRSILDNDNVYFTAPYFNKSGPGAYESGI 780  
 Db 721 FVYTDGGITRVYPKAGENWQENPETEYDSFYKRSILDNDNVYFTAPYFNKSGPGAYESGI 780  
 QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWENFTKTSIRDPCAGVPCDCRNSDVMDCVI 840  
 Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWENFTKTSIRDPCAGVPCDCRNSDVMDCVI 840  
 QY 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYOSVCEPGAAPK 900  
 Db 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYOSVCEPGAAPK 900  
 QY 901 GAGHSAYVPSIADILHIGWATAAASWSTLQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
 Db 901 GAGHSAYVPSIADILHIGWATAAASWSTLQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
 QY 961 SCITEQTOYFFDNDKSFSGVLDGNCGRIFHVEKLMNTNLIFIMVESKGTCPCDTRLII 1020  
 Db 961 SCITEQTOYFFDNDKSFSGVLDGNCGRIFHVEKLMNTNLIFIMVESKGTCPCDTRLII 1020  
 QY 1021 QAEQTSDDGPDGDMVK 1036  
 Db 1021 QAEQTSDDGPDGDMVK 1036

## RESULT 5

AAU01031

ID AAU01031 standard; Protein: 1069 AA.

XX AC

XX AAU01031;

XX 04-JUL-2001 (first entry)

XX DE

Pig secreted soluble alpha2delta calcium channel subunit #5 protein.  
 Pig; secreted calcium channel alpha2delta subunit; alpha2delta-2;  
 KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;  
 KW

gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;  
 filter binding assay; wheat germ lectin flashplate assay; porcine.

Sus scrofa.

WO200119870-A2.

22-MAR-2001.

18-SEP-2000; 2000WO-EP09137.

16-SEP-1999; 99US-0397550.

(WARN ) WARNER LAMBERT CO.

Brown JP, Bertelli F;

WPI; 2001-235262/24.

Calcium channel alpha2delta subunits, useful in e.g. SPA assays,  
 Flashplate assays, Nickel Flashplate assays, Filter binding assays or  
 Wheat Germ Lectin Flashplate assays -

Disclosure: Page 124-127; 160pp; English.

The present sequence represents pig secreted calcium channel alpha2delta  
 subunit #5 which is soluble and retains the functional characteristics  
 of the full length or wild type alpha2delta subunit from which it is  
 derived. The invention relates to truncated alpha2delta-2, alpha2delta-3  
 or alpha2delta-4 subunit soluble proteins which retain their affinity for  
 radioactively labelled gabapentin. The alpha2delta subunit is 1 of the  
 components of the heteromultimeric voltage-dependent calcium channel  
 (VDCC) complexes present in neuronal and non-neuronal tissues including  
 heart and skeletal muscle. Numerous soluble forms of the human calcium  
 channel alpha2delta subunits (AAU01014-AAU01024 and AAU01032-AAU01038)  
 and 5 soluble forms of the porcine calcium channel alpha2delta subunits  
 (AAU01027-AAU01031) are described. The secreted soluble alpha2delta  
 subunit may be used in assays e.g. scintillation proximity assay (SPA),  
 flashplate, nickel flashplate, filter binding or wheat germ lectin  
 flashplate assays to detect or measure the binding or interaction of a  
 ligand (e.g. gabapentin, L-Norleucine, L-Allo-Isoleucine, L-methionine,  
 L-Leucine, L-Isoleucine, L-Valine, Spermine and/or L-Phenylalanine) of  
 a calcium channel alpha2delta subunit.

Sequence 1069 AA;

Query Match 100.0%; Score 5446; DB 22; Length 1069;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLTLFQSLILIGPSSQEPFPPSAVTIKSWDKMQEDLVTAKTASGVNQLVDI 60

Db 1 MAAGCLLALTLTLFQSLILIGPSSQEPFPPSAVTIKSWDKMQEDLVTAKTASGVNQLVDI 60

QY 61 YEKYQDLYTVEPNARQLVEIARDIEKLLSNRSKALVRLALEAEKQVAAHQWREFASN 120

Db 61 YEKYQDLYTVEPNARQLVEIARDIEKLLSNRSKALVRLALEAEKQVAAHQWREFASN 120

QY 121 EVYVYNAKDDLDPEKNDSEPGSQRIKPVFIDDAFGQISYQHAHVHPTDIYEGSTIVL 180

Db 121 EVYVYNAKDDLDPEKNDSEPGSQRIKPVFIDDAFGQISYQHAHVHPTDIYEGSTIVL 180

QY 181 NELNWTSALEDEVEFKKREEDPSLLWQVFGSATGLARYYPASPWVNSRTPNKIDYDVRR 240

Db 181 NELNWTSALEDEVEFKKREEDPSLLWQVFGSATGLARYYPASPWVNSRTPNKIDYDVRR 240

QY 241 RPWYIOGAASPKDMLILVDVSGVSGTLKLLRTSVSEMLETSLDDDFVNVASFNSNAQ 300

Db 241 RPWYIOGAASPKDMLILVDVSGVSGTLKLLRTSVSEMLETSLDDDFVNVASFNSNAQ 300

QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGTIDYKKGFSFAFPELLNLYNVRANCNKIIML 360

Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGTIDYKKGFSFAFPELLNLYNVRANCNKIIML 360

QY 361 FTDGGERAEIYAKYNDKKYRVFTFSVQGHYDRGPQIWMACENKGYEYIEPSIGAIR 420  
 DB 361 FTDGGERAEIYAKYNDKKYRVFTFSVQGHYDRGPQIWMACENKGYEYIEPSIGAIR 420  
 QY 421 INTQEYLDVLRPMVLGAKAKOVQWNTNYLDALGLGLVITGTLVPVFNITGONENKTNLK 480  
 DB 421 INTQEYLDVLRPMVLGAKAKOVQWNTNYLDALGLGLVITGTLVPVFNITGONENKTNLK 480  
 QY 481 NQLILGVMDVDSLEDIKRLTFRFTLCNPGYYFAIDPNGYVLLHPNLPKPKSQEPVTL 540  
 DB 481 NQLILGVMDVDSLEDIKRLTFRFTLCNPGYYFAIDPNGYVLLHPNLPKPKSQEPVTL 540  
 QY 541 DFLDAELENDIKVEIRNKMIDGESGKFTRTLKVSQDERYIDKGNRTYTWTPVNGTDYSL 600  
 DB 541 DFLDAELENDIKVEIRNKMIDGESGKFTRTLKVSQDERYIDKGNRTYTWTPVNGTDYSL 600  
 QY 601 ALVLPYSEYIYAKTEETITQARSKKMKDSETLKPDNFEESGYTFIAPDNCNDLKI 660  
 DB 601 ALVLPYSEYIYAKTEETITQARSKKMKDSETLKPDNFEESGYTFIAPDNCNDLKI 660  
 QY 661 SDNTEFLNFEFIDRKTTPNPNSTDLINRVLLDAGFTNELYQYWSKOKNIKGVKAR 720  
 DB 661 SDNTEFLNFEFIDRKTTPNPNSTDLINRVLLDAGFTNELYQYWSKOKNIKGVKAR 720  
 QY 721 FVYTDGGITRVYPKEAGENQENPETEYDSFYKRSILDNDNYVFTAPYFNKSGPGAYESGI 780  
 DB 721 FVYTDGGITRVYPKEAGENQENPETEYDSFYKRSILDNDNYVFTAPYFNKSGPGAYESGI 780  
 QY 781 MYSKAVEIYIQGKLLKPAVVGKIDVNSWIENTKTSIRDPKAGPVCCKRNSDVMDCVI 840  
 DB 781 MYSKAVEIYIQGKLLKPAVVGKIDVNSWIENTKTSIRDPKAGPVCCKRNSDVMDCVI 840  
 QY 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLNLSIYAFNKSVDYQSVCEPAAAPKQ 900  
 DB 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLNLSIYAFNKSVDYQSVCEPAAAPKQ 900  
 QY 901 GAGHSAYVPSIADILHIGWATAAASLLOQFLLSLFPRLLEAVEMEDDDFTASLSKQ 960  
 DB 901 GAGHSAYVPSIADILHIGWATAAASLLOQFLLSLFPRLLEAVEMEDDDFTASLSKQ 960  
 QY 961 SCITEQYQFFNDKSKFSVGLDCGNCRIHFVEKLMNTNLIIFIMVESKGTGCPDTRLLI 1020  
 DB 961 SCITEQYQFFNDKSKFSVGLDCGNCRIHFVEKLMNTNLIIFIMVESKGTGCPDTRLLI 1020  
 QY 1021 QABQTSDDGPDPCDMVK 1036  
 DB 1021 QABQTSDDGPDPCDMVK 1036

## RESULT 6

AAB62255  
 ID AAB62255 standard; Protein; 1069 AA.

AC AAB62255;

DT 11-JUN-2001 (first entry)

XX Porcine calcium channel subunit alpha2delta-1 deletion mutant.

DE Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;  
 KW nervous system disorder; pain; epilepsy; anxiety; pig; mutant.

XX Sus scrofa.

XX WO200120336-A2.

PN 22-MAR-2001.

XX 18-SEP-2000; 2000WO-EP09136.

XX 16-SEP-1999; 99US-0397549.

XX

(WARN ) WARNER LAMBERT CO.

Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;

WPI; 2001-257902/26.

Competitive binding assay for screening ligands which bind a cerebral  
 cortical voltage-dependent calcium channel alpha2delta-1 subunit,  
 where the ligands identified are useful for treating disorders of the  
 nervous system, including pain -

Claim 8; Page 122-126; 158pp; English.

The invention relates to a new method for screening ligands which bind a  
 cerebral cortical voltage-dependent calcium channel alpha2delta subunit,  
 preferably alpha2delta-1 subunit. The method comprises contacting a  
 secreted soluble recombinant alpha2delta-1 subunit with a ligand of  
 interest and a labelled compound which binds the subunit, followed by  
 measuring the level of binding of the labelled compound to alpha2delta-1  
 subunit. The method is useful for screening ligands, preferably  
 biologically active products that modulate a nervous system function,  
 which bind a cerebral cortical voltage-dependent calcium channel  
 alpha2delta-1 subunit. The ligands identified by the method are useful  
 for treating disorders of the nervous system, including pain, epilepsy  
 and anxiety. The present sequence represents a porcine calcium channel  
 subunit alpha2delta-1 deletion mutant.

Sequence 1069 AA;

Query Match 100.0%; Score 5446; DB 22; Length 1069;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLTILFQSLIGPSSQEPSPSAVTIKSWDKMQEDLVTILAKTASGVNQLVDI 60  
 DB 1 MAAGCLLALTLTILFQSLIGPSSQEPSPSAVTIKSWDKMQEDLVTILAKTASGVNQLVDI 60  
 QY 61 YEKQDLYTVEPNAROLVEIAARDIEKLLSNRSKALVRLALEAEKVQAAHQRDFASN 120  
 DB 61 YEKQDLYTVEPNAROLVEIAARDIEKLLSNRSKALVRLALEAEKVQAAHQRDFASN 120  
 QY 121 EVVYNAKADLDLPKNDSEPGSQRIKPVFIDANFGQISYQAAVHIPDIDYEGSTIVL 180  
 DB 121 EVVYNAKADLDLPKNDSEPGSQRIKPVFIDANFGQISYQAAVHIPDIDYEGSTIVL 180  
 QY 181 NELNWT SALDEVFKKNEEDPSLLWQVFGSATGLIARYYPASPWVDSRTPNKIDLDVRR 240  
 DB 181 NELNWT SALDEVFKKNEEDPSLLWQVFGSATGLIARYYPASPWVDSRTPNKIDLDVRR 240  
 QY 241 RPWYIOGAAPKMDLILVDVSGVSGTLTKLIRTSVSEMLETISDDDFVNVASFNSNAQD 300  
 DB 241 RPWYIOGAAPKMDLILVDVSGVSGTLTKLIRTSVSEMLETISDDDFVNVASFNSNAQD 300  
 QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNNVSRANCKIIML 360  
 DB 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNNVSRANCKIIML 360  
 QY 361 FTGGEERAQEIFAKYNDKKYRVFTFSVQGHYDRGPQIWMACENKGYEYIEPSIGAIR 420  
 DB 361 FTGGEERAQEIFAKYNDKKYRVFTFSVQGHYDRGPQIWMACENKGYEYIEPSIGAIR 420  
 QY 421 INTOEYLDVLRPMVLGAKAKOVQWNTNYLDALGLGLVITGTLVPVFNITGONENKTNLK 480  
 DB 421 INTOEYLDVLRPMVLGAKAKOVQWNTNYLDALGLGLVITGTLVPVFNITGONENKTNLK 480  
 QY 481 NQLILGVMDVDSLEDIKRLTFRFTLCNPGYYFAIDPNGYVLLHPNLPKPKSQEPVTL 540  
 DB 481 NQLILGVMDVDSLEDIKRLTFRFTLCNPGYYFAIDPNGYVLLHPNLPKPKSQEPVTL 540  
 QY 541 DFLDAELENDIKVEIRNKMIDGESGKFTRTLKVSQDERYIDKGNRTYTWTPVNGTDYSL 600  
 DB 541 DFLDAELENDIKVEIRNKMIDGESGKFTRTLKVSQDERYIDKGNRTYTWTPVNGTDYSL 600

QY 601 ALVLPYTFYIIKAKIETITQARSKGKMKDSETLKPNFESGYTFIAPRDYCNLDKI 660  
 Db 601 ALVLPYTFYIIKAKIETITQARSKGKMKDSETLKPNFESGYTFIAPRDYCNLDKI 660  
 QY 661 SDNTEFLNFNEFIDRKTPNPNPSCNTDLINRVLLDAGFTNELVQNWQSKQKIKGVKAR 720  
 Db 661 SDNTEFLNFNEFIDRKTPNPNPSCNTDLINRVLLDAGFTNELVQNWQSKQKIKGVKAR 720  
 QY 721 FVVTGGITRVYKREAGENQENPETEYDSFYKRSKSLDNDNYVFTAPYFNKSGPGAYESGI 780  
 Db 721 FVVTGGITRVYKREAGENQENPETEYDSFYKRSKSLDNDNYVFTAPYFNKSGPGAYESGI 780  
 QY 781 MVSXAVEIYIOGKLLPAPVGVKIDVNSWLENFTKTSIRDPACAGVCDCKRNSDVMDCVI 840  
 Db 781 MVSXAVEIYIOGKLLPAPVGVKIDVNSWLENFTKTSIRDPACAGVCDCKRNSDVMDCVI 840  
 QY 841 LDGCGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNIISYAFNKSVDYOSVCEPGAAPQ 900  
 Db 841 LDGCGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNIISYAFNKSVDYOSVCEPGAAPQ 900  
 QY 901 GAGHRSAYVPSIADILHIGWATAAASWILQOFLSLTFPRLLAEVEMEDDDFTASLSQ 960  
 Db 901 GAGHRSAYVPSIADILHIGWATAAASWILQOFLSLTFPRLLAEVEMEDDDFTASLSQ 960  
 QY 961 SCITEQTYFFDNDKSFSGVLDCGNCRSRIFHVEKLMNTNLIPIMVESKGTCPDTRLLI 1020  
 Db 961 SCITEQTYFFDNDKSFSGVLDCGNCRSRIFHVEKLMNTNLIPIMVESKGTCPDTRLLI 1020  
 QY 1021 QAEQTSQDPPDCDMVK 1036  
 Db 1021 QAEQTSQDPPDCDMVK 1036

RESULT 7  
 AAU01027  
 ID AAU01027 standard; Protein; 1091 AA.  
 XX  
 AC AAU01027;  
 XX  
 DT 04-JUL-2001 (first entry)  
 XX  
 DE Pig secreted soluble alpha2delta calcium channel subunit #1 protein.  
 XX  
 KW Pig; secreted calcium channel alpha2delta subunit; alpha2delta-2;  
 KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;  
 KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;  
 KW filter binding assay; wheat germ lectin flashplate assay; porcine.  
 XX  
 OS Sus scrofa.  
 XX  
 PN WO200119870-A2.  
 XX  
 PD 22-MAR-2001.  
 XX  
 PF 18-SEP-2000; 2000WO-EP09137.  
 XX  
 PR 16-SEP-1999; 99US-0397550.  
 XX  
 PA (WARN ) WARNER LAMBERT CO.  
 XX  
 PI Brown JP, Bertelli F;  
 XX  
 DR WI; 2001-235262/24.  
 XX  
 DR N-PSDB; AAS01419.  
 XX  
 PT Calcium channel alpha2delta subunits, useful in e.g. SPA assays,  
 PT Flashplate assays, Nickel Flashplate assays, Filter binding assays or  
 PT Wheat Germ Lectin Flashplate assays -  
 XX  
 PS Claim 30; Page 110-113; 160pp; English.  
 XX  
 CC The present sequence represents pig secreted calcium channel alpha2delta  
 CC subunit #1 which is soluble and retains the functional characteristics

CC of the full length or wild type alpha2delta subunit from which it is  
 CC derived. The invention relates to truncated alpha2delta-2, alpha2delta-3  
 CC or alpha2delta-4 subunit soluble proteins which retain their affinity for  
 CC radioactively labelled gabapentin. The alpha2delta subunit is 1 of the  
 CC components of the heteromultimeric voltage-dependent calcium channel  
 CC (VDCC) complexes present in neuronal and non-neuronal tissues including  
 CC heart and skeletal muscle. Numerous soluble forms of the human calcium  
 CC channel alpha2delta subunits (AAU01014-AAU01024 and AAU01032-AAU01038)  
 CC and 5 soluble forms of the porcine calcium channel alpha2delta subunits  
 CC (AAU01027-AAU01031) are described. The secreted soluble alpha2delta  
 CC subunit may be used in assays e.g. scintillation proximity assay (SPA),  
 CC flashplate, nickel flashplate, filter binding or wheat germ lectin  
 CC flashplate assays to detect or measure the binding or interaction of a  
 CC ligand (e.g. gabapentin, L-Norleucine, L-Allo-Isoleucine, L-methionine,  
 CC L-Leucine, L-Isoleucine, L-Valine, Spermine and/or L-Phenylalanine) of  
 CC a calcium channel alpha2delta subunit.  
 XX  
 SQ Sequence 1091 AA;  
 Query Match 100.0%; Score 5446; DB 22; Length 1091;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAAGCLLALTTLFQSLIGPSSQBPFPSPAVTIKSWDKMQEDLVTAKTAGVNLVDI 60  
 Db 1 MAAGCLLALTTLFQSLIGPSSQBPFPSPAVTIKSWDKMQEDLVTAKTAGVNLVDI 60  
 QY 61 YEKYQDLTYVEPNNAQOLVEIAARDIEKLLSNRSKALVRLALEAEKVAQAHHQWREDFASN 120  
 Db 61 YEKYQDLTYVEPNNAQOLVEIAARDIEKLLSNRSKALVRLALEAEKVAQAHHQWREDFASN 120  
 QY 121 EYVYNAKDDLDPEKNDSPPGSGRIKPVFIDANFGROIYSQHAHVHPTDIYEGSTIVL 180  
 Db 121 EYVYNAKDDLDPEKNDSPPGSGRIKPVFIDANFGROIYSQHAHVHPTDIYEGSTIVL 180  
 QY 181 NELNWTSALEDVFKKNREEDPSLLMQVFGSATGLARYYPASPWVDSNRPKNKIDLYDVR 240  
 Db 181 NELNWTSALEDVFKKNREEDPSLLMQVFGSATGLARYYPASPWVDSNRPKNKIDLYDVR 240  
 QY 241 RPWYIOGAASPKDMLILVDVSGSVSGLTLKLI RTSVSSEMLETLDSDDFVNVASFNSAQD 300  
 Db 241 RPWYIOGAASPKDMLILVDVSGSVSGLTLKLI RTSVSSEMLETLDSDDFVNVASFNSAQD 300  
 QY 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGIDYKKGFSFAFQQLLNVNVRANCKIIML 360  
 Db 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGIDYKKGFSFAFQQLLNVNVRANCKIIML 360  
 QY 361 FTDGGEERAQEIFAKYNDKKVRFVTFVSGQHNVDGPIQWMACENKGYEIPSGAIR 420  
 Db 361 FTDGGEERAQEIFAKYNDKKVRFVTFVSGQHNVDGPIQWMACENKGYEIPSGAIR 420  
 QY 421 INTQEYLDVLGRPMVLGADKAKOVQWNTVYLDALDELGVITGTLPVFNITGQENKTNLK 480  
 Db 421 INTQEYLDVLGRPMVLGADKAKOVQWNTVYLDALDELGVITGTLPVFNITGQENKTNLK 480  
 QY 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHPNLPKPKSQEPVTL 540  
 Db 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHPNLPKPKSQEPVTL 540  
 QY 541 DFLDAELENDIKVEIRNKMIDGESGEKFTLVKQSDERYIDKGNRTTWTTPVNGTDYSL 600  
 Db 541 DFLDAELENDIKVEIRNKMIDGESGEKFTLVKQSDERYIDKGNRTTWTTPVNGTDYSL 600  
 QY 601 ALVLPYTFYIIKAKIETITQARSKGKMKDSETLKPNFESGYTFIAPRDYCNLDKI 660  
 Db 601 ALVLPYTFYIIKAKIETITQARSKGKMKDSETLKPNFESGYTFIAPRDYCNLDKI 660  
 QY 661 SDNTEFLNFNEFIDRKTPNPNPSCNTDLINRVLLDAGFTNELVQNWQSKQKIKGVKAR 720  
 Db 661 SDNTEFLNFNEFIDRKTPNPNPSCNTDLINRVLLDAGFTNELVQNWQSKQKIKGVKAR 720  
 QY 721 FVVTGGITRVYKREAGENQENPETEYDSFYKRSKSLDNDNYVFTAPYFNKSGPGAYESGI 780  
 Db 721 FVVTGGITRVYKREAGENQENPETEYDSFYKRSKSLDNDNYVFTAPYFNKSGPGAYESGI 780

Db 721 FVTDGGITRVYPKEAGENQENPETIEDSFYKRSILDNDNVYFTAPYFNKSGAYESGI 780  
 QY 781 MVS KAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVCDCKRNSDVMDCVI 840  
 Db 781 MVS KAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVCDCKRNSDVMDCVI 840  
 QY 841 LDG GFLMANHDDYTNQIGRFGEIDPDLMRHLVNSIYAFNKSYDYQSVCEPGAAPKQ 900  
 Db 841 LDG GFLMANHDDYTNQIGRFGEIDPDLMRHLVNSIYAFNKSYDYQSVCEPGAAPKQ 900  
 QY 901 GAGHRSAYVPSIADILHIGWATAAASILQOFLSLTPRLLLEAVEMEDDDFTASLSKQ 960  
 Db 901 GAGHRSAYVPSIADILHIGWATAAASILQOFLSLTPRLLLEAVEMEDDDFTASLSKQ 960  
 QY 961 SCITEQTQFFNDKSFSGVLDGNCGRIFHVEKLMNTNLIIFIMVESKGTGCPDCTRLLI 1020  
 Db 961 SCITEQTQFFNDKSFSGVLDGNCGRIFHVEKLMNTNLIIFIMVESKGTGCPDCTRLLI 1020  
 QY 1021 QABOTSDGPDPCDMVK 1036  
 Db 1021 QABOTSDGPDPCDMVK 1036  
 RESULT 8  
 ID AAB62251 standard; Protein; 1091 AA.  
 AC AAB62251;  
 XX  
 XX  
 DT 11-JUN-2001 (first entry)  
 XX Porcine calcium channel subunit alpha2delta-1.  
 DE Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;  
 KW nervous system disorder; pain; epilepsy; anxiety; pig.  
 XX  
 XX Sus scrofa.  
 OS  
 PN WO200120336-A2.  
 XX  
 PD 22-MAR-2001.  
 XX  
 PF 18-SEP-2000; 2000WO-EP09136.  
 XX  
 PR 16-SEP-1999; 99US-0397549.  
 XX  
 PA (WARN ) WARNER LAMBERT CO.  
 XX  
 PI Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;  
 XX  
 DR WPI; 2001-257902/26.  
 DR N-PSDB; AAF57556.  
 XX  
 PT Competitive binding assay for screening ligands which bind a cerebral  
 PT cortical voltage-dependent calcium channel alpha2-delta-1 subunit,  
 PT where the ligands identified are useful for treating disorders of the  
 PT nervous system, including pain -  
 XX  
 PS Claim 7; Page 109-112; 158pp; English.  
 XX  
 CC The invention relates to a new method for screening ligands which bind a  
 CC cerebral cortical voltage-dependent calcium channel alpha2delta subunit,  
 CC preferably alpha2delta-1 subunit. The method comprises contacting a  
 CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of  
 CC interest and a labelled compound which binds the subunit, followed by  
 CC measuring the level of binding of the labelled compound to alpha2delta-1  
 CC subunit. The method is useful for screening ligands, preferably  
 CC biologically active products that modulate a nervous system function,  
 CC which bind a cerebral cortical voltage-dependent calcium channel  
 CC alpha2delta-1 subunit. The ligands identified by the method are useful  
 CC for treating disorders of the nervous system, including pain, epilepsy  
 CC and anxiety. The present sequence represents a porcine calcium channel  
 CC subunit alpha2delta-1.

XX Sequence 1091 AA;  
 Query Match 100.0%; Score 5446; DB 22; Length 1091;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAACCLALALITLTPQSLLIGPSSQEPSPASVTIKSWVDKMQEDLVTIAKTASGVNQLVDI 60  
 Db 1 MAACCLALALITLTPQSLLIGPSSQEPSPASVTIKSWVDKMQEDLVTIAKTASGVNQLVDI 60  
 QY 61 YEKQDLYTYVEPNAROLVETAAARDIEKLKLSNRSKALVRLALEAEKVQAAHQHREDPASN 120  
 Db 61 YEKQDLYTYVEPNAROLVETAAARDIEKLKLSNRSKALVRLALEAEKVQAAHQHREDPASN 120  
 QY 121 EVVYNAKDDLDPEKNDSEFQSRIKPVFIDANFGFQISYQAAAHIPDIDYEGSTIVL 180  
 Db 121 EVVYNAKDDLDPEKNDSEFQSRIKPVFIDANFGFQISYQAAAHIPDIDYEGSTIVL 180  
 QY 181 NELNWTSAIDVEFKKNEEDPSLLWQVFGSATGLARYYPASPVWDNSRTNPKIDLVDVRR 240  
 Db 181 NELNWTSAIDVEFKKNEEDPSLLWQVFGSATGLARYYPASPVWDNSRTNPKIDLVDVRR 240  
 QY 241 RPWYIQGAASPDKMLILVDYSGSVSGLTLLKIRTSVSEMLETILSDDDFVNVASFNSNAQD 300  
 Db 241 RPWYIQGAASPDKMLILVDYSGSVSGLTLLKIRTSVSEMLETILSDDDFVNVASFNSNAQD 300  
 QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNNVSRANCKIIML 360  
 Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNNVSRANCKIIML 360  
 QY 361 FTDGEERAQEIFAKYNNKDKKVRVFTFESVQGHNYDRGPIQWMACENKGYGYEIPSGAIR 420  
 Db 361 FTDGEERAQEIFAKYNNKDKKVRVFTFESVQGHNYDRGPIQWMACENKGYGYEIPSGAIR 420  
 QY 421 INTOEYLDVLGRPMVLADKAKOVQNTNVLDALELGLVITGTLVPFNITQGNENKTNLK 480  
 Db 421 INTOEYLDVLGRPMVLADKAKOVQNTNVLDALELGLVITGTLVPFNITQGNENKTNLK 480  
 QY 481 NQLILGVMGVDSVLEDIKRLTPRFTLCPNGYFAIDPNGYVLLHPNLQPNKPSQBPVTL 540  
 Db 481 NQLILGVMGVDSVLEDIKRLTPRFTLCPNGYFAIDPNGYVLLHPNLQPNKPSQBPVTL 540  
 QY 541 DFLDAELENDIKVEIRNMKIDGESGKTFRTLVKSQDERVIDKGNRTYTWTPVNGTDYSL 600  
 Db 541 DFLDAELENDIKVEIRNMKIDGESGKTFRTLVKSQDERVIDKGNRTYTWTPVNGTDYSL 600  
 QY 601 ALVLPTYSFYIYKAKIETITQARSKKMKDSFTLKPDNFEESGYTFTAPRDYCNLDKI 660  
 Db 601 ALVLPTYSFYIYKAKIETITQARSKKMKDSFTLKPDNFEESGYTFTAPRDYCNLDKI 660  
 QY 661 SDNTEFLNFEIDRKTNNFSCNTDLINRVLLDAGFTNELVQNVWSKQNKIGVKAR 720  
 Db 661 SDNTEFLNFEIDRKTNNFSCNTDLINRVLLDAGFTNELVQNVWSKQNKIGVKAR 720  
 QY 721 FVTDGGITRVYPKEAGENQENPETIEDSFYKRSILDNDNVYFTAPYFNKSGAYESGI 780  
 Db 721 FVTDGGITRVYPKEAGENQENPETIEDSFYKRSILDNDNVYFTAPYFNKSGAYESGI 780  
 QY 781 MVS KAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVCDCKRNSDVMDCVI 840  
 Db 781 MVS KAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVCDCKRNSDVMDCVI 840  
 QY 841 LDG GFLMANHDDYTNQIGRFGEIDPDLMRHLVNSIYAFNKSYDYQSVCEPGAAPKQ 900  
 Db 841 LDG GFLMANHDDYTNQIGRFGEIDPDLMRHLVNSIYAFNKSYDYQSVCEPGAAPKQ 900  
 QY 901 GAGHRSAYVPSIADILHIGWATAAASILQOFLSLTPRLLLEAVEMEDDDFTASLSKQ 960  
 Db 901 GAGHRSAYVPSIADILHIGWATAAASILQOFLSLTPRLLLEAVEMEDDDFTASLSKQ 960  
 QY 961 SCITEQTQFFNDKSFSGVLDGNCGRIFHVEKLMNTNLIIFIMVESKGTGCPDCTRLLI 1020  
 Db 961 SCITEQTQFFNDKSFSGVLDGNCGRIFHVEKLMNTNLIIFIMVESKGTGCPDCTRLLI 1020





ID XX AAB62257 standard; Protein; 1036 AA.  
 AC XX AAB62257;  
 XX DT 11-JUN-2001 (first entry)  
 XX DE Porcine calcium channel alpha2delta subunit.  
 XX KW Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;  
 KW nervous system disorder; pain; epilepsy; anxiety; pig.  
 XX OS Sus scrofa.  
 XX PN WO200120336-A2.  
 XX PD 22-MAR-2001.  
 XX PF 18-SEP-2000; 2000WO-EP09136.  
 XX PR 16-SEP-1999; 99US-0397549.  
 XX PA (WARN ) WARNER LAMBERT CO.  
 PI Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;  
 DR WPI; 2001-257902/26.  
 DR N-PSDB; AAF57561.  
 XX CC Competitive binding assay for screening ligands which bind a cerebral  
 PT cortical voltage-dependent calcium channel alpha2-delta-1 subunit,  
 PT where the ligands identified are useful for treating disorders of the  
 PT nervous system, including pain -  
 XX Claim 8; Page 132-135; 158pp; English.  
 XX CC The invention relates to a new method for screening ligands which bind a  
 CC cerebral cortical voltage-dependent calcium channel alpha2delta subunit,  
 CC preferably alpha2delta-1 subunit. The method comprises contacting a  
 CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of  
 CC interest and a labelled compound which binds the subunit, followed by  
 CC measuring the level of binding of the labelled compound to alpha2delta-1  
 CC subunit. The method is useful for screening ligands, preferably  
 CC biologically active products that modulate a nervous system function,  
 CC which bind a cerebral cortical voltage-dependent calcium channel  
 CC alpha2delta-1 subunit. The ligands identified by the method are useful  
 CC for treating disorders of the nervous system, including pain, epilepsy  
 CC and anxiety. The present sequence represents a porcine calcium channel  
 CC alpha2delta subunit.  
 XX SQ Sequence 1036 AA;

Query Match 98.8%; Score 5380; DB 22; Length 1036;  
 Best Local Similarity 98.7%; Pred. No. 0;  
 Matches 1023; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLFQSLIGPSQEPFSAVTKSWDKMQEDLVTLAKTASGVNQLVDI 60  
 DB 1 MAAGCLLALTLFQSLIGPSQEPFSAVTKSWDKMQEDLVTLAKTASGVNQLVDI 60  
 QY 61 YEKYQDLYVEPNARQLVEIAARDIEKLLSNRSLALVRLALEAKKVOAAHQWREDFASN 120  
 DB 61 YEKYQDLYVEPNARQLVEIAARDIEKLLSNRSLALVRLALEAKKVOAAHQWREDFASN 120  
 QY 121 FVYYNAKDDLDPKNDSEPGSQRIKPVIEDANFGRIQISYQHAHVHIPTDIYEGSTIVL 180  
 DB 121 FVYYNAKDDLDPKNDSEPGSQRIKPVIEDANFGRIQISYQHAHVHIPTDIYEGSTIVL 180  
 QY 181 NELNWTSSALDEVFKKNREDEPSLLMQVFGSATGLARYTPASFWVDNSRTPNKIDLYDVR 240  
 DB 181 NELNWTSSALDEVFKKNREDEPSLLMQVFGSATGLARYTPASFWVDNSRTPNKIDLYDVR 240  
 QY 241 RPWYIQGAASPRDKMLILVDVSGVSGLTGLKLRISVSEMLETSLDDDFVNVASFNSNAQD 300  
 DB 241 RPWYIQGAASPRDKMLILVDVSGVSGLTGLKLRISVSEMLETSLDDDFVNVASFNSNAQD 300

Db 241 RPWYIQGAASPRDKMLILVDVSGVSGLTGLKLRISVSEMLETSLDDDFVNVASFNSNAQD 300  
 QY 301 VSCFQHLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFQOLLNINYSRANCNKIIML 360  
 Db 301 VSCFQHLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFQOLLNINYSRANCNKIIML 360  
 QY 361 FTDGGERAQEIIPAKYNDKKVRVFTFSVQOHNYDRGPIQWMACENKGYEIPSTIGAIR 420  
 Db 361 FTDGGERAQEIIPAKYNDKKVRVFTFSVQOHNYDRGPIQWMACENKGYEIPSTIGAIR 420  
 QY 421 INTQEVLDVLGRPMVLADGKAKQVQWNTVYLDALGLVITGLTFVFNITGQENKTNLK 480  
 Db 421 INTQEVLDVLGRPMVLADGKAKQVQWNTVYLDALGLVITGLTFVFNITGQENKTNLK 480  
 QY 481 NQILGVMGVDVSLIEDIKRLTPRFTLCPNGYFAIDPNGYVLLHNLQPKPKSPEPTL 540  
 Db 481 NQILGVMGVDVSLIEDIKRLTPRFTLCPNGYFAIDPNGYVLLHNLQPKPKSPEPTL 540  
 QY 541 DFLDAELENDIKVEIRNKMIDGESGEKTFRTLVKSQDERYIDKGNRTYTWTVPNGTDYSL 600  
 Db 541 DFLDAELENDIKVEIRNKMIDGESGEKTFRTLVKSQDERYIDKGNRTYTWTVPNGTDYSL 600  
 QY 601 ALVLPTYSPYIIKAKIETITQARSKKGMKDSKSETLKPDPNFEESGYTFIAPRDYCNLDKI 660  
 Db 601 ALVLPTYSPYIIKAKIETITQARSKKGMKDSKSETLKPDPNFEESGYTFIAPRDYCNLDKI 660  
 QY 661 SDNTEFLNFNEFIDRKTNNPSCNTDLINRVLLDAGFTNELYQWYWSKOKNKGYKAR 720  
 Db 661 SDNTEFLNFNEFIDRKTNNPSCNTDLINRVLLDAGFTNELYQWYWSKOKNKGYKAR 720  
 QY 721 FVVDGGITRVYKPEAGENWQENPETVEDSFYKRSQDNDVFTAPYFNKSGPGAYESGI 780  
 Db 721 FVVDGGITRVYKPEAGENWQENPETVEDSFYKRSQDNDVFTAPYFNKSGPGAYESGI 780  
 QY 781 MVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPGAGVDCRNSDVMDCVI 840  
 Db 781 MVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPGAGVDCRNSDVMDCVI 840  
 QY 841 LDDGGLLMANHDYTNQIGRFFGEIDPMSLRHLVNIISVYAFNKSVDYQSVCEPGAAPKQ 900  
 Db 841 LDDGGLLMANHDYTNQIGRFFGEIDPMSLRHLVNIISVYAFNKSVDYQSVCEPGAAPKQ 900  
 QY 901 GAGHSRVAVPSADIHLIGWATAAANSIIQQFLLSTFPRLLEAVEMEDDDFTASLSKQ 960  
 Db 901 GAGHSRVAVPSADIHLIGWATAAANSIIQQFLLSTFPRLLEAVEMEDDDFTASLSKQ 960  
 QY 961 SCITEQTYQFFDNDKSFSGVLDGCGNCSRIHFVHEKLMNTNLIIFTMVESKGTCPDTRLLI 1020  
 Db 961 SCITEQTYQFFDNDKSFSGVLDGCGNCSRIHFVHEKLMNTNLIIFTMVESKGTCPDTRLLI 1020  
 QY 1021 QAEQTSQDGPDCDMVK 1036  
 Db 1021 QAEQTSQDGPDCDMVK 1036

RESULT 11

AAU01034

ID AAU01034 standard; Protein; 1063 AA.

XX AC AAU01034;

XX AC AAU01034;

DT 04-JUL-2001 (first entry)

DE Human secreted soluble alpha2delta calcium channel subunit #14 protein.

XX KW Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;

KW gabapentin; scintillation proximity assay; sPA; nickel flashplate assay;

XX KW filter binding assay; wheat germ lectin flashplate assay.

OS Homo sapiens.

XX KW

PN WO200119870-A2.

XX 22-MAR-2001.  
 XX 18-SEP-2000; 2000WO-EP09137.  
 XX 16-SEP-1999; 99US-0397550.  
 XX (WARN ) WARNER LAMBERT CO.  
 XX Brown JP, Bertelli F;  
 XX WPI; 2001-235262/24.  
 XX N-PSDB; AAS01425.  
 XX Calcium channel alpha2delta subunits, useful in e.g. SPA assays,  
 XX Flashplate assays, Nickel Flashplate assays, Filter binding assays or  
 XX Wheat Germ Lectin Flashplate assays -  
 XX Claim 31; Page 137-140; 160pp; English.  
 XX The present sequence represents human secreted calcium channel  
 XX alpha2delta subunit #14 which is soluble and retains the functional  
 XX characteristics of the full length or wild type alpha2delta subunit  
 XX (AAU01025) from which it is derived. The invention relates to truncated  
 XX alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins  
 XX which retain their affinity for radioactively labelled gabapentin. The  
 XX alpha2delta subunit is 1 of the components of the heteromultimeric  
 XX voltage-dependent calcium channel (VDCC) complexes present in neuronal  
 XX and non-neuronal tissues including heart and skeletal muscle. Numerous  
 XX soluble forms of the human calcium channel alpha2delta subunits  
 XX (AAU01014-AAU01024 and AAU01022-AAU01038) and 5 soluble forms of the  
 XX porcine calcium channel alpha2delta subunits (AAU01027-AAU01031) are  
 XX described. The secreted soluble alpha2delta subunit may be used in assays  
 XX e.g. scintillation proximity assay (SPA), flashplate, nickel flashplate,  
 XX filter binding or wheat germ lectin flashplate assays to detect or  
 XX measure the binding or interaction of a ligand (e.g. gabapentin,  
 XX L-Norleucine, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Isoleucine,  
 XX L-Valine, Spermine and/or L-phenylalanine) of a calcium channel  
 XX alpha2delta subunit.  
 XX Sequence 1063 AA;  
 Query Match 98.8%; Score 5380; DB 22; Length 1063;  
 Best Local Similarity 98.7%; Pred. NO. 0;  
 Matches 1023; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 MAAGCLLALTLFOSLLIGSPSPFPFSAVTIKSWDKMQEDLVTLAKTAGSVNQLYDI 60  
 DB 1 MAAGCLLALTLFOSLLIGSPSPFPFSAVTIKSWDKMQEDLVTLAKTAGSVNQLYDI 60  
 QY 61 YEKYQDLYTVEPNNAQLVEIAARDIEKLLSNRSLVLALEAEKVQAAHQWREDFASN 120  
 DB 61 YEKYQDLYTVEPNNAQLVEIAARDIEKLLSNRSLVLALEAEKVQAAHQWREDFASN 120  
 QY 121 EVVYNAKDDLPKNDSEPGSQRIKPFIDDAFGRIQISQHAHVHPTDIYEGSTVL 180  
 DB 121 EVVYNAKDDLPKNDSEPGSQRIKPFIDDAFGRIQISQHAHVHPTDIYEGSTVL 180  
 QY 181 NELNWTSSALDEVFKKREDEPSLLMQVFGSATGLARYYPASWPVDNSRTPNKKIDLYDVR 240  
 DB 181 NELNWTSSALDEVFKKREDEPSLLMQVFGSATGLARYYPASWPVDNSRTPNKKIDLYDVR 240  
 QY 241 RPWYIQGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
 DB 241 RPWYIQGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
 QY 301 VSCFQHLVQANVRNKKVLKADVNNITAKGIDYKKGFSFAPQLLNNVNSRANCNKIIML 360  
 DB 301 VSCFQHLVQANVRNKKVLKADVNNITAKGIDYKKGFSFAPQLLNNVNSRANCNKIIML 360  
 QY 361 FTDGGEERAQEIFAKYNDKKVRVTFVSGQHNVDGRPTQWACENKGYEYIPSIGAIR 420  
 DB 361 FTDGGEERAQEIFAKYNDKKVRVTFVSGQHNVDGRPTQWACENKGYEYIPSIGAIR 420

QY 421 INTQEYLDVLGRPMVLGADRAKQVQWTVNYDLDALELGLVITGTLPVFNITQGNENKTNLK 480  
 DB 421 INTQEYLDVLGRPMVLGADRAKQVQWTVNYDLDALELGLVITGTLPVFNITQGNENKTNLK 480  
 QY 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYYPALDPNGYVLLHPNLPKPKSQBPVTL 540  
 DB 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYYPALDPNGYVLLHPNLPKPKSQBPVTL 540  
 QY 541 DFLDAELENDIKVEIRNKMIDGESGEKTFRTLVKQSQDERYIDKGNRTYTTVPNGTDSL 600  
 DB 541 DFLDAELENDIKVEIRNKMIDGESGEKTFRTLVKQSQDERYIDKGNRTYTTVPNGTDSL 600  
 QY 601 ALVLPYTSFYIRAKIETITQARSKGKMKDSETLKPDMFESGYTFIAPRYCNDLKI 660  
 DB 601 ALVLPYTSFYIRAKIETITQARSKGKMKDSETLKPDMFESGYTFIAPRYCNDLKI 660  
 QY 661 SDNTEELLNFNEFIDRKTNNPSCNTDLLNRVLLDAGFTNELLVQVYWSKQNKIKGVKAR 720  
 DB 661 SDNTEELLNFNEFIDRKTNNPSCNTDLLNRVLLDAGFTNELLVQVYWSKQNKIKGVKAR 720  
 QY 721 FVVTGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
 DB 721 FVVTGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
 QY 781 MVSXAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRDPCAGPVCDCRNSDVMDCVI 840  
 DB 781 MVSXAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRDPCAGPVCDCRNSDVMDCVI 840  
 QY 841 LDDGGFLLMANHDDYTNOIGRFFGEIDPISLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 900  
 DB 841 LDDGGFLLMANHDDYTNOIGRFFGEIDPISLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 900  
 QY 901 GAGHRSAYVPSIADILHIGWATAAAWSILQOFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960  
 DB 901 GAGHRSAYVPSIADILHIGWATAAAWSILQOFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960  
 QY 961 SCITEQTYQYFFDNDKSFSGVLDGCGNCSRIHFHVEKLMNTNLIFIMVESKGTCPDTRLLI 1020  
 DB 961 SCITEQTYQYFFDNDKSFSGVLDGCGNCSRIHFHVEKLMNTNLIFIMVESKGTCPDTRLLI 1020  
 QY 1021 QAEQTSQDGPDCDMVK 1036  
 DB 1021 QAEQTSQDGPDCDMVK 1036  
 RESULT 12  
 AAB62258  
 ID AAB62258 standard; Protein; 1063 AA.  
 XX AAB62258;  
 XX 11-JUN-2001 (first entry)  
 XX Porcine calcium channel alpha2delta subunit.  
 XX Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;  
 XX nervous system disorder; pain; epilepsy; anxiety; pig.  
 XX Sus scrofa.  
 XX WO200120336-A2.  
 XX 22-MAR-2001.  
 XX 18-SEP-2000; 2000WO-EP09136.  
 XX 16-SEP-1999; 99US-0397549.  
 XX (WARN ) WARNER LAMBERT CO.  
 XX Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;  
 XX

DR WPI: 2001-257902/26.  
 XX N-PSDB; AAF57562.  
 PT Competitive binding assay for screening ligands which bind a cerebral  
 PT cortical voltage-dependent calcium channel alpha2-delta-1 subunit,  
 PT where the ligands identified are useful for treating disorders of the  
 PT nervous system, including pain -  
 XX  
 PS Claim 8; Page 135-139; 158pp; English.  
 XX The invention relates to a new method for screening ligands which bind a  
 CC cerebral cortical voltage-dependent calcium channel alpha2delta subunit,  
 CC preferably alpha2delta-1 subunit. The method comprises contacting a  
 CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of  
 CC interest and a labelled compound which binds the subunit, followed by  
 CC measuring the level of binding of the labelled compound to alpha2delta-1  
 CC subunit. The method is useful for screening ligands, preferably  
 CC biologically active products that modulate a nervous system function,  
 CC which bind a cerebral cortical voltage-dependent calcium channel  
 CC alpha2delta-1 subunit. The ligands identified by the method are useful  
 CC for treating disorders of the nervous system, including pain, epilepsy  
 CC and anxiety. The present sequence represents a porcine calcium channel  
 CC alpha2delta subunit.  
 XX  
 SQ Sequence 1063 AA;

Query Match 98.8%; Score 5380; DB 22; Length 1063;  
 Best Local Similarity 98.7%; Pred. No. 0;  
 Matches 1023; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLFQSLILIGSPSPSPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60  
 DB 1 MAAGCLLALTTLFQSLILIGSPSPSPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60  
 QY 61 YEKYQDLTVTEPNARQLVEIAARDIEKLLSNRSKALVRLALEAEKVQAAHOWREDFASN 120  
 DB 61 YEKYQDLTVTEPNARQLVEIAARDIEKLLSNRSKALVRLALEAEKVQAAHOWREDFASN 120  
 QY 121 EYVYNAKDDLDPEKNDSEPSQRIKPVFIDDANFGRIQISYQHAHVHIPTDIYEGSTIVL 180  
 DB 121 EYVYNAKDDLDPEKNDSEPSQRIKPVFIEDANFGRQISYQHAHVHIPTDIYEGSTIVL 180  
 QY 181 NELNWTALDEVFKNRDEPSSLVQVFGSATGLARYYPASPDWNSRTPNKIDLYDVR 240  
 DB 181 NELNWTALDEVFKNRDEPSSLVQVFGSATGLARYYPASPDWNSRTPNKIDLYDVR 240  
 QY 241 RPWYIQGAASPKDMLILVDVSGVSGLTLLKIRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
 DB 241 RPWYIQGAASPKDMLILVDVSGVSGLTLLKIRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
 QY 301 VSCFOHLVQANVRNKKVLLKDAVNITAKGITDYKKGFSFAPEQLLNTVNSRANCKIIML 360  
 DB 301 VSCFOHLVQANVRNKKVLLKDAVNITAKGITDYKKGFSFAPEQLLNTVNSRANCKIIML 360  
 QY 361 FTDGEERAQEIFAKYKNDKVRVFTSVGQHNDRGPDIOWMACENKGYIYEIPSIGAIR 420  
 DB 361 FTDGEERAQEIFAKYKNDKVRVFTSVGQHNDRGPDIOWMACENKGYIYEIPSIGAIR 420  
 QY 421 INTQBYLDVLGRPMVLGADKAKQVQWNTNVLDALELGLVITGTLVPVFNITQGNENKTLK 480  
 DB 421 INTQBYLDVLGRPMVLGADKAKQVQWNTNVLDALELGLVITGTLVPVFNITQGNENKTLK 480  
 QY 481 NOLLIGVMGVDSLEIDIKRLTPRTLCPNGYFFAIDPNGYVLLHPNLOPNKPSQEPVTL 540  
 DB 481 NOLLIGVMGVDSLEIDIKRLTPRTLCPNGYFFAIDPNGYVLLHPNLOPNKPSQEPVTL 540  
 QY 541 DFLDALENDIKVEIRNKMIDGESGKTFRTLKVSQDERYIDKGNRTYTTPVNGTDYSL 600  
 DB 541 DFLDALENDIKVEIRNKMIDGESGKTFRTLKVSQDERYIDKGNRTYTTPVNGTDYSL 600  
 QY 601 ALVLPYTSFYIYKAKIETITQARSKKGMKDSSTLKPDPNFESGYFTFIAPRYCNDLKI 660  
 DB 601 ALVLPYTSFYIYKAKIETITQARSKKGMKDSSTLKPDPNFESGYFTFIAPRYCNDLKI 660

QY 661 SDNTEFLNNEFIDRKTPNPNPSCNTDLINRVLLDAGFTNELVQYWSKQNIKGVKAR 720  
 DB 661 SDNTEFLNNEFIDRKTPNPNPSCNTDLINRVLLDAGFTNELVQYWSKQNIKGVKAR 720  
 QY 721 FVYTDGGITRVYPKEAGENQWENPETYEDSFYKRSLDNDNYVFTAFYFNKSGPAYESGI 780  
 DB 721 FVYTDGGITRVYPKEAGENQWENPETYEDSFYKRSLDNDNYVFTAFYFNKSGPAYESGI 780  
 QY 781 MVSKAVEIYIQGKLLPAPVVGIIKIDVNSWTENFTKTSIRDPACAGPVCDCKRNSDVMDCVI 840  
 DB 781 MVSKAVEIYIQGKLLPAPVVGIIKIDVNSWTENFTKTSIRDPACAGPVCDCKRNSDVMDCVI 840  
 QY 841 LDGSGFLLMANHDDYTNQIGRFFGEIDPSSLMRLHVNISYVAFNKSVDYQSVCEPGAAPQ 900  
 DB 841 LDGSGFLLMANHDDYTNQIGRFFGEIDPSSLMRLHVNISYVAFNKSVDYQSVCEPGAAPQ 900  
 QY 901 GAGHRSAYVPSVADIIQIGMWATAAAWSILQQFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
 DB 901 GAGHRSAYVPSVADIIQIGMWATAAAWSILQQFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
 QY 961 SCITEQTOYFFDNDKSFSGVLDCGNCSTRIFHVEKLMNTNLIFIMVESKGTCPCDTRLII 1020  
 DB 961 SCITEQTOYFFDNDKSFSGVLDCGNCSTRIFHVEKLMNTNLIFIMVESKGTCPCDTRLII 1020  
 QY 1021 QAEQTSDDGPPDCDMVK 1036  
 DB 1021 QAEQTSDDGPPDCDMVK 1036

RESULT 13  
 AAR71011  
 ID AAR71011 standard; Protein; 1091 AA.  
 XX  
 AC AAR71011;  
 XX  
 DT 01-DEC-1995 (first entry)  
 XX  
 DE Human neuronal calcium channel subunit alpha 2b.  
 XX  
 KW Calcium channel subunit; antagonist; agonist; diagnosis;  
 KW Lambert Eaton Syndrome.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9504822-A.  
 XX  
 PD 16-FEB-1995.  
 XX  
 PF 11-AUG-1994; 94WO-US09230.  
 XX  
 PR 11-AUG-1993; 93US-0105536.  
 PR 05-NOV-1993; 93US-0149097.  
 XX  
 PA (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.  
 XX  
 XX Ellis SB, Gillespie A, Harpold MW, Mccue AF, Williams ME;  
 PI WPI; 1995-090900/12.  
 DR N-PSDB; AAQ84664.  
 XX  
 PT DNA encoding human calcium channel sub-unit(s) - used for  
 PT developing prods. for studying calcium channels, e.g. for  
 PT obtaining agonists and antagonists  
 XX  
 PS Disclosure; Page 166-171; 285pp; English.  
 XX  
 CC Human neuronal alpha 2 coding sequence (AAQ84664) transcript is  
 CC differentially processed in skeletal muscle, aorta, and CNS in  
 CC the region corresp. to nt 1595-1942 of AAQ84664 in each of the  
 CC tissues. Five alternatively spliced variant transcripts that differ  
 CC in the presence or absence or one to three different portions of  
 CC this region. There are three sequences involved (see AAQ84664 FT

CC and AAQ84665 FT), sequence 1, sequence 2 and sequence 3. The five  
CC alpha 2 encoding transcripts from the different tissues include  
CC different combinations of the three sequences, except for one of  
CC the alpha 2 transcripts expressed in aorta which lacks all three  
CC sequences. The five alpha 2 forms identified are (1) a form that  
CC lacks sequence 3 called alpha 2a, expressed in skeletal muscle  
CC (2) one that lacks sequence 1 called alpha 2b, expressed in CNS  
CC (3) one that lacks sequences 1 and 2 called alpha 2c, expressed in  
CC aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,  
CC expressed in aorta and (5) one that lacks sequences 1 and 3  
CC called alpha 2e.

XX Sequence 1091 AA;

Query Match 98.8%; Score 5380; DB 16; Length 1091;  
Best Local Similarity 98.7%; Pred. No. 0;  
Matches 1023; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLFQSLIGSSQEPFSAVTIKSWDKQEDLVTAKTASGVNQLVDI 60  
DB 1 MAAGCLLALTTLFQSLIGSSQEPFSAVTIKSWDKQEDLVTAKTASGVNQLVDI 60  
QY 61 YEKYODLYTVENPNARQLVETAAARDIEKLLNSRSKALVRLALEAKVQAAHOREDFASN 120  
DB 61 YEKYODLYTVENPNARQLVETAAARDIEKLLNSRSKALVRLALEAKVQAAHOREDFASN 120  
QY 121 EVVYNAKDDLDPEKNDEPQSQRIPKPFIDDAFNGRQISYQAAVHIPTDIYEGSTIVL 180  
DB 121 EVVYNAKDDLDPEKNDEPQSQRIPKPFIDDAFNGRQISYQAAVHIPTDIYEGSTIVL 180  
QY 181 NELNWTSSALDEVFKNREDEPSLLMQVFGSATGLARYPPASPVWDNSRTPNKKIDLYVRR 240  
DB 181 NELNWTSSALDEVFKNREDEPSLLMQVFGSATGLARYPPASPVWDNSRTPNKKIDLYVRR 240  
QY 241 RPWYLOGAASPKDMLILVDVSGVSGLTLLKLRISVSEMLETLSDDDFVNVASFNSNAQD 300  
DB 241 RPWYLOGAASPKDMLILVDVSGVSGLTLLKLRISVSEMLETLSDDDFVNVASFNSNAQD 300  
QY 301 VSCFQHLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFEQLLNNVSRANCKIIML 360  
DB 301 VSCFQHLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFEQLLNNVSRANCKIIML 360  
QY 361 FTDGGEERAQETFAKYNKDKKVRVTFSSVGHNYDRGPLOWMACENKGYEYIIPSIGAIR 420  
DB 361 FTDGGEERAQETFAKYNKDKKVRVTFSSVGHNYDRGPLOWMACENKGYEYIIPSIGAIR 420  
QY 421 INTQYLDVLRPMVLGADKAKOVQWTVNYLDALGLVITGTLVPFNITGQENKTNLK 480  
DB 421 INTQYLDVLRPMVLGADKAKOVQWTVNYLDALGLVITGTLVPFNITGQENKTNLK 480  
QY 481 NQLILGVMGVDSLEDIKRLTFRFTLCPNGYYFAIDPNGYVLLHLPNLPKPKSQEPVTL 540  
DB 481 NQLILGVMGVDSLEDIKRLTFRFTLCPNGYYFAIDPNGYVLLHLPNLPKPKSQEPVTL 540  
QY 541 DELDAELNDIKVEIRNKMIDGESKEFTRLVKSQDERYIDKGNRTYTWTVPVNGTDYSL 600  
DB 541 DELDAELNDIKVEIRNKMIDGESKEFTRLVKSQDERYIDKGNRTYTWTVPVNGTDYSL 600  
QY 601 ALVLPYTFYIYKAKLEETITQARSKKGMKDSITLKPDNFESGYTFIAPDYCNLDKI 660  
DB 601 ALVLPYTFYIYKAKLEETITQARSKKGMKDSITLKPDNFESGYTFIAPDYCNLDKI 660  
QY 661 SONNTEFLNFBNEFIDRKTPNPNPCNTDLINRVLLDAGFTNELVQYNSKQKNIKGVAR 720  
DB 661 SONNTEFLNFBNEFIDRKTPNPNPCNTDLINRVLLDAGFTNELVQYNSKQKNIKGVAR 720  
QY 721 FVYTDGGITRVYPKEAGENKQENPETEYDSFKRSIDNDNYYFTAPYFNKSGPGAYESGI 780  
DB 721 FVYTDGGITRVYPKEAGENKQENPETEYDSFKRSIDNDNYYFTAPYFNKSGPGAYESGI 780  
QY 781 MYSKAVEIYIQGLKLPVAVVGKIDVNSWNIENFTKTSIRDPKAGPVCDCKRNSDVMDCVI 840  
DB 781 MYSKAVEIYIQGLKLPVAVVGKIDVNSWNIENFTKTSIRDPKAGPVCDCKRNSDVMDCVI 840

QY 841 LDGGFLLMANHDDYTNQIGRFFGETDPSLMRHLNVISYAFNKSVDYQSVCEPGAAPKQ 900  
DB 841 LDGGFLLMANHDDYTNQIGRFFGETDPSLMRHLNVISYAFNKSVDYQSVCEPGAAPKQ 900  
QY 901 GAGHRSAVPSIADILHIGWATAAAWSILQFLLSLTTPRLLAEVEMEDDDFTASLSKQ 960  
DB 901 GAGHRSAVPSIADILHIGWATAAAWSILQFLLSLTTPRLLAEVEMEDDDFTASLSKQ 960  
QY 961 SCITEQTQYFFDNDKSFSGVLDCGNCRSRIFHVEKLMNTNLIFIMVESKGTGCPDRLLI 1020  
DB 961 SCITEQTQYFFDNDKSFSGVLDCGNCRSRIFHVEKLMNTNLIFIMVESKGTGCPDRLLI 1020  
QY 1021 QAEQTSDDGPPCDMWK 1036  
DB 1021 QAEQTSDDGPPCDMWK 1036

#### RESULT 14

AAW63145  
ID AAW63145 standard; Protein; 1091 AA.

XX AAW63145;

XX AC AC

DT 12-OCT-1998 (first entry)

XX Human calcium channel alpha-2 subunit.

XX Alpha-2 subunit; human; calcium channel; assay; detection;

KW characterisation; Lambert Eaton Syndrome; LES; diagnosis.

XX Homo sapiens.

XX US5792846-A.

XX 11-AUG-1998.

XX 31-MAY-1995; 95US-0455543.

XX 04-APR-1994; 94US-0223305.

PR 04-APR-1988; 88US-0176899.

PR 04-APR-1989; 89US-0603751.

PR 04-APR-1989; 89WO-US01408.

PR 20-FEB-1990; 90US-0482384.

PR 30-NOV-1990; 90US-0620250.

PR 15-AUG-1991; 91US-0745206.

PR 31-MAY-1995; 95US-0455543.

XX (SIBI-) SIBIA NEUROSCIENCES INC.

XX Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;

PI Williams ME;

XX WPI; 1998-456192/39.

DR N-PSDB; AAV42689.

XX Claim 4; Columns 283-288; 166pp; English.

CC The present sequence represents the alpha-2 subunit of a human calcium  
CC channel. Calcium channels are membrane-spanning, multi-subunit proteins  
CC that allow controlled entry of calcium ions into cells. This leads  
CC to depolarisation events required for muscle contraction. The recombinant  
CC subunit, when expressed with nucleic acids encoding the complete calcium  
CC channel, can be used in assays for the detection and characterisation of  
CC compounds that modulate the channel. The DNA encoding the subunits can  
CC be alternatively spliced when transcribed, giving more than one form of  
CC the protein from the same transcript, each having slightly different  
CC properties. In addition, the reactivity of the alpha 1 subunit with IgG  
CC molecules from the serum of an individual with Lambert Eaton Syndrome

CC (LES) can be used as a diagnostic for the disease.

```

SQ Sequence 1091 AA;
Query Match 98.8%; Score 5380; DB 19; Length 1091;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1023; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAACCLALTLTQSLIGSPSSQEPSPSAVITKSWYDKMQEDLVTLAKTASGVNQLVDI 60
DQ 1 MAACCLALTLTQSLIGSPSSQEPSPSAVITKSWYDKMQEDLVTLAKTASGVNQLVDI 60
QY 61 YEKQDLYTVEPNARQLVEIARDIEKLLSNRSKALVRLALEAEKVAQAAHQWREDFASN 120
DQ 61 YEKQDLYTVEPNARQLVEIARDIEKLLSNRSKALVRLALEAEKVAQAAHQWREDFASN 120
QY 121 EVVYNAKDDLDPEKNDSEPGSRIRKPVFTDDANFRQISYQHAHVHPTDIYEGSTIVL 180
DQ 121 EVVYNAKDDLDPEKNDSEPGSRIRKPVFTDDANFRQISYQHAHVHPTDIYEGSTIVL 180
QY 181 NELNWTSALEDEVKKNREEDPSLLQWFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240
DQ 181 NELNWTSALEDEVKKNREEDPSLLQWFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240
QY 241 RPWYIOGAASPDKMLILVDVSGVSGLTGLIRTSYSEMLETLSDDDFVNVSFNSNAQD 300
DQ 241 RPWYIOGAASPDKMLILVDVSGVSGLTGLIRTSYSEMLETLSDDDFVNVSFNSNAQD 300
QY 301 VSCFQHLVQANVRNKKVLDVANNITAKITDYKKGFSFAFQOLLNYSRANCKNIIML 360
DQ 301 VSCFQHLVQANVRNKKVLDVANNITAKITDYKKGFSFAFQOLLNYSRANCKNIIML 360
QY 361 FTGGGERAEQIEFAKNKKQKVFVFTSVQGHYDRGPQWACENKGYEIPSGAIR 420
DQ 361 FTGGGERAEQIEFAKNKKQKVFVFTSVQGHYDRGPQWACENKGYEIPSGAIR 420
QY 421 INTQEYLDVLRPMVLGAKAKQVQNTVYLDALGLVITGTLPVFNITGQENKNTLK 480
DQ 421 INTQEYLDVLRPMVLGAKAKQVQNTVYLDALGLVITGTLPVFNITGQENKNTLK 480
QY 481 NQILGVMGVDVSLDIKRLTPRTLCNPGYFAIDPNCYVLLHNPQKPKSQEPVTL 540
DQ 481 NQILGVMGVDVSLDIKRLTPRTLCNPGYFAIDPNCYVLLHNPQKPKSQEPVTL 540
QY 541 DFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSODERYIDKGNRTYTWTPVNGTDSL 600
DQ 541 DFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSODERYIDKGNRTYTWTPVNGTDSL 600
QY 601 ALVLPYSFYIYKAKTEITTOARSKKGMKDSKSETLKPDPNFEESGYTFTAPRDYCNLKI 660
DQ 601 ALVLPYSFYIYKAKLEETITTOARSKKGMKDSKSETLKPDPNFEESGYTFTAPRDYCNLKI 660
QY 661 SDNNTFELNFEFTDRKTPNPNPSCNTDLINRVLLDAGFTNELVONYSKQKNIKGVKAR 720
DQ 661 SDNNTFELNFEFTDRKTPNPNPSCNADLINRVLLDAGFTNELVONYSKQKNIKGVKAR 720
QY 721 FVVTGGITRVYPKEAGENQENPETEYDFYKSLDNDVYVFTAPYFNKSGPGAYESGI 780
DQ 721 FVVTGGITRVYPKEAGENQENPETEYDFYKSLDNDVYVFTAPYFNKSGPGAYESGI 780
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWNIENFTKTSIRDPAGVPCDKRNSDVMDCVI 840
DQ 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWNIENFTKTSIRDPAGVPCDKRNSDVMDCVI 840
QY 841 LDGCGFLMANHDDVTNIGRFFGEIDPSLMHLNLSVYAFNKSVDYQSCVCEGAAAPKQ 900
DQ 841 LDGCGFLMANHDDVTNIGRFFGEIDPSLMHLNLSVYAFNKSVDYQSCVCEGAAAPKQ 900
QY 901 GAGHSAYVPSTADILHIGWATAAASILQOFLLSLTFPRLLEAVEMDDDFASLSKQ 960
DQ 901 GAGHSAYVPSTADILHIGWATAAASILQOFLLSLTFPRLLEAVEMDDDFASLSKQ 960
QY 961 SCITEQTQFFDNDKSFSGVLDGNCGRIFHEKLMNTNLIFIMVESKGTCPDTRLII 1020
```

```

Db 961 SCITEQTQFFDNDKSFSGVLDGNCGRIFHEKLMNTNLIFIMVESKGTCPDTRLII 1020
QY 1021 QAEQTSDDGPDPCDMVK 1036
DQ 1021 QAEQTSDDGPDPCDMVK 1036
Db 1021 QAEQTSDDGPDPCDMVK 1036
```

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RESULT 15
AAB10576
ID AAB10576 standard; Protein; 1091 AA.
XX AC AAB10576;
XX DT 22-DEC-2000 (first entry)
XX DE Human calcium channel alpha-2 subunit protein.
XX KW Human; calcium channel; calcium channel subunit; diagnosis;
KW Lambert Eaton Syndrome; calcium channel subunit alpha-2.
XX OS Homo sapiens.
XX PN US6096514-A.
XX PD 01-AUG-2000.
XX PF 25-MAY-1995; 95US-0450562.
XX PR 04-APR-1988; 88US-0176899.
XX PR 02-FEB-1990; 90US-0482384.
XX PR 08-NOV-1990; 90US-0603751.
XX PR 30-NOV-1990; 90US-0620250.
XX PR 15-AUG-1991; 91US-0745206.
XX PR 10-APR-1992; 92US-0868354.
XX PR 13-JUL-1992; 92US-0914231.
XX PR 11-AUG-1993; 93US-0105536.
XX PR 05-NOV-1993; 93US-0149097.
XX PR 07-FEB-1994; 94US-0193078.
XX PR 04-APR-1994; 94US-0223305.
XX PR 11-AUG-1994; 94US-0290012.
XX PR 23-SEP-1994; 94US-0311363.
XX PR 28-SEP-1994; 94US-0314083.
XX PR 07-NOV-1994; 94US-0336257.
XX PR 13-MAR-1995; 95US-0404950.
```

(SIBI-) SIBIA NEUROSCIENCES INC.

Ellis SB, Williams ME, McCue AP, Harpold MM;

WPI; 2000-548230/50.

N-PSDB; AAA71707.

Human calcium channel beta subunit polynucleotides, useful for producing recombinant eukaryotic cells and for diagnosing Lambert Eaton Syndrome

Example IV; Column 135-144; 153pp; English.

This invention describes a novel isolated DNA molecule (I) comprising a sequence encoding a beta3-1 subunit of a human calcium channel. Nucleic acid probes comprising 14-30 contiguous nucleotides of beta3 subunit encoding DNA are useful for isolation and cloning of calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that express heterologous calcium channel are useful for identifying compounds that modulate calcium channel activity and in assays for identifying agonists and antagonists of calcium channel activity in humans. Human calcium channel subunit or eukaryotic cells expressing the channel are useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This sequence represents the human calcium channel alpha-2 subunit which is described in the method of the invention.

Sequence 1091 AA;

Query Match 98.8%; Score 5380; DB 21; Length 1091;  
Best Local Similarity 98.7%; Pred. No. 0;  
Matches 1023; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MAAGCLLALTTLTQSLGSPSSPPFPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
Db 1 MAAGCLLALTTLTQSLGSPSSPPFPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

Qy 61 YEKYQDLTVPEPNARQIUEIAARDIEKLLNSRKALVRLALEAEKVAQAAHOWREDFASN 120  
Db 61 YEKYQDLTVPEPNARQIUEIAARDIEKLLNSRKALVRLALEAEKVAQAAHOWREDFASN 120

Qy 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIYSQHAHVHIPTDIYEGSTIVL 180  
Db 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIYSQHAHVHIPTDIYEGSTIVL 180

Qy 181 NELNWTSALEDEVFKKNREDEPSLLMQVFGSATGLARYYPASPVVDNSRTPNKIDLYDVR 240  
Db 181 NELNWTSALEDEVFKKNREDEPSLLMQVFGSATGLARYYPASPVVDNSRTPNKIDLYDVR 240

Qy 241 RPWYIQAASPKDMLILYDVSGVSGLTCLKIRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
Db 241 RPWYIQAASPKDMLILYDVSGVSGLTCLKIRTSVSEMLETSLDDDFVNVASFNSNAQD 300

Qy 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGIDYKKGFSFAFEQLINYNVSRANCNKIIML 360  
Db 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGIDYKKGFSFAFEQLINYNVSRANCNKIIML 360

Qy 361 FTDGGEERAQEIFAKYKDKKVRVFTFVGQHNVDGRPIOMACENKGYEYIIPSIGAIR 420  
Db 361 FTDGGEERAQEIFAKYKDKKVRVFTFVGQHNVDGRPIOMACENKGYEYIIPSIGAIR 420

Qy 421 INTQYVLDVGLGPMVLGDKAKQVQWNTVYLDALGLVITGTLVPVFNITGONENKTNLK 480  
Db 421 INTQYVLDVGLGPMVLGDKAKQVQWNTVYLDALGLVITGTLVPVFNITGONENKTNLK 480

Qy 481 NQILILGVMGVDSLEDIKRLTPRFTLCPPNGYFFAIDPNGYVLLHPNLQPKPKSQEPVTL 540  
Db 481 NQILILGVMGVDSLEDIKRLTPRFTLCPPNGYFFAIDPNGYVLLHPNLQPKPKSQEPVTL 540

Qy 541 DFLDAELENDIIVEIRNKMIDGESKEFTRLVKSQDERYIDKGNRTYTTPVNGTDYSL 600  
Db 541 DFLDAELENDIIVEIRNKMIDGESKEFTRLVKSQDERYIDKGNRTYTTPVNGTDYSL 600

Qy 601 ALVLPYSPYIYAKAETITQARSKKGMKDSITLKPDPNPEESGYTFIAPRDYCNDLKI 660  
Db 601 ALVLPYSPYIYAKAETITQARSKKGMKDSITLKPDPNPEESGYTFIAPRDYCNDLKI 660

Qy 661 SDNTEFLNFEFIDRKTPNPNPCNTDLINRVLLDAGFTNELVQNYWSKQKNIKGVKAR 720  
Db 661 SDNTEFLNFEFIDRKTPNPNPCNTDLINRVLLDAGFTNELVQNYWSKQKNIKGVKAR 720

Qy 721 FVYTDGGITRVTPKEAGENWQENPETYEDSFYKRSLDNDNYFTAPYFNKSGPGAYESGI 780  
Db 721 FVYTDGGITRVTPKEAGENWQENPETYEDSFYKRSLDNDNYFTAPYFNKSGPGAYESGI 780

Qy 781 MYSKAVEIYIQGLKLPVVGKIDVNSWIENTFTKTSIRDPKAGVPCDCKRNSDVMDCVI 840  
Db 781 MYSKAVEIYIQGLKLPVVGKIDVNSWIENTFTKTSIRDPKAGVPCDCKRNSDVMDCVI 840

Qy 841 LDDGGFLMANHDDYTNQIGREFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 900  
Db 841 LDDGGFLMANHDDYTNQIGREFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 900

Qy 901 GAGHSAYVPSADIHIGHWATAAWSILOQFLSLTFPRLEAVEMEDDDFTASLSKQ 960  
Db 901 GAGHSAYVPSADIHIGHWATAAWSILOQFLSLTFPRLEAVEMEDDDFTASLSKQ 960

Qy 961 SCITEQTYFFDNDKSFSGVLDGNCRI FHWKLMNTNLIFIMVESKGTCTCDTRLII 1020  
Db 961 SCITEQTYFFDNDKSFSGVLDGNCRI FHWKLMNTNLIFIMVESKGTCTCDTRLII 1020

Qy 1021 QAEQTSDDGPDPCDMVK 1036  
Db 1021 QAEQTSDDGPNPCDMVK 1036

Search completed: February 10, 2003, 14:18:05  
Job time : 37.6207 secs





GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 10, 2003, 14:13:55 ; Search time 11.4906 Seconds  
(without alignments)  
2652.785 Million cell updates/sec

Title: US-10-090-827-7  
Perfect score: 5446  
Sequence: 1 MAAGCLLALTLTLFQSLIG.....RLLIQABQTSQDPDPCDMVK 1036

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5380	98.8	1091	1	US-07-745-206A-25
2	5380	98.8	1091	1	US-08-455-543A-52
3	5380	98.8	1091	2	US-08-223-305C-52
4	5380	98.8	1091	2	US-08-311-363-25
5	5376	98.7	1091	3	US-08-713-118-4
6	5376	98.7	1091	4	US-09-452-007-4
7	5340.5	98.1	1086	1	US-08-455-543A-54
8	5340.5	98.1	1086	2	US-08-223-305C-54
9	5323.5	97.8	1084	1	US-08-455-543A-56
10	5323.5	97.8	1084	2	US-08-223-305C-56
11	5304	97.4	1103	1	US-08-455-543A-53
12	5304	97.4	1103	2	US-08-223-305C-53
13	5284	97.0	1079	1	US-08-455-543A-55
14	5284	97.0	1079	2	US-08-223-305C-55
15	5258.5	96.6	1106	1	US-08-435-675B-5
16	5240.5	96.2	1106	1	US-08-336-257A-8
17	5007.5	91.9	1086	6	5386025-8
18	2924.5	53.7	1145	4	US-09-470-443-2
19	2924.5	53.7	1145	4	US-09-470-443-4
20	2903.5	53.3	1076	4	US-09-470-443-6
21	2563.5	47.1	1084	1	US-08-435-675B-6
22	185	3.4	885	3	US-09-074-579-5
23	185	3.4	885	4	US-09-388-774-5
24	164.5	3.0	789	1	US-08-471-033-32
25	164.5	3.0	789	2	US-08-471-044-32
26	164.5	3.0	789	2	US-08-463-483A-32
27	164.5	3.0	789	2	US-08-471-046A-32

28	164.5	3.0	789	2	US-08-470-566B-32	Sequence 32, Appl
29	164.5	3.0	789	2	US-08-838-219B-4	Sequence 4, Appl
30	164.5	3.0	789	2	US-08-469-334-32	Sequence 32, Appl
31	164.5	3.0	789	3	US-09-300-529-32	Sequence 32, Appl
32	164.5	3.0	789	3	US-09-233-336A-4	Sequence 4, Appl
33	164.5	3.0	789	4	US-09-233-752A-4	Sequence 4, Appl
34	164.5	3.0	789	4	US-09-402-036-4	Sequence 4, Appl
35	164.5	3.0	789	4	US-09-904-226-4	Sequence 4, Appl
36	161.5	3.0	746	2	US-08-838-219B-6	Sequence 6, Appl
37	161.5	3.0	746	3	US-09-233-336A-6	Sequence 6, Appl
38	161.5	3.0	746	4	US-09-233-752A-6	Sequence 6, Appl
39	161.5	3.0	746	4	US-09-402-036-6	Sequence 6, Appl
40	161.5	3.0	746	4	US-09-904-226-6	Sequence 6, Appl
41	160.5	2.9	790	4	US-08-960-780-4	Sequence 4, Appl
42	160.5	2.9	790	4	US-09-073-898-4	Sequence 4, Appl
43	160.5	2.9	946	3	US-09-074-579-3	Sequence 3, Appl
44	160.5	2.9	946	4	US-09-388-774-3	Sequence 3, Appl
45	157.5	2.9	789	4	US-08-960-780-6	Sequence 6, Appl

## ALIGNMENTS

RESULT 1  
US-07-745-206A-25  
; Sequence 25, Application US/07745206A  
; Patent No. 5429921  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark  
; APPLICANT: McGue, Ann  
; APPLICANT: Feldman, Daniel  
; TITLE OF INVENTION: Human Calcium Channel Compositions and  
; TITLE OF INVENTION: Methods  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fitch, Even, Tabin & Flannery  
; STREET: 135 S. LaSalle  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: U.S.A.  
; ZIP: 60603

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07745,206A  
FILING DATE: 19910815  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Feder, Scott B  
REFERENCE/DOCKET NUMBER: 51504  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-372-7842  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1091 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-745-206A-25

Query Match 98.8%; Score 5380; DB 1; Length 1091;  
Best Local Similarity 98.7%; Pred. No. 0;  
Matches 1023; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLTLFQSLIGPSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

Db 1 MAAGCLLALTLTLFQSLIGPSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

QY 61 YEKYQDLYTVEPNNAQLVEITAARDIEKLLSNRSKALVRLALEAEKVOAAHQWREDFASN 120  
Db 61 YEKYQDLYTVEPNNAQLVEITAARDIEKLLSNRSKALVRLALEAEKVOAAHQWREDFASN 120  
QY 121 EVVYNNAKDDDDPEKNDSEPSQRIKPVFIIDANFGROISYHOAAVHIPTDIYEGSTIVL 180  
Db 121 EVVYNNAKDDDDPEKNDSEPSQRIKPVFIIDANFGROISYHOAAVHIPTDIYEGSTIVL 180  
QY 181 NELNWTSSALDEVEFKKNREDESLWQVFGSATGLARYYPASPWVNSRTPNKIDLYDVR 240  
Db 181 NELNWTSSALDEVEFKKNREDESLWQVFGSATGLARYYPASPWVNSRTPNKIDLYDVR 240  
QY 241 RPWYTOGAASPKDMLILVDVSGVSGSLPLKLI RTSVSMLETLSDDDPVNVASFNNAQD 300  
Db 241 RPWYTOGAASPKDMLILVDVSGVSGSLPLKLI RTSVSMLETLSDDDPVNVASFNNAQD 300  
QY 301 VSCFOHLVQANVRNKKVLKDAVNNTITAGITDYKKGFSFAEQLLNVNVRANCNKIIML 360  
Db 301 VSCFOHLVQANVRNKKVLKDAVNNTITAGITDYKKGFSFAEQLLNVNVRANCNKIIML 360  
QY 361 FTDGGEERAQAEIFAKYNDKKVRVFTSVGQHNYDRGPIONMACENKGYEIPSGAIR 420  
Db 361 FTDGGEERAQAEIFAKYNDKKVRVFTSVGQHNYDRGPIONMACENKGYEIPSGAIR 420  
QY 421 INTQEYLDVGRPMVLADKAKQVQWTVNYLDALGLVITGTLDPVFNITQONENKTNLK 480  
Db 421 INTQEYLDVGRPMVLADKAKQVQWTVNYLDALGLVITGTLDPVFNITQONENKTNLK 480  
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Db 481 NQILGVGMVDVSLIEDIKRLTPRFTLPCNGYFAIDPNGYVLLHPNLOPKPKSQEPVTL 540  
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Db 541 DFLDALENDIKVEIRNKMIDGSEKTRTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
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Db 601 ALVLPYTSFYIYKAKLEETITQARSKKGMKDSSETLKPDPNFEESGYTFIAPRDYCNLDKI 660  
QY 661 SONNTEFLNFEFIDRKTTPNPNCSNADLINRVLLDAGFTNELVQYWSKQKNIKGVKAR 720  
Db 661 SONNTEFLNFEFIDRKTTPNPNCSNADLINRVLLDAGFTNELVQYWSKQKNIKGVKAR 720  
QY 721 FVYTDGGITRVYPKRAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSPGAYESGI 780  
Db 721 FVYTDGGITRVYPKRAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSPGAYESGI 780  
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTKTSIRDPGAGVPCDCKRNSDVMDCVI 840  
Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTKTSIRDPGAGVPCDCKRNSDVMDCVI 840  
QY 841 LDDGGFLMANHDDYTQIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCPEGAAPKQ 900  
Db 841 LDDGGFLMANHDDYTQIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCPEGAAPKQ 900  
QY 901 GAGHRSAYPSTADILHIGWATAAWSILQOFLSLFPRLLEAVEMEDDDFTASLSKQ 960  
Db 901 GAGHRSAYPSTADILHIGWATAAWSILQOFLSLFPRLLEAVEMEDDDFTASLSKQ 960  
QY 961 SCITEQOTQFFNDKSKFSGVLDGNCNRSIFHVEKLMNTNLFIMVESKGTGCPDTRLLI 1020  
Db 961 SCITEQOTQFFNDKSKFSGVLDGNCNRSIFHVEKLMNTNLFIMVESKGTGCPDTRLLI 1020  
QY 1021 QABQTSQDGPDCDMVK 1036  
Db 1021 QABQTSQDGPDCDMVK 1036

## RESULT 2

US-08-455-543A-52  
; Sequence 52, Application US/0845543A  
; Patent No. 5792846

GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,543A  
FILING DATE: May 31, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/223,305  
FILING DATE: April 4, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-52517  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1091 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-455-543A-52

Query Match 98.8%; Score 5380; DB 1; Length 1091;  
Best Local Similarity 98.7%; Pred. No. 0;  
Matches 1023; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLTLFQSLILIGPSSQEPFSPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

Db 1 MAAGCLLALTLTLFQSLILIGPSSQEPFSPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

QY 61 YEKYQDLYTVEPNNAQVLEIAARDIEKLLSNRSKALVRLAEAEKVQAAHQRDFASN 120  
Db 61 YEKYQDLYTVEPNNAQVLEIAARDIEKLLSNRSKALVRLAEAEKVQAAHQRDFASN 120  
QY 121 EVVYNAKDDLDPEKNDSPGSRQIKPVFIDANFGRLSYOAAVHIPTDIYEGSTVL 180  
Db 121 EVVYNAKDDLDPEKNDSPGSRQIKPVFIDANFGRLSYOAAVHIPTDIYEGSTVL 180  
QY 181 NELNWTSALEDFVFKKNEEDPSLLMQVFGSATGLARYYPASPVNDNSRTPNKIDLYDVR 240  
Db 181 NELNWTSALEDFVFKKNEEDPSLLMQVFGSATGLARYYPASPVNDNSRTPNKIDLYDVR 240  
QY 241 RPYIOGAASPKDMLILVDVSGVSLTLKLRITSVSEMLETLDSDDFVNVASFNSAQD 300  
Db 241 RPYIOGAASPKDMLILVDVSGVSLTLKLRITSVSEMLETLDSDDFVNVASFNSAQD 300  
QY 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGIDYKKGFFAPBOLLNYNVSRANCKIIML 360  
Db 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGIDYKKGFFAPBOLLNYNVSRANCKIIML 360  
QY 361 FTDGGERAQEITAKYKNDKKVVFVTFSSVGHNYDRGPQIOMACENKGYEYIPIPSIGAIR 420  
Db 361 FTDGGERAQEITAKYKNDKKVVFVTFSSVGHNYDRGPQIOMACENKGYEYIPIPSIGAIR 420  
QY 421 INTOEYLDVLRPMVLADGKAKOVQWTVNYLDALGLVITGTLVPFNITGONENKTNLK 480  
Db 421 INTOEYLDVLRPMVLADGKAKOVQWTVNYLDALGLVITGTLVPFNITGONENKTNLK 480  
QY 481 NQILILGVMGVDSLEDIKRLTPRFLCPNGYYFADPNGYVLLHLPNPKPKSQEPVTL 540  
Db 481 NQILILGVMGVDSLEDIKRLTPRFLCPNGYYFADPNGYVLLHLPNPKPKSQEPVTL 540  
QY 541 DFLDALENDIKVEIRNKMIDGSEKFTRLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
Db 541 DFLDALENDIKVEIRNKMIDGSEKFTRLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
QY 601 ALVLPYTFYIYKAKIETITQARSKKGMKDSFTLKPDPNFEESGYTPIAPRDYCNLDKI 660  
Db 601 ALVLPYTFYIYKAKIETITQARSKKGMKDSFTLKPDPNFEESGYTPIAPRDYCNLDKI 660  
QY 661 SDNTEFLNFEFIDRKTTPNPNPCNTDILNRVLLDAGFTNVLVONYWSKOKNIKGKVKAR 720  
Db 661 SDNTEFLNFEFIDRKTTPNPNPCNTDILNRVLLDAGFTNVLVONYWSKOKNIKGKVKAR 720  
QY 721 FVVTGGITRVYPKAGENWQENPTYEDSYKRSNDNDNVFTAPYFNKSGPGAYESGI 780  
Db 721 FVVTGGITRVYPKAGENWQENPTYEDSYKRSNDNDNVFTAPYFNKSGPGAYESGI 780  
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIGNFTKTSIRDPGAGVCDCKRNSDVMDCVI 840  
Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIGNFTKTSIRDPGAGVCDCKRNSDVMDCVI 840  
QY 841 LDGGLLMAHDDYTNQIGRFFGIDPSLMRHLVNIISVYAFNKSVDYQSVCEPGAAPKQ 900  
Db 841 LDGGLLMAHDDYTNQIGRFFGIDPSLMRHLVNIISVYAFNKSVDYQSVCEPGAAPKQ 900  
QY 901 GAGHSAYVPSADILHGWATAAAMSILQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
Db 901 GAGHSAYVPSADILHGWATAAAMSILQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
QY 961 SCITETQYFFDNDSKFSGLVDCGNCNCRIFHVEKLMNTNLIIFWVSKGTCPCDTRLII 1020  
Db 961 SCITETQYFFDNDSKFSGLVDCGNCNCRIFHVEKLMNTNLIIFWVSKGTCPCDTRLII 1020  
QY 1021 QAEQTSQDGPDCDMVK 1036  
Db 1021 QAEQTSQDGPDCDMVK 1036

RESULT 3

US-08-223-305C-52

; Sequence 52, Application US/08223305C

Patent No. 5851824  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/223,305C  
FILING DATE: April 4, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 52516 (P519739)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1091 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-223-305C-52

Query Match 98.8%; Score 5380; DB 2; Length 1091;  
Best Local Similarity 98.7%; Pred. No. 0;  
Matches 1023; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLTFLQSLIGPSSQEPFPSPAVTIKSWDKMQEDLVTLAKTASGVNOLVDI 60

Db 1 MAAGCLLALTLTFLQSLIGPSSQEPFPSPAVTIKSWDKMQEDLVTLAKTASGVNOLVDI 60

QY 61 YEKYQDLYTVEPNNAQVLEIAARDIEKLLSNRSKALVRLAEAEKVQAAHQRDFASN 120

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Db 61 YEKYQDLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSLAEAEKVQAAHQRDEFSN 120
QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIDDFANFRQISQYHAAVHIPTDIYEGSTIVL 180
Db 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIDDFANFRQISQYHAAVHIPTDIYEGSTIVL 180
QY 181 NELNWTSDALDEVFKKNEEDPSLLWQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240
Db 181 NELNWTSDALDEVFKKNEEDPSLLWQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240
QY 241 RPWYIOGAASPKDMLILVDVSGVSGLTLLKLRISYSEMLETLSDDDFFNVASFSNAQD 300
Db 241 RPWYIOGAASPKDMLILVDVSGVSGLTLLKLRISYSEMLETLSDDDFFNVASFSNAQD 300
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNNVSRANCKIIML 360
Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNNVSRANCKIIML 360
QY 361 FTDGGERAQEIIFAKYKNDKKVRVFTFSVQGHNYDRGPIQWACENKGYIYEPSIGAIR 420
Db 361 FTDGGERAQEIIFAKYKNDKKVRVFTFSVQGHNYDRGPIQWACENKGYIYEPSIGAIR 420
QY 421 INTQEVYLDVLRPMWLAGKAKOVQNTVYLDALGLVITGTLPVFNITGQENKTNLK 480
Db 421 INTQEVYLDVLRPMWLAGKAKOVQNTVYLDALGLVITGTLPVFNITGQENKTNLK 480
QY 481 NQILGVMGVDVSLIEDIKRLTPRTLCPCNGYPAIDPNGYVLLHPLNLPKPKSQEPVTL 540
Db 481 NQILGVMGVDVSLIEDIKRLTPRTLCPCNGYPAIDPNGYVLLHPLNLPKPKSQEPVTL 540
QY 541 DFLDAELENDIKVEIKRMKIDGSGEKTERTLVKSODERYIDKGNRTYTWTVPNGTIDYSL 600
Db 541 DFLDAELENDIKVEIKRMKIDGSGEKTERTLVKSODERYIDKGNRTYTWTVPNGTIDYSL 600
QY 601 ALVLPYSFYIIKAKIEETITQARSKKGMKDSITLKPDPNFESGYTFTAPDYNCLDKI 660
Db 601 ALVLPYSFYIIKAKIEETITQARSKKGMKDSITLKPDPNFESGYTFTAPDYNCLDKI 660
QY 661 SDNTEFLNPNFIDRKTTPNPNPSCNADLINRVLLDAGFTNELVQYWSKQNKIRGVKAR 720
Db 661 SDNTEFLNPNFIDRKTTPNPNPSCNADLINRVLLDAGFTNELVQYWSKQNKIRGVKAR 720
QY 721 FVYTDGGITRVYKPEAGENQENPEYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
Db 721 FVYTDGGITRVYKPEAGENQENPEYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
QY 781 MVS KAVEIYIQGKLLKPAVVGKIDVNSWIENTFTKTSIRDPKAGPVCDCKRNSDMDCVI 840
Db 781 MVS KAVEIYIQGKLLKPAVVGKIDVNSWIENTFTKTSIRDPKAGPVCDCKRNSDMDCVI 840
QY 841 LDGGLFLLMANHDDYTNOIGRFGEIDPSLMRLHVNISYAFNKSVDYQSVCEPGAAPKQ 900
Db 841 LDGGLFLLMANHDDYTNOIGRFGEIDPSLMRLHVNISYAFNKSVDYQSVCEPGAAPKQ 900
QY 901 GAGHSAYVPSIADILHIGWATAAWSILQOFLLSLTPRLLEAVEMEDDDFTASLSKQ 960
Db 901 GAGHSAYVPSIADILHIGWATAAWSILQOFLLSLTPRLLEAVEMEDDDFTASLSKQ 960
QY 961 SCITEQTQTFDNDKSFSGVLDCGNCRIHFHVEKLMNNTLIFIMVESKGTCPDTRLLI 1020
Db 961 SCITEQTQTFDNDKSFSGVLDCGNCRIHFHVEKLMNNTLIFIMVESKGTCPDTRLLI 1020
QY 1021 QABQTSIDGPPCDMWK 1036
Db 1021 QABQTSIDGPPCDMWK 1036
```

## RESULT 4

US-08-311-363-25

; Sequence 25, Application US/08311363

; Patent No. 5876958

; GENERAL INFORMATION:

```
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: Human Calcium Channel Compositions and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311.363
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-51506
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1091 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-311-363-25
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Query Match 98.8%; Score 5380; DB 2; Length 1091;

Best Local Similarity 98.7%; Pred. No. 0;

Matches 1023; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLTFLQSLIGPSQEPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

Db 1 MAAGCLLALTTLTFLQSLIGPSQEPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

QY 61 YEKYQDLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSLAEAEKVQAAHQRDEFSN 120

Db 61 YEKYQDLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSLAEAEKVQAAHQRDEFSN 120

QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIDDFANFRQISQYHAAVHIPTDIYEGSTIVL 180

Db 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIDDFANFRQISQYHAAVHIPTDIYEGSTIVL 180

QY 181 NELNWTSDALDEVFKKNEEDPSLLWQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240

Db 181 NELNWTSDALDEVFKKNEEDPSLLWQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240

QY 241 RPWYIOGAASPKDMLILVDVSGVSGLTLLKLRISYSEMLETLSDDDFFNVASFSNAQD 300

Db 241 RPWYIOGAASPKDMLILVDVSGVSGLTLLKLRISYSEMLETLSDDDFFNVASFSNAQD 300

QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNNVSRANCKIIML 360

Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNNVSRANCKIIML 360

QY 361 FTDGGERAQEIIFAKYKNDKKVRVFTFSVQGHNYDRGPIQWACENKGYIYEPSIGAIR 420

Db 361 FTDGGERAQEIIFAKYKNDKKVRVFTFSVQGHNYDRGPIQWACENKGYIYEPSIGAIR 420

```

QY 421 INTQYLDVLRPMVLAGDKAKQVQWNTVYLDALGLVITGTLPVFNITQGNENKTLK 480
Db 421 INTQYLDVLRPMVLAGDKAKQVQWNTVYLDALGLVITGTLPVFNITQGNENKTLK 480
QY 481 NQILGVMGVDVSLIEDIKRLTPFTLCPNGYFAIDPNGVYLLHPNLQPNKSPQEPVTL 540
Db 481 NQILGVMGVDVSLIEDIKRLTPFTLCPNGYFAIDPNGVYLLHPNLQPNKSPQEPVTL 540
QY 541 DFLDAELNDIKVEIRNKMIDGESGKFTLVKSODERYIDKGNRTYTWTVPNGDYSL 600
Db 541 DFLDAELNDIKVEIRNKMIDGESGKFTLVKSODERYIDKGNRTYTWTVPNGDYSL 600
QY 601 ALVLPYTFYIIKAKLEETITQARSKKGMKDSSETLKPDPNFEESGYTFIAPDYCNLDKI 660
Db 601 ALVLPYTFYIIKAKLEETITQARSKKGMKDSSETLKPDPNFEESGYTFIAPDYCNLDKI 660
QY 661 SDNTEFLNFEFIDRKTPNPNPCNTDLINRVLLDAGFTNELVQYNSKQNIKGVKAR 720
Db 661 SDNTEFLNFEFIDRKTPNPNPCNTDLINRVLLDAGFTNELVQYNSKQNIKGVKAR 720
QY 721 FVYTDGGITRVYPKEAGENQENPETEYDSFYKRSILDNDNYVFTAPYFNKSGPGAYESGI 780
Db 721 FVYTDGGITRVYPKEAGENQENPETEYDSFYKRSILDNDNYVFTAPYFNKSGPGAYESGI 780
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTKTSIRDPGAGVDCCKRNSDVMDCVI 840
Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTKTSIRDPGAGVDCCKRNSDVMDCVI 840
QY 841 LDGGFLLMANHDDYTNQIGREFGIDPSLMRHLNYSVYAFNPKSYDYQSCVCEPAAKQ 900
Db 841 LDGGFLLMANHDDYTNQIGREFGIDPSLMRHLNYSVYAFNPKSYDYQSCVCEPAAKQ 900
QY 901 GAGHSAYVPSADIILHGWATAAASILQOFLSLTFPRLLAEVEMEDDDFTASLSKQ 960
Db 901 GAGHSAYVPSADIILHGWATAAASILQOFLSLTFPRLLAEVEMEDDDFTASLSKQ 960
QY 961 SCITQTOYFFDNDKSFSGVLDCGNCGRIFHVEKLMNTLIFIMVESKGTCPCDTRLII 1020
Db 961 SCITQTOYFFDNDKSFSGVLDCGNCGRIFHVEKLMNTLIFIMVESKGTCPCDTRLII 1020
QY 1021 QAEQTSQDGPDCMYK 1036
Db 1021 QAEQTSQDGPDCMYK 1036

```

## RESULT 5

```

US-08-713-118-4
; Sequence 4, Application US/08713118
; Patent No. 6040436
; GENERAL INFORMATION:
; APPLICANT: Franco, Rodrigo
; APPLICANT: Sun Chen, Ai Ru
; APPLICANT: Suey, David J.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL
; TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,118
; FILING DATE: 16-SEP-1996
; CLASSIFICATION: 435

```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Mata, Elizabeth W.
; REGISTRATION NUMBER: 38,236
; REFERENCE/DOCKET NUMBER: ACC96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1091 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-713-118-4

```

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Query Match 98.7%; Score 5376; DB 3; Length 1091;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 1022; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLTQSLIGPSSQPEPPSAVTIKSWDKMQEDLVTLAKTAGSYNQLVDI 60
Db 1 MAAGCLLALTTLTQSLIGPSSQPEPPSAVTIKSWDKMQEDLVTLAKTAGSYNQLVDI 60
QY 61 YEKYQDLYTVEPNNAQQLVEIAARDIEKLSNRSKALVRLALEAEKYOAAHQRWEDFASN 120
Db 61 YEKYQDLYTVEPNNAQQLVEIAARDIEKLSNRSKALVRLALEAEKYOAAHQRWEDFASN 120
QY 121 EVVYNNAKDDLDPKNSQEPGSRQIKPVFIDANFGROIQSYQAAVHIPTDIYEGSTIVL 180
Db 121 EVVYNNAKDDLDPKNSQEPGSRQIKPVFIDANFGROIQSYQAAVHIPTDIYEGSTIVL 180
QY 181 NELNWT SALDEVFVKKNREEDPSLLQWVFGSATGLARYYPASPWVDNSRTNPKIDLYDVR 240
Db 181 NELNWT SALDEVFVKKNREEDPSLLQWVFGSATGLARYYPASPWVDNSRTNPKIDLYDVR 240
QY 241 RPWTIOGAASPKDMLILVDVSGVSGTLKLIRTSVSEMLETSDDDFVNVAFNSNAQ 300
Db 241 RPWTIOGAASPKDMLILVDVSGVSGTLKLIRTSVSEMLETSDDDFVNVAFNSNAQ 300
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGSPAFEPQLLNVNVRANCKIIML 360
Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGSPAFEPQLLNVNVRANCKIIML 360
QY 361 FTDGGEERAQEIFAKYKDKKRVVFTSVGOHNYDROPIOMACENKGYIYEIPSTGAI 420
Db 361 FTDGGEERAQEIFAKYKDKKRVVFTSVGOHNYDROPIOMACENKGYIYEIPSTGAI 420
QY 421 INTQYLDVLRPMVLAGDKAKQVQWNTVYLDALGLVITGTLPVFNITQGNENKTLK 480
Db 421 INTQYLDVLRPMVLAGDKAKQVQWNTVYLDALGLVITGTLPVFNITQGNENKTLK 480
QY 481 NQILGVMGVDVSLIEDIKRLTPFTLCPNGYFAIDPNGVYLLHPNLQPNKSPQEPVTL 540
Db 481 NQILGVMGVDVSLIEDIKRLTPFTLCPNGYFAIDPNGVYLLHPNLQPNKSPQEPVTL 540
QY 541 DFLDAELNDIKVEIRNKMIDGESGKFTLVKSODERYIDKGNRTYTWTVPNGDYSL 600
Db 541 DFLDAELNDIKVEIRNKMIDGESGKFTLVKSODERYIDKGNRTYTWTVPNGDYSL 600
QY 601 ALVLPYTFYIIKAKLEETITQARSKKGMKDSSETLKPDPNFEESGYTFIAPDYCNLDKI 660
Db 601 ALVLPYTFYIIKAKLEETITQARSKKGMKDSSETLKPDPNFEESGYTFIAPDYCNLDKI 660
QY 661 SDNTEFLNFEFIDRKTPNPNPCNTDLINRVLLDAGFTNELVQYNSKQNIKGVKAR 720
Db 661 SDNTEFLNFEFIDRKTPNPNPCNTDLINRVLLDAGFTNELVQYNSKQNIKGVKAR 720
QY 721 FVYTDGGITRVYPKEAGENQENPETEYDSFYKRSILDNDNYVFTAPYFNKSGPGAYESGI 780
Db 721 FVYTDGGITRVYPKEAGENQENPETEYDSFYKRSILDNDNYVFTAPYFNKSGPGAYESGI 780
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTKTSIRDPGAGVDCCKRNSDVMDCVI 840

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Db 781 MVS KAVEIYIOGKLLKPAVVGKIDVNSWIENTKTSTIRDCAGPVCDCRNSDVMDCVI 840  
QY 841 LDDGGFLMANHDDYTNOIGRFFGIDPSLMRHLVNSVYAFNKSVDYQSVCEGAPKQ 900  
Db 841 LDDGGFLMANHDDYTNOIGRFFGIDPSLMRHLVNSVYAFNKSVDYQSVCEGAPKQ 900  
QY 901 GAGHSAYVPSIADILHIGWATAAASIILOQFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960  
Db 901 GAGHSAYVPSIADILHIGWATAAASIILOQFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960  
QY 961 SCITEQTFYFFDNDKSFSGVLDGNCGRIFHVEKLMNTNLIIFIMVESKGTCPDTRLLI 1020  
Db 961 SCITEQTFYFFDNDKSFSGVLDGNCGRIFHVEKLMNTNLIIFIMVESKGTCPDTRLLI 1020  
QY 1021 QAEQTS DGPDCDMVK 1036  
Db 1021 QAEQTS DGPDCDMVK 1036

RESULT 6  
US-09-452-007-4  
; Sequence 4, Application US/09452007  
; Patent No. 6140485  
; GENERAL INFORMATION:  
; APPLICANT: Franco, Rodrigo  
; APPLICANT: Sun Chen, Ai Ru  
; APPLICANT: Suey, David J.  
; TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL  
; TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173-4799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/452,007  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/713,118  
; FILING DATE: 16-SEP-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mata, Elizabeth W.  
; REGISTRATION NUMBER: 38,236  
; REFERENCE/DOCKET NUMBER: ACC96-01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-861-6240  
; TELEFAX: 617-861-9540  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1091 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-09-452-007-4  
Query Match 98.7%; Score 5376; DB 4; Length 1091;  
Best Local Similarity 98.6%; Pred. No. 0;  
Matches 1022; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLTQSLIGPSSQEPFPPSAVTIKSWDKMQEDLVLTAKTASGVNOLVDI 60  
Db 1 MAAGCLLALTLTQSLIGPSSQEPFPPSAVTIKSWDKMQEDLVLTAKTASGVNOLVDI 60  
QY 61 YEKYQDLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSLAEAEKVQAAHQRDEFASN 120

Db 61 YEKYQDLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSLAEAEKVQAAHQRDEFASN 120  
QY 121 EVVYVNAKDDLDPEKNDSSEPGSQRIKPVIEDANFGQISYQHAHAHIPDTDIYEGSTIVL 180  
Db 121 EVVYVNAKDDLDPEKNDSSEPGSQRIKPVIEDANFGQISYQHAHAHIPDTDIYEGSTIVL 180  
QY 181 NELNWTSALEDFVKKKNEEDPSSLQWVFGSATGLIARYYPASPWVDSNRTPNKIDLYDVR 240  
Db 181 NELNWTSALEDFVKKKNEEDPSSLQWVFGSATGLIARYYPASPWVDSNRTPNKIDLYDVR 240  
QY 241 RPYWYTOGAASPKDMLILVDVSGSVGLTLKLIIRISVSEMLETISDDDFVNAVAFNSNAQ 300  
Db 241 RPYWYTOGAASPKDMLILVDVSGSVGLTLKLIIRISVSEMLETISDDDFVNAVAFNSNAQ 300  
QY 301 VSCFOHLYQVANYRNKKVLKDAVNITAKGIDYKKGSFAFEQQLLNYSRANCNKIIML 360  
Db 301 VSCFOHLYQVANYRNKKVLKDAVNITAKGIDYKKGSFAFEQQLLNYSRANCNKIIML 360  
QY 361 FTDGGEERAQEIFAKYKNDKVKVRVFTFSVGHNYDRGPQIMMACENKGYEYIPSGAIR 420  
Db 361 FTDGGEERAQEIFAKYKNDKVKVRVFTFSVGHNYDRGPQIMMACENKGYEYIPSGAIR 420  
QY 421 INTQEWYLDVLRPMVLGADKAKQVQWNTVYLDALGLVITGTLPVENITGONENKTNLK 480  
Db 421 INTQEWYLDVLRPMVLGADKAKQVQWNTVYLDALGLVITGTLPVENITGONENKTNLK 480  
QY 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYFYFAIDPNGYVLLHPNLQPNKPSQEPVTL 540  
Db 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYFYFAIDPNGYVLLHPNLQPNKPSQEPVTL 540  
QY 541 DFLDAELENDIKVEIRNKMIDGESCEKTFRLVKSQDERYIDKGNRYTWTVPNGTDSL 600  
Db 541 DFLDAELENDIKVEIRNKMIDGESCEKTFRLVKSQDERYIDKGNRYTWTVPNGTDSL 600  
QY 601 ALVLPYSPYIYKAKTEETITQARSKKGMKDSITLKPDNFEESGYTFIAPRDYCNLDKI 660  
Db 601 ALVLPYSPYIYKAKTEETITQARSKKGMKDSITLKPDNFEESGYTFIAPRDYCNLDKI 660  
QY 661 SDNTEFLNFEFIDRKTTPNPNPCNTDLINRVLLDAGFTNELVQNYWSKOKNKGKVKAR 720  
Db 661 SDNTEFLNFEFIDRKTTPNPNPCNTDLINRVLLDAGFTNELVQNYWSKOKNKGKVKAR 720  
QY 721 FVYTDGGITRVYPKEAGENQENPETEYDSFYKRSLDNDNVFTAPYFNKSGPGAYESGI 780  
Db 721 FVYTDGGITRVYPKEAGENQENPETEYDSFYKRSLDNDNVFTAPYFNKSGPGAYESGI 780  
QY 781 MVS KAVEIYIOGKLLKPAVVGKIDVNSWIENTKTSTIRDCAGPVCDCRNSDVMDCVI 840  
Db 781 MVS KAVEIYIOGKLLKPAVVGKIDVNSWIENTKTSTIRDCAGPVCDCRNSDVMDCVI 840  
QY 841 LDDGGFLMANHDDYTNOIGRFFGIDPSLMRHLVNSVYAFNKSVDYQSVCEGAPKQ 900  
Db 841 LDDGGFLMANHDDYTNOIGRFFGIDPSLMRHLVNSVYAFNKSVDYQSVCEGAPKQ 900  
QY 901 GAGHSAYVPSIADILHIGWATAAASIILOQFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960  
Db 901 GAGHSAYVPSIADILHIGWATAAASIILOQFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960  
QY 961 SCITEQTFYFFDNDKSFSGVLDGNCGRIFHVEKLMNTNLIIFIMVESKGTCPDTRLLI 1020  
Db 961 SCITEQTFYFFDNDKSFSGVLDGNCGRIFHVEKLMNTNLIIFIMVESKGTCPDTRLLI 1020  
QY 1021 QAEQTS DGPDCDMVK 1036  
Db 1021 QAEQTS DGPDCDMVK 1036

RESULT 7  
US-08-455-543A-54  
; Sequence 54, Application US/08455543A  
; Patent No. 5792846  
; GENERAL INFORMATION:

APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US 07/455,543A  
FILING DATE: May 31, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/223,305  
FILING DATE: April 4, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-52517  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1086 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-455-543A-54

Query Match 98.1%; Score 5340.5; DB 1; Length 1086;  
Best Local Similarity 98.3%; Pred. No. 0;  
Matches 1018; Conservative 6; Mismatches 7; Indels 5; Gaps 1;  
QY 1 MAAGCLLALTLTQSLIGSPSEPPPSAVTISKWVDKMQEDLVTLAKTAGSGVNLVDI 60  
Db 1 MAAGCLLALTLTQSLIGSPSEPPPSAVTISKWVDKMQEDLVTLAKTAGSGVNLVDI 60

QY 61 YEKYQDLTYTVEPNNAQOLVEIAARDIEKLLSNRSKALVRLALEAEKQVAAHQRDEFASN 120  
Db 61 YEKYQDLTYTVEPNNAQOLVEIAARDIEKLLSNRSKALVRLALEAEKQVAAHQRDEFASN 120  
QY 121 EVYYNNAKDDLDPEKNDSEPGSQRIKPVFIDANFGHQISYQHAHVHIPTDIYEGSTIVL 180  
Db 121 EVYYNNAKDDLDPEKNDSEPGSQRIKPVFIDANFGHQISYQHAHVHIPTDIYEGSTIVL 180  
QY 181 NELNWTSAIDDEVFKKNNREEDPSLLQVFGSATGLARYPASPWVDNSTRPNKIDLYDVR 240  
Db 181 NELNWTSAIDDEVFKKNNREEDPSLLQVFGSATGLARYPASPWVDNSTRPNKIDLYDVR 240  
QY 241 RPWYIOGAASPKDMLILVDVSGSVGLTLKLRITSVSEMLETSLDDDFVNVASFNSNAQD 300  
Db 241 RPWYIOGAASPKDMLILVDVSGSVGLTLKLRITSVSEMLETSLDDDFVNVASFNSNAQD 300  
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAGTIDYKGSFAFEQLLNLYNVRANCNKTIIML 360  
Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAGTIDYKGSFAFEQLLNLYNVRANCNKTIIML 360  
QY 361 FTDCGEERAQEIFAKYKNDKKVRVFTFSVGHNYDRGPIQWMACENKGYEYIPIPSIGAIR 420  
Db 361 FTDCGEERAQEIFAKYKNDKKVRVFTFSVGHNYDRGPIQWMACENKGYEYIPIPSIGAIR 420  
QY 421 INTQEYLDVLRPMVLAGDKAKOVQNTVYLDALGLVITGTLPVENITQENKTNLK 480  
Db 421 INTQEYLDVLRPMVLAGDKAKOVQNTVYLDALGLVITGTLPVENITQENKTNLK 480  
QY 481 NQLILGYMGVDVSLIEDIKRLTPRTLCPNGYYFAIDPNGVYLLHNPKNKQSBPVTL 540  
Db 481 NQLILGYMGVDVSLIEDIKRLTPRTLCPNGYYFAIDPNGVYLLHNPKNKQSBPVTL 540  
QY 541 DFLDAELENDIKVEIRNKMIDGESGKTRTLVKSQDERYIDKGNRTYTTPVNGTDYSL 600  
Db 541 DFLDAELENDIKVEIRNKMIDGESGKTRTLVKSQDERYIDKGNRTYTTPVNGTDYSL 600  
QY 596 ALVLPYTSFYIYKAKLEETITQARSKKGMKDSSETLKPDPNFEEGYTFFIAPDYCNDLKI 655  
Db 596 ALVLPYTSFYIYKAKLEETITQARSKKGMKDSSETLKPDPNFEEGYTFFIAPDYCNDLKI 655  
QY 661 SDNTEPELLNFNEFIDRKTPNPNPSCNTDILNRLVLLDAGFTNELVQYWSKQKNIKGVKAR 720  
Db 661 SDNTEPELLNFNEFIDRKTPNPNPSCNTDILNRLVLLDAGFTNELVQYWSKQKNIKGVKAR 720  
QY 721 FVYTDGGITRVYPKEAGENQENPETEYDSFYKRSLDNDNVFTAPVFNKSGPGAYESGI 780  
Db 721 FVYTDGGITRVYPKEAGENQENPETEYDSFYKRSLDNDNVFTAPVFNKSGPGAYESGI 780  
QY 776 MVSKAVEIYIQGLKLLKPAVVGKIDVNSWTENFTKTSIRDPCAGPVCDCCKRNSDVMDCVI 840  
Db 776 MVSKAVEIYIQGLKLLKPAVVGKIDVNSWTENFTKTSIRDPCAGPVCDCCKRNSDVMDCVI 840  
QY 841 LDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLNLSVYAPNKSVDYQSVCEPGAAPKQ 900  
Db 841 LDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLNLSVYAPNKSVDYQSVCEPGAAPKQ 900  
QY 836 LDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLNLSVYAFNKSVDYQSVCEPGAAPKQ 895  
Db 836 LDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLNLSVYAFNKSVDYQSVCEPGAAPKQ 895  
QY 901 GAGHRSAYVPSIADILHIGHWATAAASWILQQLLSLTPRLLEAVEMEDDDFTASLSKQ 960  
Db 901 GAGHRSAYVPSIADILHIGHWATAAASWILQQLLSLTPRLLEAVEMEDDDFTASLSKQ 960  
QY 961 SCITEQTQTFDNDKSFSGVLDGCGNCSRFHFHVEKLMNTNLIFIMVESKGTCPDTRLLI 1020  
Db 961 SCITEQTQTFDNDKSFSGVLDGCGNCSRFHFHVEKLMNTNLIFIMVESKGTCPDTRLLI 1020  
QY 1021 QABQTSIDGDPDCDMVK 1036  
Db 1021 QABQTSIDGDPDCDMVK 1036  
QY 1016 QAEQTSIDGDPDCDMVK 1031  
Db 1016 QAEQTSIDGDPDCDMVK 1031

RESULT 8  
US-08-223-305C-54  
; Sequence 54, Application US/08223305C  
; Patent No. 5851824

GENERAL INFORMATION:  
 APPLICANT: Harpold, Michael  
 APPLICANT: Ellis, Steven  
 APPLICANT: Williams, Mark  
 APPLICANT: Feldman, Daniel  
 APPLICANT: McCue, Ann  
 APPLICANT: Brenner, Robert  
 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
 TITLE OF INVENTION: METHODS  
 NUMBER OF SEQUENCES: 57  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Brown, Martin, Haller & McClain  
 STREET: 1660 Union Street  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92101-2926  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/223,305C  
 FILING DATE: April 4, 1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/868,354  
 FILING DATE: April 10, 1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/745,206  
 FILING DATE: 15-AUG-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/620,250  
 FILING DATE: 30-NOV-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/482,384  
 FILING DATE: 20-FEB-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/603,751  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/US89/01408  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/176,899  
 FILING DATE: 04-APR-1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie L.  
 REGISTRATION NUMBER: 33,779  
 REFERENCE/DOCKET NUMBER: 52516 (P519739)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619)238-0999  
 TELEFAX: (619)238-0062  
 INFORMATION FOR SEQ ID NO: 54:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1086 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-223-305C-54

Query Match 98.1%; Score 5340.5; DB 2; Length 1086;  
 Best Local Similarity 98.3%; Pred. No. 0;  
 Matches 1018; Conservative 6; Mismatches 7; Indels 5; Gaps 1;

QY 1 MAAGCLLALTTLTFLQSLIGPSSPPFPSSAVTIKSWVDKMQEDLVTLAKTAGSYGNQLVDI 60  
 DB 1 MAAGCLLALTTLTFLQSLIGPSSPPFPSSAVTIKSWVDKMQEDLVTLAKTAGSYGNQLVDI 60  
 QY 61 YEKYQDLYTVEPNNAQLVEIAARDIEKLLSNRSKALVSLALEAEKVKQAQAHQWREDFASN 120

DB 61 YEKYQDLYTVEPNNAQLVEIAARDIEKLLSNRSKALVSLALEAEKVKQAQAHQWREDFASN 120  
 QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFTIDANFRQISYQAAVHIPTDIYEGSTIVL 180  
 DB 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFTIDANFRQISYQAAVHIPTDIYEGSTIVL 180  
 QY 181 NELNWTLSALDEVFKKNEEDPSLLQVFGSATGLARYYPASPVWDNSRTPNKIDLYDVR 240  
 DB 181 NELNWTLSALDEVFKKNEEDPSLLQVFGSATGLARYYPASPVWDNSRTPNKIDLYDVR 240  
 QY 241 RPWYIOGAASPKDMLILVDVSGVSGLTLLKLRISYSEMLETLSDDDFVNVASFNSNAOD 300  
 DB 241 RPWYIOGAASPKDMLILVDVSGVSGLTLLKLRISYSEMLETLSDDDFVNVASFNSNAOD 300  
 QY 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGITYKGFSAFEGQLLNYSRANCNKIIML 360  
 DB 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGITYKGFSAFEGQLLNYSRANCNKIIML 360  
 QY 361 FTDGGERAQEIPAKYKNDKKVVFVTFVSGOHNYDRGPLOWMACENKGYIYIETSPISGAIR 420  
 DB 361 FTDGGERAQEIPAKYKNDKKVVFVTFVSGOHNYDRGPLOWMACENKGYIYIETSPISGAIR 420  
 QY 421 INTQEYLDVLGRPMVLGDKAKOVQWNTVYLDALGLVITGTPVFNITGQENKTNLK 480  
 DB 421 INTQEYLDVLGRPMVLGDKAKOVQWNTVYLDALGLVITGTPVFNITGQENKTNLK 480  
 QY 481 NQLILGVMGVDSLEDITKRLTPRFTLCPNGYPAIDPNGYVLLHPLNPKNSOBPVTL 540  
 DB 481 NQLILGVMGVDSLEDITKRLTPRFTLCPNGYPAIDPNGYVLLHPLNPKNSOBPVTL 540  
 QY 541 DFLDAELENDIKVEIRNKMIDGESGKTRTLVKSDERYIDKGNRTYTWTVPNGDYSL 600  
 DB 541 DFLDAELENDIKVEIRNKMIDGESGKTRTLVKSDERYIDKGNRTYTWTVPNGDYSL 600  
 QY 601 ALVLTYSFYIYKAKLEETITQARSKKGMKDSSETLKPDNFEESGYTFIAPRDYCNLDKI 660  
 DB 601 ALVLTYSFYIYKAKLEETITQARSKKGMKDSSETLKPDNFEESGYTFIAPRDYCNLDKI 660  
 QY 661 SDNTEFLNFEFIDRKTPNPNPSCNTDLINRVLLDAGFTNELVQNSKQKNIKGVKAR 720  
 DB 661 SDNTEFLNFEFIDRKTPNPNPSCNTDLINRVLLDAGFTNELVQNSKQKNIKGVKAR 720  
 QY 721 FVYTDGGITRVYPKEAGENQENPETEYDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
 DB 721 FVYTDGGITRVYPKEAGENQENPETEYDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
 QY 781 MVS KAVEIYIQQKLLKPAVVGIKIDVNSWIENFTKTSIRDPGAPVCDCKRNSDVMDCVI 840  
 DB 781 MVS KAVEIYIQQKLLKPAVVGIKIDVNSWIENFTKTSIRDPGAPVCDCKRNSDVMDCVI 840  
 QY 841 LDDGGFLLMANHDDYTNQIGRPFGEIDPSIMRHLVNI SVYAFNKSVDYOSVCEPGAAPKQ 900  
 DB 841 LDDGGFLLMANHDDYTNQIGRPFGEIDPSIMRHLVNI SVYAFNKSVDYOSVCEPGAAPKQ 900  
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 QY 1021 QAEQTSDDGPPDCDMVK 1036  
 DB 1016 QAEQTSDDGPPDCDMVK 1031  
 RESULT 9  
 US-08-455-543A-56  
 ; Sequence 56, Application US/0845543A  
 ; Patent No. 5792846  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Harpold, Michael



APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,543A  
FILING DATE: May 31, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/223,305  
FILING DATE: April 4, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-52517  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1084 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-455-543A-56

Query Match 97.88; Score 5323.5; DB 1; Length 1084;  
Best Local Similarity 98.08; Pred. No. 0;  
Matches 1015; Conservative 6; Mismatches 8; Indels 7; Gaps 1;  
QY 1 MAACCLALTLTLFQSLIGSPSPPPSAVTIKSWDKMQEDLVTLAKTAGSGVNLVDI 60  
DB 1 MAACCLALTLTLFQSLIGSPSPPPSAVTIKSWDKMQEDLVTLAKTAGSGVNLVDI 60  
QY 61 YEKQDLYTVEPNNAARQLVEITAARDIEKLLNSRKALVLALEAEKVAQAHHQWREDFASN 120

DB 61 YEKQDLYTVEPNNAARQLVEITAARDIEKLLNSRKALVLALEAEKVAQAHHQWREDFASN 120  
QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIDDANFGRQISYQHAHVHIPTDIYEGSTIVL 180  
DB 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISYQHAHVHIPTDIYEGSTIVL 180  
QY 181 NELNWTSADEVFKKNREEDPSLLWQVFGSATGLARYYPASPVWDNRTPNKIDLYDVR 240  
DB 181 NELNWTSADEVFKKNREEDPSLLWQVFGSATGLARYYPASPVWDNRTPNKIDLYDVR 240  
QY 241 RPWYIQGAASPKDMLILVDVSGSYGLTLKLRISVSEMLETLSDDDFVNVASNSNAQD 300  
DB 241 RPWYIQGAASPKDMLILVDVSGSYGLTLKLRISVSEMLETLSDDDFVNVASNSNAQD 300  
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAGTIDYKKGFSFAFEQLLNVSRANCKIIML 360  
DB 301 VSCFQHLVQANVRNKKVLDKAVNNITAGTIDYKKGFSFAFEQLLNVSRANCKIIML 360  
QY 361 FTDGGEERAQEIFAKYNKDKKVRVFTSVGQHNKYDRGPIOMMACENKGYEYIETPSICAIR 420  
DB 361 FTDGGEERAQEIFAKYNKDKKVRVFTSVGQHNKYDRGPIOMMACENKGYEYIETPSICAIR 420  
QY 421 INTOEYLDVLRPMVLAGDKAKOVQWTVNYDLDELGLVITGTLPVFNITGQENKTNLK 480  
DB 421 INTOEYLDVLRPMVLAGDKAKOVQWTVNYDLDELGLVITGTLPVFNITGQENKTNLK 480  
QY 481 NOLLGVNGVDVSLIEDIKRLTPRTLCNPGYFAIDPNGYVLLHNPKNPKSQEPVTL 540  
DB 481 NOLLGVNGVDVSLIEDIKRLTPRTLCNPGYFAIDPNGYVLLHNPKNPKSQEPVTL 540  
QY 541 DFLDAELENDIKVEIRNKMIDGESGEKTFRTLVKSQDERYIDKGNRTYTPTVNGTDYSL 600  
DB 541 DFLDAELENDIKVEIRNKMIDGESGEKTFRTLVKSQDERYIDKGNRTYTPTVNGTDYSL 600  
QY 601 ALVLPYTSFYIIKAKIEETITQARSKGKMKDSETLKPDNFEESGYTFFIAPRYCNDLKI 660  
DB 601 ALVLPYTSFYIIKAKIEETITQARSKGKMKDSETLKPDNFEESGYTFFIAPRYCNDLKI 660  
QY 661 SDNTEFLNFEFIDRKTNPNSCNTDLINRVLLDAGFTNELVQYWSKQKNIKGVKAR 720  
DB 661 SDNTEFLNFEFIDRKTNPNSCNTDLINRVLLDAGFTNELVQYWSKQKNIKGVKAR 720  
QY 721 FVVTGGITRVYPKEAGENQENPETEYDSFYKRSIDNDNYVFTAPYFNKSGPGAYESGI 780  
DB 721 FVVTGGITRVYPKEAGENQENPETEYDSFYKRSIDNDNYVFTAPYFNKSGPGAYESGI 780  
QY 781 MVSKAVEIYIQGLKLLKPAVVGKIDVNSWIENFTKTSIRDPCAGPYCDCKRNSDMDCVI 840  
DB 781 MVSKAVEIYIQGLKLLKPAVVGKIDVNSWIENFTKTSIRDPCAGPYCDCKRNSDMDCVI 840  
QY 841 LDGSGFLLMANHDDYTNOIGRPFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPQGAAPK 900  
DB 841 LDGSGFLLMANHDDYTNOIGRPFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPQGAAPK 900  
QY 901 GAGHRSAYVPSADIHLHIGMWATAAASLIQOFLLSLTPRLEAVEMEDDDFTASLSKQ 960  
DB 901 GAGHRSAYVPSADIHLHIGMWATAAASLIQOFLLSLTPRLEAVEMEDDDFTASLSKQ 960  
QY 961 SCITEQTYFFDNDKSKFSGLVDCGNCISRFHVEKLMNTNLIFIMVESGTCPCDTRLLI 1020  
DB 961 SCITEQTYFFDNDKSKFSGLVDCGNCISRFHVEKLMNTNLIFIMVESGTCPCDTRLLI 1020  
QY 1021 QAEQTSDDGPNPCDMVK 1036  
DB 1021 QAEQTSDDGPNPCDMVK 1036  
DB 1014 QAEQTSDDGPNPCDMVK 1029

RESULT 10  
US-08-223-305C-56  
; Sequence 56, Application US/08223305C  
; Patent No. 5851824  
; GENERAL INFORMATION:

APPLICANT: Harpold, Michael  
 APPLICANT: Ellis, Steven  
 APPLICANT: Williams, Mark  
 APPLICANT: Feldman, Daniel  
 APPLICANT: McCue, Ann  
 APPLICANT: Brenner, Robert  
 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
 TITLE OF INVENTION: METHODS  
 NUMBER OF SEQUENCES: 57  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Brown, Martin, Haller & McClain  
 STREET: 1660 Union Street  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92101-2926  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/223,305C  
 FILING DATE: April 4, 1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/868,354  
 FILING DATE: April 10, 1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/745,206  
 FILING DATE: 13-AUG-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/620,250  
 FILING DATE: 30-NOV-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/482,384  
 FILING DATE: 20-FEB-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/603,751  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/US89/01408  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/176,899  
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 ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie L.  
 REGISTRATION NUMBER: 33,779  
 REFERENCE/DOCKET NUMBER: 52516 (P519739)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619)238-0999  
 TELEFAX: (619)238-0062  
 INFORMATION FOR SEQ ID NO: 56:  
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 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: Internal  
 US-08-223-305C-56

Query Match 97.8%; Score 5323.5; DB 2; Length 1084;  
 Best Local Similarity 98.0%; Pred. No. 0;  
 Matches 1015; Conservative 6; Mismatches 8; Indels 7; Gaps 1;

QY 1 MAAGCLLALTLTFQSLIGPSSPEPPSAVTIKSWDKMQEDLVTLAKTAGVNLVDI 60  
 DB 1 MAAGCLLALTLTFQSLIGPSSPEPPSAVTIKSWDKMQEDLVTLAKTAGVNLVDI 60  
 QY 61 YEKQDLYTVEPNARQLVLAARDIEKLLSNRSKALVRLALEAEKVQAAHQWREDFASN 120  
 DB 61 YEKQDLYTVEPNARQLVLAARDIEKLLSNRSKALVRLALEAEKVQAAHQWREDFASN 120

QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIDDAFNGRQISYQHAHVHPTDIEGSTITV 180  
 DB 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISYQHAHVHPTDIEGSTITV 180  
 QY 181 NELNWTSLALDEVFKKNEEDPSLLWQVFGSATGLARYYPASPVWVNSRTPNKIDLYDVR 240  
 DB 181 NELNWTSLALDEVFKKNEEDPSLLWQVFGSATGLARYYPASPVWVNSRTPNKIDLYDVR 240  
 QY 241 RPWYIOGAASPKDMLILVDVSGSVGLTLKLRITSVSEMLETLSDDDFVNVASFNSNAQ 300  
 DB 241 RPWYIOGAASPKDMLILVDVSGSVGLTLKLRITSVSEMLETLSDDDFVNVASFNSNAQ 300  
 QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLLNYSRANCNKIIML 360  
 DB 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLLNYSRANCNKIIML 360  
 QY 361 FTDGGEERAQEIFAKYNNKDKKVRVFTSVGQHNVDGRPIQWACENKGYIYEIPSIGAIR 420  
 DB 361 FTDGGEERAQEIFNKYNNKDKKVRVFTSVGQHNVDGRPIQWACENKGYIYEIPSIGAIR 420  
 QY 421 INTOEYLDVLGRPMVLADGKAKOVQWNTNVLDALELGLVITGTLPVFNITGQENKTNLK 480  
 DB 421 INTOEYLDVLGRPMVLADGKAKOVQWNTNVLDALELGLVITGTLPVFNITGQENKTNLK 480  
 QY 481 NOLILGVMGVDVSLIEDIKRLTPRETLCPNGYFAIDPNGYVLLHPNLOPKNPKSQEPVTL 540  
 DB 481 NOLILGVMGVDVSLIEDIKRLTPRETLCPNGYFAIDPNGYVLLHPNLOPKNPKSQEPVTL 540  
 QY 541 DFLDAELENDIKVEIRNMKIDGESGKTFRLVKSQDERYIDKGNRTYTTPVNGTDYSL 600  
 DB 541 DFLDAELENDIKVEIRNMKIDGESGKTFRLVKSQDERYIDKGNRTYTTPVNGTDYSL 600  
 QY 601 ALVLPYTFYIYKAKIETITQARSKGKMDSETLPDNEEESGYTFIAPRDYCNLDKI 660  
 DB 601 ALVLPYTFYIYKAKLEETITQARY-----SETLPDNEEESGYTFIAPRDYCNLDKI 660  
 QY 661 SDNTEFLLNFEFIDRKTNNPCNTDLINRVLLDAGFTNELVQNYWSKOKNIKGVYKAR 720  
 DB 661 SDNTEFLLNFEFIDRKTNNPCNTDLINRVLLDAGFTNELVQNYWSKOKNIKGVYKAR 720  
 QY 721 FVWTDGGITRVYPKEAGENWQENPETEDSYKRSKLDNDNVFTAPYFNKSGPGAYESGI 780  
 DB 721 FVWTDGGITRVYPKEAGENWQENPETEDSYKRSKLDNDNVFTAPYFNKSGPGAYESGI 780  
 QY 773 FVWTDGGITRVYPKEAGENWQENPETEDSYKRSKLDNDNVFTAPYFNKSGPGAYESGI 773  
 DB 773 FVWTDGGITRVYPKEAGENWQENPETEDSYKRSKLDNDNVFTAPYFNKSGPGAYESGI 773  
 QY 841 LDGGLFLMANHDDYTNOIGRFFGEIDPSLMRHLVNTISVYAFNKSVDYQSVCEPGAAPKQ 900  
 DB 841 LDGGLFLMANHDDYTNOIGRFFGEIDPSLMRHLVNTISVYAFNKSVDYQSVCEPGAAPKQ 900  
 QY 901 GAGHSAYVPSIADILHIGWATAAASILQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
 DB 901 GAGHSAYVPSIADILHIGWATAAASILQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
 QY 953 GAGHSAYVPSIADILHIGWATAAASILQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ 953  
 DB 953 GAGHSAYVPSIADILHIGWATAAASILQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ 953  
 QY 1021 QAEQTSDDGPDPCDMVK 1036  
 DB 1021 QAEQTSDDGPDPCDMVK 1036  
 QY 1014 QAEQTSDDGPDPCDMVK 1029  
 DB 1014 QAEQTSDDGPDPCDMVK 1029

RESULT 11  
 US-08-455-543A-53  
 ; Sequence 53, Application US/08455543A  
 ; Patent No. 5792846  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Harpold, Michael  
 ; APPLICANT: Ellis, Steven

APPLICANT: Williams, Mark  
 APPLICANT: Feldman, Daniel  
 APPLICANT: McCue, Ann  
 APPLICANT: Brenner, Robert  
 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
 TITLE OF INVENTION: METHODS  
 NUMBER OF SEQUENCES: 57  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Brown, Martin, Haller & McClain  
 STREET: 1660 Union Street  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92101-2926  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: Fast-SEQ version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/455,543A  
 FILING DATE: May 31, 1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/223,305  
 FILING DATE: April 4, 1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/868,354  
 FILING DATE: April 10, 1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/745,206  
 FILING DATE: 15-AUG-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/620,250  
 FILING DATE: 30-NOV-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/482,384  
 FILING DATE: 20-FEB-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/603,751  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/US89/01408  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/176,899  
 FILING DATE: 04-APR-1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie L.  
 REGISTRATION NUMBER: 33,779  
 REFERENCE/DOCKET NUMBER: 6362-52517  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619)238-0999  
 TELEFAX: (619)238-0062  
 INFORMATION FOR SEQ ID NO: 53:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1103 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-455-543A-53

Query Match 97.4%; Score 5304; DB 1; Length 1103;  
 Best Local Similarity 96.2%; Pred. No. 0;  
 Matches 1015; Conservative 6; Mismatches 8; Indels 26; Gaps 2;

Qy 1 MAAGCLLALTLTFLQSLIGSPSPPEPPSAVTIKSWDKMQEDLVTLAKTAGVNLQVLDI 60  
 Db 1 MAAGCLLALTLTFLQSLIGSPSPPEPPSAVTIKSWDKMQEDLVTLAKTAGVNLQVLDI 60  
 Qy 61 YEKYQDLYTVEPNNAQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDFASN 120

Db 61 YEKYQDLYTVEPNNAQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDFASN 120  
 Qy 121 EVVYVNAKDDLDPEKNDSPEGSQRKPVFIDANFGRQISYQHAHVHIPTDIYEGSTIVL 180  
 Db 121 EVVYVNAKDDLDPEKNDSPEGSQRKPVFIDANFGRQISYQHAHVHIPTDIYEGSTIVL 180  
 Qy 181 NELNWTSAIDVEFKKNREEDPSLLQWVFGSATGLARYYPASPWVDSNRTPKNKIDLYDVR 240  
 Db 181 NELNWTSAIDVEFKKNREEDPSLLQWVFGSATGLARYYPASPWVDSNRTPKNKIDLYDVR 240  
 Qy 241 RPWYIQGAASPKDMLILVDVSGSVSGLTKLIRTSVSEMLETLDSDDFVNVASFNSNAQD 300  
 Db 241 RPWYIQGAASPKDMLILVDVSGSVSGLTKLIRTSVSEMLETLDSDDFVNVASFNSNAQD 300  
 Qy 301 VSCFQHLVQANVRNKKVLDKAVNNITAGITDYKKGSEFAFEQLLNLYNVRANCKIIML 360  
 Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAGITDYKKGSEFAFEQLLNLYNVRANCKIIML 360  
 Qy 361 FTDGGEERAQEIFAKYNNKKVRYFTFSVGOHNYDRGPIONMACENKGYIYEIPSIGAIR 420  
 Db 361 FTDGGEERAQEIFAKYNNKKVRYFTFSVGOHNYDRGPIONMACENKGYIYEIPSIGAIR 420  
 Qy 421 INTQEYLDVLRPMVLGADKAKOVQNTVYLDALGLVITGTLPVFNITQONENKTNLK 480  
 Db 421 INTQEYLDVLRPMVLGADKAKOVQNTVYLDALGLVITGTLPVFNITQONENKTNLK 480  
 Qy 481 NQLILGVMGVDVSLIEDIKRLTPRTLCPNGYIFAIDPNGVYVLLHPNLQPK----- 530  
 Db 481 NQLILGVMGVDVSLIEDIKRLTPRTLCPNGYIFAIDPNGVYVLLHPNLQPK----- 530  
 Qy 531 -----NPKSQEPVTLDFDLAELENDLKVEIRNMKIDGESGEKFTLVLSQDERYI 581  
 Db 531 -----NPKSQEPVTLDFDLAELENDLKVEIRNMKIDGESGEKFTLVLSQDERYI 581  
 Qy 582 DGNRTYTWTPVNGTDYSLALVLPYTFYIYKAKIEFTITQAKSKGKMKDSSETLKPDNF 641  
 Db 582 DGNRTYTWTPVNGTDYSLALVLPYTFYIYKAKIEFTITQAKSKGKMKDSSETLKPDNF 641  
 Qy 641 DGNRTYTWTPVNGTDYSLALVLPYTFYIYKAKIEFTITQAKSKGKMKDSSETLKPDNF 653  
 Db 641 DGNRTYTWTPVNGTDYSLALVLPYTFYIYKAKIEFTITQAKSKGKMKDSSETLKPDNF 653  
 Qy 654 EESGYTFIAPRDYCNLDKISDNNTFLLNFNEFTDRKTPNNPSCNTDILNRLVLDAGFTN 701  
 Db 654 EESGYTFIAPRDYCNLDKISDNNTFLLNFNEFTDRKTPNNPSCNTDILNRLVLDAGFTN 713  
 Qy 702 ELVONYWSKOKNIKGKAREVVTDDGTRVYPKEAGENMOENPETVEDSFYKRSNDNDY 761  
 Db 702 ELVONYWSKOKNIKGKAREVVTDDGTRVYPKEAGENMOENPETVEDSFYKRSNDNDY 761  
 Qy 714 ELVONYWSKOKNIKGKAREVVTDDGTRVYPKEAGENMOENPETVEDSFYKRSNDNDY 773  
 Db 714 ELVONYWSKOKNIKGKAREVVTDDGTRVYPKEAGENMOENPETVEDSFYKRSNDNDY 773  
 Qy 762 VFTAPYFNKSGPAYESGIMVSKAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRD 821  
 Db 762 VFTAPYFNKSGPAYESGIMVSKAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRD 821  
 Qy 774 VFTAPYFNKSGPAYESGIMVSKAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRD 833  
 Db 774 VFTAPYFNKSGPAYESGIMVSKAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRD 833  
 Qy 822 CAGPVCDCRNSDVMDCVILDDGGFLIMANHDDYTNOIGRFFGEIDPSLMRHLVNLISVA 881  
 Db 822 CAGPVCDCRNSDVMDCVILDDGGFLIMANHDDYTNOIGRFFGEIDPSLMRHLVNLISVA 881  
 Qy 834 CAGPVCDCRNSDVMDCVILDDGGFLIMANHDDYTNOIGRFFGEIDPSLMRHLVNLISVA 893  
 Db 834 CAGPVCDCRNSDVMDCVILDDGGFLIMANHDDYTNOIGRFFGEIDPSLMRHLVNLISVA 893  
 Qy 882 FNKSYDYQSVCEPGAAPKOGAGHRSAYVPSIADILHIGMWATAAAMSILQQFLSLTFFR 941  
 Db 882 FNKSYDYQSVCEPGAAPKOGAGHRSAYVPSIADILHIGMWATAAAMSILQQFLSLTFFR 941  
 Qy 894 FNKSYDYQSVCEPGAAPKOGAGHRSAYVPSIADILHIGMWATAAAMSILQQFLSLTFFR 953  
 Db 894 FNKSYDYQSVCEPGAAPKOGAGHRSAYVPSIADILHIGMWATAAAMSILQQFLSLTFFR 953  
 Qy 942 LLEAVEMEDDDFTASLSKOSCIETEQTQYFFDNDKSKFSFSGVLDGCGNCSRIHFHEKLMNTNL 1001  
 Db 942 LLEAVEMEDDDFTASLSKOSCIETEQTQYFFDNDKSKFSFSGVLDGCGNCSRIHFHEKLMNTNL 1013  
 Qy 1002 IFIMVESKGTCPCDTRLLIQAEQTSDDGPPCDMVK 1036  
 Db 1002 IFIMVESKGTCPCDTRLLIQAEQTSDDGPPCDMVK 1036  
 Qy 1014 IFIMVESKGTCPCDTRLLIQAEQTSDDGPPCDMVK 1048  
 Db 1014 IFIMVESKGTCPCDTRLLIQAEQTSDDGPPCDMVK 1048

RESULT 12  
 US-08-223-305C-53  
 ; Sequence 53, Application US/08223305C  
 ; Patent No. 5851824  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Harpold, Michael

APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
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NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Hallier & McClain  
STREET: 1660 Union Street  
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COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/223,305C  
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REFERENCE/DOCKET NUMBER: 52516 (P519739)  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
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SEQUENCE CHARACTERISTICS:  
LENGTH: 1103 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-223-305C-53

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QY 1 MAACGLALTLTILFOSLLIGPSSQPPSAVTIKSWDKMOEDLVTLAKTASGVNQLVDI 60  
DB 1 MAACGLALTLTILFOSLLIGPSSQPPSAVTIKSWDKMOEDLVTLAKTASGVNQLVDI 60  
QY 61 YEKQDLYTVEPNNAQRLVETAAKDIEKLLSNRSKALVRLALEAEKVQAAHQWREDFASN 120  
DB 61 YEKQDLYTVEPNNAQRLVETAAKDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120

QY 121 EVVYVYNAKDDLDPEKNDSEPGSQRIKPVFTDDANFORQISYQAAVHIPTDIYEGSTIVL 180  
DB 121 EVVYVYNAKDDLDPEKNDSEPGSQRIKPVFTEDANFORQISYQAAVHIPTDIYEGSTIVL 180  
QY 181 NELNWTSALEDEVFKKNEEDPSLLQVFGSATGLARYYPASPMVDNSRTPNKIDLDYDVR 240  
DB 181 NELNWTSALEDEVFKKNEEDPSLLQVFGSATGLARYYPASPMVDNSRTPNKIDLDYDVR 240  
QY 241 RPYWIOGAASPKDMLILVDYSGVSGILTKLIRTSVSEMLETILSDDDFVNVSFNSNAQ 300  
DB 241 RPYWIOGAASPKDMLILVDYSGVSGILTKLIRTSVSEMLETILSDDDFVNVSFNSNAQ 300  
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSFAFEOILLNYSRANCNKIIML 360  
DB 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSFAFEOILLNYSRANCNKIIML 360  
QY 361 FTGGEERAQEIFAKYKNDKKVRVFTSVGOHNYDROPIOWMACENKGGYIYEPSIGAIR 420  
DB 361 FTGGEERAQEIFAKYKNDKKVRVFTSVGOHNYDROPIOWMACENKGGYIYEPSIGAIR 420  
QY 421 INTOEYLDVLRPMVLADGKAKOVQWNTNVYLDALALEGLVITGTLVPVNI'GQENKTNLK 480  
DB 421 INTOEYLDVLRPMVLADGKAKOVQWNTNVYLDALALEGLVITGTLVPVNI'GQENKTNLK 480  
QY 481 NQILGYMGVDVLSLEIKRLTPRETLCNPGYFAIDPNGYVLLHPNLOPK----- 530  
DB 481 NQILGYMGVDVLSLEIKRLTPRETLCNPGYFAIDPNGYVLLHPNLOPK----- 530  
QY 531 -----NPKSQEPVTLDFDAELENDIKVEIRNKMIDGESGEKTFRTLVKSODRYI 581  
DB 531 -----NPKSQEPVTLDFDAELENDIKVEIRNKMIDGESGEKTFRTLVKSODRYI 581  
QY 581 LKRRPNQNPCKSOEPTVTLDFDAELENDIKVEIRNKMIDGESGEKTFRTLVKSODRYI 600  
DB 581 LKRRPNQNPCKSOEPTVTLDFDAELENDIKVEIRNKMIDGESGEKTFRTLVKSODRYI 600  
QY 601 DKGRTYVTPVNGTDYSLALVLPYFYIKAKIETITQARSKKGMKMDSETLKPDNF 641  
DB 601 DKGRTYVTPVNGTDYSLALVLPYFYIKAKIETITQARSKKGMKMDSETLKPDNF 641  
QY 642 EESGYTFIAPRDYCNLDKISDNTEFLLNFEFTDRTPNPNPCNTDLINRVLLDAGFTN 701  
DB 642 EESGYTFIAPRDYCNLDKISDNTEFLLNFEFTDRTPNPNPCNTDLINRVLLDAGFTN 701  
QY 654 EESGYTFIAPRDYCNLDKISDNTEFLLNFEFTDRTPNPNPCNTDLINRVLLDAGFTN 713  
DB 654 EESGYTFIAPRDYCNLDKISDNTEFLLNFEFTDRTPNPNPCNTDLINRVLLDAGFTN 713  
QY 702 ELVQYNSKQKNIKGVKARFVVTGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDY 761  
DB 702 ELVQYNSKQKNIKGVKARFVVTGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDY 761  
QY 714 ELVQYNSKQKNIKGVKARFVVTGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDY 773  
DB 714 ELVQYNSKQKNIKGVKARFVVTGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDY 773  
QY 762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDP 821  
DB 762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDP 821  
QY 774 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDP 833  
DB 774 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDP 833  
QY 822 CAGPVCDCKRNSDVNDCVILDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNSIYVA 881  
DB 822 CAGPVCDCKRNSDVNDCVILDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNSIYVA 881  
QY 834 CAGPVCDCKRNSDVNDCVILDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNSIYVA 893  
DB 834 CAGPVCDCKRNSDVNDCVILDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNSIYVA 893  
QY 882 FNKSYDYQSVCEPGAAPKQAGAGHSAYVPSIADILHIGWATAAAWSILOQFLSLTFPR 941  
DB 882 FNKSYDYQSVCEPGAAPKQAGAGHSAYVPSIADILHIGWATAAAWSILOQFLSLTFPR 941  
QY 894 FNKSYDYQSVCEPGAAPKQAGAGHSAYVPSIADILHIGWATAAAWSILOQFLSLTFPR 953  
DB 894 FNKSYDYQSVCEPGAAPKQAGAGHSAYVPSIADILHIGWATAAAWSILOQFLSLTFPR 953  
QY 942 LLEAVEMEDDDFTASLSKQSCITEQTYFFDNDSKFSFSGVLDGCGNSRIFHVEKIMNTNL 1001  
DB 942 LLEAVEMEDDDFTASLSKQSCITEQTYFFDNDSKFSFSGVLDGCGNSRIFHVEKIMNTNL 1001  
QY 954 LLEAVEMEDDDFTASLSKQSCITEQTYFFDNDSKFSFSGVLDGCGNSRIFHVEKIMNTNL 1013  
DB 954 LLEAVEMEDDDFTASLSKQSCITEQTYFFDNDSKFSFSGVLDGCGNSRIFHVEKIMNTNL 1013  
QY 1002 IFIMVESKGTCTPCDTRLLIQAEQTSDDGPPDCDMVK 1036  
DB 1014 IFIMVESKGTCTPCDTRLLIQAEQTSDDGPPDCDMVK 1048

RESULT 13  
US-08-543A-55  
; Sequence 55, Application US/08455543A  
; Patent No. 5792846  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark

APPLICANT: Feldman, Daniel  
 APPLICANT: McCue, Ann  
 APPLICANT: Brenner, Robert  
 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
 TITLE OF INVENTION: METHODS  
 NUMBER OF SEQUENCES: 57  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Brown, Martin, Haller & McClain  
 STREET: 1660 Union Street  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92101-2926  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/455,543A  
 FILING DATE: May 31, 1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/223,305  
 FILING DATE: April 4, 1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/868,354  
 FILING DATE: April 10, 1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/745,206  
 FILING DATE: 15-AUG-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/620,250  
 FILING DATE: 30-NOV-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/482,384  
 FILING DATE: 20-FEB-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/603,751  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/US89/01408  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/176,899  
 FILING DATE: 04-APR-1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie L.  
 REGISTRATION NUMBER: 33,779  
 REFERENCE/DOCKET NUMBER: 6362-52517  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619)238-0999  
 TELEFAX: (619)238-0062  
 INFORMATION FOR SEQ ID NO: 55:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1079 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-455-543A-55

Query Match 97.0%; Score 5284; DB 1; Length 1079;  
 Best Local Similarity 97.5%; Pred. No. 0;  
 Matches 1010; Conservative 6; Mismatches 8; Indels 12; Gaps 2;

QY 1 MAAGCLLALTTLTFLFOSLLIGSPSPFPFSAVTIKSWVDKMQEDLVTLAKTAGSYNQLVDI 60  
 DB 1 MAAGCLLALTTLTFLFOSLLIGSPSPFPFSAVTIKSWVDKMQEDLVTLAKTAGSYNQLVDI 60  
 QY 61 YEKYODLYTVEPNARQLVEIAARDIEKLLNSRSKALVRLALEAEKVAQAAHQWREDFASN 120  
 DB 61 YEKYODLYTVEPNARQLVEIAARDIEKLLNSRSKALVRLALEAEKVAQAAHQWREDFASN 120

QY 121 EVVYNAKDDLDPEKNDSEPGSQRKPVFIDANFGROISYQHAAYHIPTDIYEGSTIVL 180  
 DB 121 EVVYNAKDDLDPEKNDSEPGSQRKPVFIDANFGROISYQHAAYHIPTDIYEGSTIVL 180  
 QY 181 NELNWTSDALDEVFKKNREEDPSLLWQVFGSATGLARYYPASPWDNSRTPKNKIDLYDVR 240  
 DB 181 NELNWTSDALDEVFKKNREEDPSLLWQVFGSATGLARYYPASPWDNSRTPKNKIDLYDVR 240  
 QY 241 RPWYIQAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETLDSDDFVNVASNSNAQD 300  
 DB 241 RPWYIQAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETLDSDDFVNVASNSNAQD 300  
 QY 301 VSCFQHLVQANVRNKKVLKDAVNNTAKITDYKKGFSFAFEQLLNNVNSRANCKIIML 360  
 DB 301 VSCFQHLVQANVRNKKVLKDAVNNTAKITDYKKGFSFAFEQLLNNVNSRANCKIIML 360  
 QY 361 FTDGGEERAQEIFAKYKNDKVRVFTFSVGOHNYDRGPIONMACENKGYEYIEISGAIR 420  
 DB 361 FTDGGEERAQEIFAKYKNDKVRVFTFSVGOHNYDRGPIONMACENKGYEYIEISGAIR 420  
 QY 421 INTQEYLDVLRPVMVLADGKAKQVQWNTNYLDALGLVITGTLPVFNITQGNENKTNLK 480  
 DB 421 INTQEYLDVLRPVMVLADGKAKQVQWNTNYLDALGLVITGTLPVFNITQGNENKTNLK 480  
 QY 481 NQLILGVMGVDVSLIEDIKRLTPRTLCPNGYFFAIDPNGYVLLHPNLQPKPKSQEPVTL 540  
 DB 481 NQLILGVMGVDVSLIEDIKRLTPRTLCPNGYFFAIDPNGYVLLHPNLQPKPKSQEPVTL 540  
 QY 541 DFLDAELNDIKVEIRNKMIDGESGEKTFRTLVKSQDERYIDKGNRTYTTWTPVNGTDSL 600  
 DB 541 DFLDAELNDIKVEIRNKMIDGESGEKTFRTLVKSQDERYIDKGNRTYTTWTPVNGTDSL 600  
 QY 601 ALVLTYSFYIKAKIETITQARKSKGKMDSETLPADNPEESGYTFIAPRDYCNDLKI 660  
 DB 601 ALVLTYSFYIKAKIETITQARKSKGKMDSETLPADNPEESGYTFIAPRDYCNDLKI 660  
 QY 661 SDNTEFLNENEFIDRKTNNPNSCNTDLINRVLLDAGFTNELVQNTWSKOKNIKGVKAR 720  
 DB 661 SDNTEFLNENEFIDRKTNNPNSCNTDLINRVLLDAGFTNELVQNTWSKOKNIKGVKAR 720  
 QY 721 FVVTGGITRVYKPEAGENWOENPETYEDSFYKRSNDNDNYVFTAPYFNKSGPGAYESGI 780  
 DB 721 FVVTGGITRVYKPEAGENWOENPETYEDSFYKRSNDNDNYVFTAPYFNKSGPGAYESGI 780  
 QY 781 MYSKAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRDPACGVCDCCKRNSDVMDCVI 840  
 DB 781 MYSKAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRDPACGVCDCCKRNSDVMDCVI 840  
 QY 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNSVYAFNKSVDYQSVCEPFGAAPKQ 900  
 DB 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNSVYAFNKSVDYQSVCEPFGAAPKQ 900  
 QY 901 GAGHRSAYVPSIADILHIGWATAAASIIQQFLLSTFPRLLEAVEMEDDDFTASLSKQ 960  
 DB 901 GAGHRSAYVPSIADILHIGWATAAASIIQQFLLSTFPRLLEAVEMEDDDFTASLSKQ 960  
 QY 961 SCITEQTYFFDNDKSKFSGLDCGNCGRIFHVEKLMNTNLIFTWVESKGTCTCDTRLII 1020  
 DB 961 SCITEQTYFFDNDKSKFSGLDCGNCGRIFHVEKLMNTNLIFTWVESKGTCTCDTRLII 1020  
 QY 1021 QAEQTSQDGPDCDMVK 1036  
 DB 1021 QAEQTSQDGPDCDMVK 1036  
 QY 1009 QAEQTSQDGPDCDMVK 1024  
 DB 1009 QAEQTSQDGPDCDMVK 1024  
 RESULT 14  
 US-08-223-305C-55  
 ; Sequence 55, Application US/08223305C  
 ; Patent No. 5851824  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Harpold, Michael  
 ; APPLICANT: Ellis, Steven

APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/223,305C  
FILING DATE: April 4, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 52516 (P519739)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1079 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-223-305C-55

Query Match 97.0%; Score 5284; DB 2; Length 1079;  
Best Local Similarity 97.5%; Pred. No. 0;  
Matches 1010; Conservative 6; Mismatches 8; Indels 12; Gaps 2;

QY 1 MAAGCLLALTLTFLQSLILGPSSEPPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60  
Db 1 MAAGCLLALTLTFLQSLILGPSSEPPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60  
QY 61 YEKYQDLYTVEPNNAQLVEIARDEKLLSNRSKALVRLALEAEKVQAAHQRDFASN 120  
Db 61 YEKYQDLYTVEPNNAQLVEIARDEKLLSNRSKALVRLALEAEKVQAAHQRDFASN 120  
QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFRQISYQHAHVHIPTDIYEGSTIVL 180

Db 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFRQISYQHAHVHIPTDIYEGSTIVL 180  
QY 181 NELNWTLSALDEVFKKNREEDPSLLWQVFGSATGLARYYPASPVWDNSRTPNKIDLDYVRR 240  
Db 181 NELNWTLSALDEVFKKNREEDPSLLWQVFGSATGLARYYPASPVWDNSRTPNKIDLDYVRR 240  
QY 241 RPWYIOGAASPKDMLILVDVSGSVGLTLKIRTSVSEMLETSDDDFVNVASFNSNAQD 300  
Db 241 RPWYIOGAASPKDMLILVDVSGSVGLTLKIRTSVSEMLETSDDDFVNVASFNSNAQD 300  
QY 301 VSCFOHLVQANVRNKKVLDVANNITAKGITYDKKGFSAFECOLLNANVSRANCNKIIML 360  
Db 301 VSCFOHLVQANVRNKKVLDVANNITAKGITYDKKGFSAFECOLLNANVSRANCNKIIML 360  
QY 361 FTDGGEERAQEIFAKYNKDKKRVFTFSVQGHNYDRGPIQWMACENKNGYYEIPSGAIR 420  
Db 361 FTDGGEERAQEIFAKYNKDKKRVFTFSVQGHNYDRGPIQWMACENKNGYYEIPSGAIR 420  
QY 421 INTQEYLDVLGRPMVLAGDKAKQVQWNTNVYLDALGLVITGLPVFNITQGNENKTNLK 480  
Db 421 INTQEYLDVLGRPMVLAGDKAKQVQWNTNVYLDALGLVITGLPVFNITQGNENKTNLK 480  
QY 481 NQLILGVMGVDVSLDIKRLTPRFTLCPNGYFPAIDPNGYVLLHPNLQPNKPSQBPVTL 540  
Db 481 NQLILGVMGVDVSLDIKRLTPRFTLCPNGYFPAIDPNGYVLLHPNLQPNKPSQBPVTL 540  
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Db 541 DFLDAELENDIKVEIRNMIDGESGKFTFTLVKSDQERYIDKGNRTYTWTPVNGTDYSL 600  
QY 596 ALVLTYSFYIYKAKLEETITQARY-----SETLKPDPNFEESGYTFIAPROYCNDLKI 648  
Db 596 ALVLTYSFYIYKAKLEETITQARY-----SETLKPDPNFEESGYTFIAPROYCNDLKI 648  
QY 661 SDNTEFLNFEPIIDRKTNNPSCNTDLINRVLLDAGFTNELVQYWSKOKNIKGVKAR 720  
Db 649 SDNTEFLNFEPIIDRKTNNPSCNTDLINRVLLDAGFTNELVQYWSKOKNIKGVKAR 708  
QY 721 FVVTDDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
Db 709 FVVTDDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 768  
QY 781 MYSKAVEIYIOGKLLKPAVVGIIKIDVNSWIENTFKTSIRDCPAGPCVDCRNSDVMDCVI 840  
Db 769 MYSKAVEIYIOGKLLKPAVVGIIKIDVNSWIENTFKTSIRDCPAGPCVDCRNSDVMDCVI 828  
QY 841 LDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 900  
Db 829 LDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 888  
QY 901 GAGHSAYVPSIADILHIGWATAAASIIQQFLLSLTFPRLLBAVEMEDDDFTASLSKQ 960  
Db 889 GAGHSAYVPSIADILHIGWATAAASIIQQFLLSLTFPRLLBAVEMEDDDFTASLSKQ 948  
QY 961 SCITEQTYQYFFDNDKSKFSGVLDGCGNSRIFHVEKLMNTNLIIFIMVESKGTCPCDTRLLI 1020  
Db 949 SCITEQTYQYFFDNDKSKFSGVLDGCGNSRIFHVEKLMNTNLIIFIMVESKGTCPCDTRLLI 1008  
QY 1021 QAEQTSDDGPDPCDMVK 1036  
Db 1009 QAEQTSDDGPDPCDMVK 1024  
RESULT 15  
US-08-435-675B-5  
; Sequence 5, Application US/08435675B  
; Patent No. 5710250  
; GENERAL INFORMATION:  
; APPLICANT: Ellis, Steven Bradley  
; APPLICANT: Williams, Mark E.  
; APPLICANT: Harpold, Michael  
; APPLICANT: Schwartz, Arnold

APPLICANT: Brenner, Robert  
 TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller & McClain  
 STREET: 1660 Union Street  
 CITY: San Diego  
 STATE: CA

COUNTRY: USA

ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/435,675B

FILING DATE: 05-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/314,083

FILING DATE: 28-SEP-1994

APPLICATION NUMBER: US 07/914,231

FILING DATE: 13-JUL-1992

APPLICATION NUMBER: US 07/603,751

FILING DATE: 08-NOV-1990

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L

REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 6362-53193

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-238-0999

TELEFAX: 619-238-0062

TELEX:

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1106 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

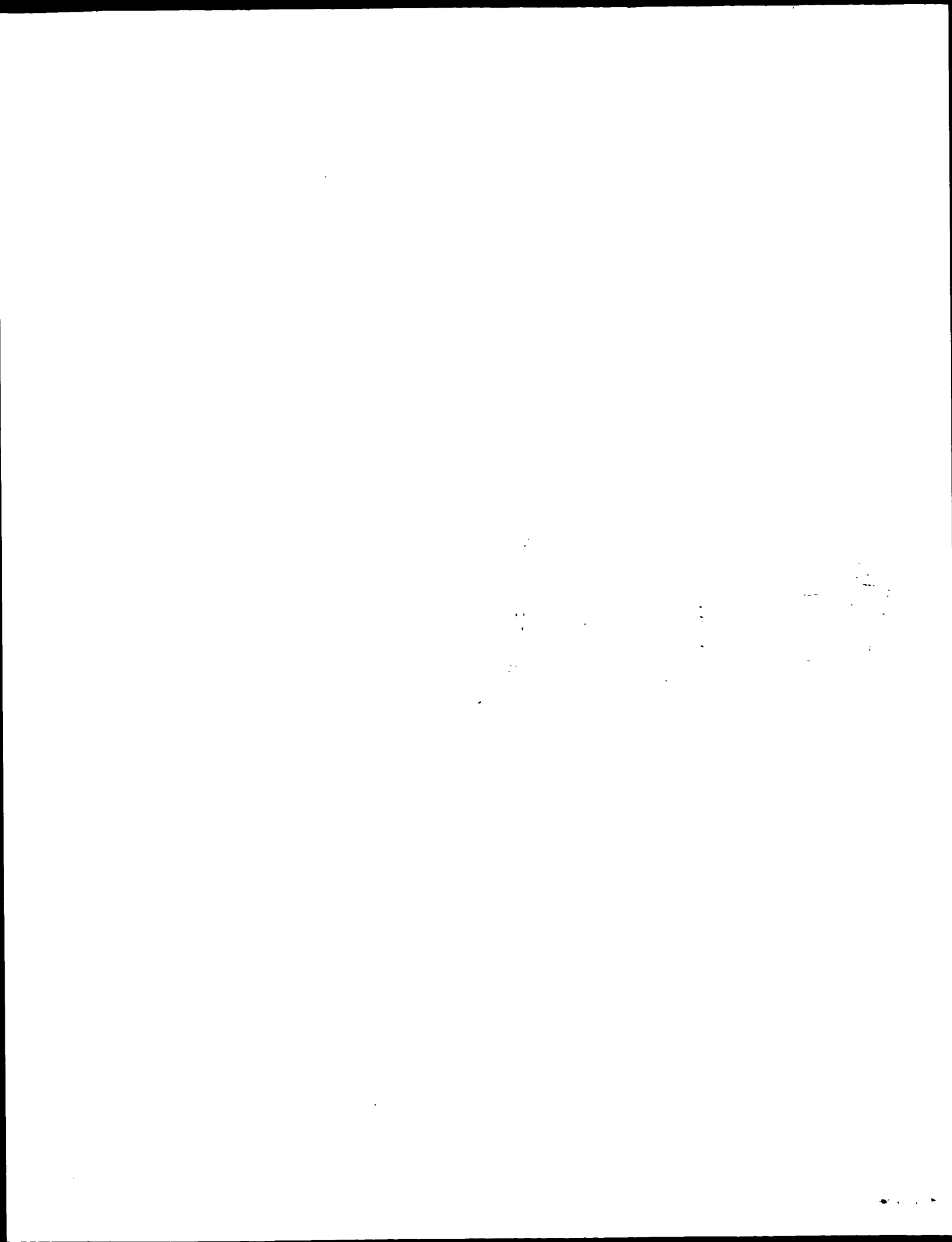
US-08-435-675B-5

Query Match 96.6%; Score 5258.5; DB 1; Length 1106;  
 Best Local Similarity 95.5%; Pred. No. 0;  
 Matches 1010; Conservative 10; Mismatches 9; Indels 29; Gaps 4;

QY 1 MAAGCLLALTTLTFS--LLIGPSOEPPPSAVTIKSWVDKMOEDLYTLAKTASGVNOLV 58  
 DB 1 MAAGRPLAWTLTQAWLILIGPSEEPSPSAVTIKSWVDKMOEDLYTLAKTASGVNOLV 60  
 QY 59 DIYEKQDLYTVEPNARQLVEIARDEKLLSNRSKALVRLALEAEKVQAAHQWREDA 118  
 DB 61 DIYEKQDLYTVEPNARQLVEIARDEKLLSNRSKALVRLALEAEKVQAAHQWREDA 120  
 QY 119 SNEVYYNAKDDLPKNDSEPGSQRIKPVFIDANFRQISYOHAAVHIPTDIYEGSTI 178  
 DB 121 SNEVYYNAKDDLPKNDSEPGSQRIKPVFIDANFRQISYOHAAVHIPTDIYEGSTI 180  
 QY 179 VLNELNWTSLADVEFKKNEEDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKIDLYDV 238  
 DB 181 VLNELNWTSLADVEFKKNEEDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKIDLYDV 240  
 QY 239 RRRPWYIQAASPKDMLILVDVSGVSGLTCLKLRTSVSEMLETSLDDDFNVNVPNSNA 298  
 DB 241 RRRPWYIQAASPKDMLILVDVSGVSGLTCLKLRTSVSEMLETSLDDDFNVNVPNSNA 300  
 QY 299 QDVSCFOHLVQANVRNKKVLDVNNITAGITDYKKGFSAFAPQLLNNVVRANCNKII 358  
 DB 301 QDVSCFOHLVQANVRNKKVLDVNNITAGITDYKKGFSAFAPQLLNNVVRANCNKII 360  
 QY 359 MLFTDGGERAQEIFAKYNDKKVYVFTSVGQHNDRGPIQWACENKGYIYEIPSIGA 418

DB 361 MLFTDGGERAQEIFAKYNDKKVYVFTSVGQHNDRGPIQWACENKGYIYEIPSIGA 420  
 QY 419 IRIINTQEYLDVLGRPMVLAKQKQVQWNTVYLDALGLVITGTLPVFNITQONENKTN 478  
 DB 421 IRIINTQEYLDVLGRPMVLAKQKQVQWNTVYLDALGLVITGTLPVFNITQONENKTN 480  
 QY 479 LKNOLILGVMGVDSLEDIKRLTPTFTLCPNGYFAIDPNGYVLLHNPQLPK-----530  
 DB 481 LKNOLILGVMGVDSLEDIKRLTPTFTLCPNGYFAIDPNGYVLLHNPQLPKPGVGIPT 540  
 QY 531 -----NPKSQEPVTLDFLDAELENDIKVEIRKMKIDGSGEKTFTLVKSODER 579  
 DB 541 INLRKRPRNVQPKSQEPVTLDFLDAELENDIKVEIRKMKIDGSGEKTFTLVKSODER 600  
 QY 580 YIDKGNRTYTWTPVNGTDY-SLALVLPYTSFYIYAKIETITQARSKKKGMKMDSETLKP 638  
 DB 601 YIDKGNRTYTWTPVNGTDYSSALVLPYTSFYIYAKIETITQARY-----SETLKP 653  
 QY 639 DNFEESGYTFIAPRDYCNLDKISDNTEFLNFEFIDRKTNNPNSCNTDLINRVLLDAG 698  
 DB 654 DNFEESGYTFIAPRDYCNLDKISDNTEFLNFEFIDRKTNNPNSCNTDLINRVLLDAG 713  
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 DB 714 FTNELVQYWSKQKNIKGVKARFVVTGGITRVYKPEAGENQWENPETYEDSFYKRSLDN 773  
 QY 759 DNYVFTAPYFNKSGPGAYESGIMYKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSI 818  
 DB 774 DNYVFTAPYFNKSGPGAYESGIMYKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSI 833  
 QY 819 RDCAGPVCDCCKRNSDVMDCVILDDGGFLLMANHDDYTNOIGREFGEIDPSLMRHLVNI 878  
 DB 834 RDCAGPVCDCCKRNSDVMDCVILDDGGFLLMANHDDYTNOIGREFGEIDPSLMRHLVNI 893  
 QY 879 VYAFNKSYDYOSVCEPGAAPKQAGHRSAYVPSIADILHIGWATAAASILQOFLLSLT 938  
 DB 894 VYAFNKSYDYOSVCEPGAAPKQAGHRSAYVPSIADILHIGWATAAASILQOFLLSLT 953  
 QY 939 FPRLLAEVEMEDDDFTASLSKQSCITEQTQYFFDNDKSFSGVLDGNCNCRIFHVEKLMN 998  
 DB 954 FPRLLAEVEMEDDDFTASLSKQSCITEQTQYFFDNDKSFSGVLDGNCNCRIFHVEKLMN 1013  
 QY 999 TNLIFINVESKGTCPCDTRLIIQAEQTSDDGPDPCDMVK 1036  
 DB 1014 TNLIFINVESKGTCPCDTRLIIQAEQTSDDGPDPCDMVK 1051

Search completed: February 10, 2003, 14:23:12  
 Job time : 15.4906 secs





GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 10, 2003, 14:13:50 ; Search time 33.0366 Seconds  
(without alignments)  
4106.031 Million cell updates/sec

Title: US-10-090-827-13

Perfect score: 5346

Sequence: 1 MAAGCLLALTLFQSLIG.....TNLIFIMVSGKTCPCDTRL 1018

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5346	100.0	1018	22 AAU01032	Human secreted sol
2	5346	100.0	1018	22 AAB62256	Porcine calcium ch
3	5346	100.0	1036	22 AAU01033	Human secreted sol
4	5346	100.0	1036	22 AAB62257	Porcine calcium ch
5	5346	100.0	1063	22 AAU01034	Human secreted sol
6	5346	100.0	1063	22 AAB62258	Porcine calcium ch
7	5346	100.0	1091	16 AAR71011	Human neuronal cal
8	5346	100.0	1091	19 AAB63145	Human calcium chan
9	5346	100.0	1091	21 AAB10576	Human calcium chan
10	5346	100.0	1091	22 AAU01035	Human secreted sol

11	5346	100.0	1091	22 AAB62259	Porcine calcium ch
12	5342	99.9	1091	19 AAR37879	Human calcium chan
13	5340	99.9	1091	14 AAR33553	Sequence of the al
14	5326.5	99.6	1110	19 AAB63148	Human calcium chan
15	5306.5	99.3	1086	16 AAR71013	Human neuronal cal
16	5306.5	99.3	1086	19 AAB63153	Human calcium chan
17	5306.5	99.3	1086	21 AAB10587	Human calcium chan
18	5289.5	98.9	1084	16 AAR71015	Human neuronal cal
19	5289.5	98.9	1084	19 AAB63155	Human calcium chan
20	5289.5	98.9	1084	21 AAB10589	Human calcium chan
21	5288	98.9	1018	22 AAU01028	Pig secreted solub
22	5288	98.9	1018	22 AAB62252	Porcine calcium ch
23	5288	98.9	1036	22 AAU01029	Pig secreted solub
24	5288	98.9	1036	22 AAB62253	Porcine calcium ch
25	5288	98.9	1063	22 AAU01030	Pig secreted solub
26	5288	98.9	1063	22 AAB62254	Porcine calcium ch
27	5288	98.9	1069	22 AAU01031	Pig secreted solub
28	5288	98.9	1069	22 AAB62255	Porcine calcium ch
29	5288	98.9	1091	22 AAU01027	Pig secreted solub
30	5288	98.9	1091	22 AAB62251	Porcine calcium ch
31	5270	98.6	1103	16 AAR71012	Human neuronal cal
32	5270	98.6	1103	19 AAB63151	Human calcium chan
33	5270	98.6	1103	21 AAB10586	Human calcium chan
34	5250	98.2	1079	19 AAB63154	Human calcium chan
35	5250	98.2	1079	21 AAB10588	Human calcium chan
36	5244	98.1	1079	16 AAR71014	Human neuronal cal
37	5137.5	96.1	1106	18 AAR37712	Rabbit skeletal ca
38	5137.5	96.1	1106	18 AAB18389	Rabbit calcium cha
39	5137.5	96.1	1106	21 AAR77545	Rabbit skeletal ca
40	5116.5	95.7	1106	16 AAR73056	Rabbit skeletal ca
41	5009.5	93.7	1100	10 AAR95644	Rabbit skeletal mus
42	2872.5	53.7	1062	22 AAU01014	Human secreted sol
43	2872.5	53.7	1062	22 AAB62238	Human calcium chan
44	2872.5	53.7	1082	22 AAU01015	Human secreted sol
45	2872.5	53.7	1082	22 AAB62239	Human calcium chan

#### ALIGNMENTS

##### RESULT 1

AAU01032  
ID AAU01032 standard; Protein; 1018 AA.

AC AAU01032;

DT 04-JUL-2001 (first entry)

XX Human secreted soluble alpha2delta calcium channel subunit #12 protein.

XX Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;

XX alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;

XX gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;

XX filter binding assay; wheat germ lectin flashplate assay.

XX Homo sapiens.

XX WO200119870-A2.

XX 22-MAR-2001.

XX 18-SEP-2000; 2000WO-EF09137.

XX 16-SEP-1999; 99US-0397550.

XX (WARN ) WARNER LAMBERT CO.

XX Brown JP, Bertelli F;

XX WPI: 2001-235262/24.

XX N-PSDB; AAS01423.

XX Calcium channel alpha2delta subunits, useful in e.g. SPA assays,

PT Flashplate assays, Nickel Flashplate assays, Filter binding assays or  
 XX Wheat Germ Lectin Flashplate assays -  
 PS Claim 31; Page 130-133; 160pp; English.

XX The present sequence represents human secreted calcium channel  
 CC alpha2delta subunit #12 which is soluble and retains the functional  
 CC characteristics of the full length or wild type alpha2delta subunit  
 CC (AAU01025) from which it is derived. The invention relates to truncated  
 CC alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins  
 CC which retain their affinity for radioactively labelled gabapentin. The  
 CC alpha2delta subunit is 1 of the components of the heteromultimeric  
 CC voltage-dependent calcium channel (VDCC) complexes present in neuronal  
 CC and non-neuronal tissues including heart and skeletal muscle. Numerous  
 CC soluble forms of the human calcium channel alpha2delta subunits  
 CC (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the  
 CC porcine calcium channel alpha2delta subunits (AAU01027-AAU01031) are  
 CC described. The secreted soluble alpha2delta subunit may be used in assays  
 CC e.g. scintillation proximity assay (SPA), flashplate, nickel flashplate,  
 CC filter binding or wheat germ lectin flashplate assays to detect or  
 CC measure the binding or interaction of a ligand (e.g. gabapentin,  
 CC L-Norleucine, L-Allo-Isoleucine, L-methionine, L-leucine, L-Isoleucine,  
 CC L-Valine, Spermine and/or L-Phenylalanine) of a calcium channel  
 CC alpha2delta subunit.

XX Sequence 1018 AA;

Query Match 100.0%; Score 5346; DB 22; Length 1018;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLFOSLLIGPSSSEPPFSAVTIKSWDKQMEDLVTLAKTAGVYNQLVDI 60  
 DB 1 MAAGCLLALTTLFOSLLIGPSSSEPPFSAVTIKSWDKQMEDLVTLAKTAGVYNQLVDI 60  
 QY 61 YEKYQDLYTVEPNNAQOLVETAAARDIEKLLNSRKALYSALAEKVAQAAHOWREDFASN 120  
 DB 61 YEKYQDLYTVEPNNAQOLVETAAARDIEKLLNSRKALYSALAEKVAQAAHOWREDFASN 120  
 QY 121 EYVYTNAKDDLDPENKDESPQSQRKPVFIEDANFGROISYQHAHAVHIPTDIYEGSTIVL 180  
 DB 121 EYVYTNAKDDLDPENKDESPQSQRKPVFIEDANFGROISYQHAHAVHIPTDIYEGSTIVL 180  
 QY 181 NELNWTSLALDEVFKNREDESLWQVFGSATGLARYYPASPWDNSRTPNKIDLYDVR 240  
 DB 181 NELNWTSLALDEVFKNREDESLWQVFGSATGLARYYPASPWDNSRTPNKIDLYDVR 240  
 QY 241 RPWYIQAASPKDMLILVDVSGVSGSLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
 DB 241 RPWYIQAASPKDMLILVDVSGVSGSLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
 QY 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGITDYKKGFSFAEQLLLNYSRANCNKIIML 360  
 DB 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGITDYKKGFSFAEQLLLNYSRANCNKIIML 360  
 QY 361 FTDGGEERAQAEIFNKNKDKVRFRFSGVGHNYERGPQIOMACENKGYIYEIPSGAIR 420  
 DB 361 FTDGGEERAQAEIFNKNKDKVRFRFSGVGHNYERGPQIOMACENKGYIYEIPSGAIR 420  
 QY 421 INTQEYLDVLGRPMVLADGAKAQVQWTVNYLDALGLVITGTLPVFNIITQGFENKTNLK 480  
 DB 421 INTQEYLDVLGRPMVLADGAKAQVQWTVNYLDALGLVITGTLPVFNIITQGFENKTNLK 480  
 QY 481 NQLILGVMGVDSLEEDIKRLPRFTLCPNGYFFAIDPNGYVLLHPNPKPKSQEPVTL 540  
 DB 481 NQLILGVMGVDSLEEDIKRLPRFTLCPNGYFFAIDPNGYVLLHPNPKPKSQEPVTL 540  
 QY 541 DFLDALENDIKVEIRNKMIDGSEKFRTLVKQSODERYIDKGNRTYTWPNVNGTDSL 600  
 DB 541 DFLDALENDIKVEIRNKMIDGSEKFRTLVKQSODERYIDKGNRTYTWPNVNGTDSL 600  
 QY 601 ALVLPYTFYIIKALEETITQARSKKMKDSETLKPDNFEEESGYTFTIAPRDYCNLDKI 660

DB 601 ALVLPYTFYIIKALEETITQARSKKMKDSETLKPDNFEEESGYTFTIAPRDYCNLDKI 660  
 QY 661 SDNTEFLNFEFIDRKTPNNPSCNADLINRVLLDAGETNELVQVWSKQKNKGVKAR 720  
 DB 661 SDNTEFLNFEFIDRKTPNNPSCNADLINRVLLDAGETNELVQVWSKQKNKGVKAR 720  
 QY 721 FVYTDGGITRVYPKAAGENWQENPEYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
 DB 721 FVYTDGGITRVYPKAAGENWQENPEYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
 QY 781 MVSKAVEIYIQGKLLAPVAVGIIKIDVNSWIENTFKTSIRDPACAGPVCDCKRNSDVMDCVI 840  
 DB 781 MVSKAVEIYIQGKLLAPVAVGIIKIDVNSWIENTFKTSIRDPACAGPVCDCKRNSDVMDCVI 840  
 QY 841 LDGGLFLMANHDDYTNQIGRFFEGEIDPSLMRHLVNIISVYAFNKSYDYQSVCEPGAAPKQ 900  
 DB 841 LDGGLFLMANHDDYTNQIGRFFEGEIDPSLMRHLVNIISVYAFNKSYDYQSVCEPGAAPKQ 900  
 QY 901 GAGHSAYVPSVADIIQIGWWTAAAWSILOQFLLSLTFPRLLAEVEMEDDDFTASLSKQ 960  
 DB 901 GAGHSAYVPSVADIIQIGWWTAAAWSILOQFLLSLTFPRLLAEVEMEDDDFTASLSKQ 960  
 QY 961 SCITEQTQYFFDNDKSFSGVLDCGNCGRIFHGEKLMNTNLIIFIMVESKGTGCPDTRL 1018  
 DB 961 SCITEQTQYFFDNDKSFSGVLDCGNCGRIFHGEKLMNTNLIIFIMVESKGTGCPDTRL 1018

RESULT 2  
 AAB62256  
 ID AAB62256 standard; Protein; 1018 AA.

AC AAB62256;

XX 11-JUN-2001 (first entry)

XX Porcine calcium channel alpha2delta subunit.

XX Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;  
 KW nervous system disorder; pain; epilepsy; anxiety; pig.

OS Sus scrofa.

XX WO200120336-A2.

XX 22-MAR-2001.

XX 18-SEP-2000; 2000WO-BF09136.

XX 16-SEP-1999; 99US-0397549.

XX (WARN ) WARNER LAMBERT CO.

XX Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;

XX WPI: 2001-257902/26.

XX N-PSDB; AAF57560.

XX Competitive binding assay for screening ligands which bind a cerebral  
 PT cortical voltage-dependent calcium channel alpha2-delta-1 subunit,  
 PT where the ligands identified are useful for treating disorders of the  
 PT nervous system, including pain -

XX Claim 8; Page 129-132; 158pp; English.

XX The invention relates to a new method for screening ligands which bind a  
 CC cerebral cortical voltage-dependent calcium channel alpha2delta subunit,  
 CC preferably alpha2delta-1 subunit. The method comprises contacting a  
 CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of  
 CC interest and a labelled compound which binds the subunit, followed by  
 CC measuring the level of binding of the labelled compound to alpha2delta-1  
 CC subunit. The method is useful for screening ligands, preferably  
 CC biologically active products that modulate a nervous system function,  
 CC which bind a cerebral cortical voltage-dependent calcium channel

CC alpha2delta-1 subunit. The ligands identified by the method are useful  
for treating disorders of the nervous system, including pain, epilepsy  
CC and anxiety. The present sequence represents a porcine calcium channel  
CX alpha2delta subunit.  
XX  
SQ Sequence 1018 AA;

Query Match 100.0%; Score 5346; DB 22; Length 1018;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLFOSLLIGSPSEPPFSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60  
DB 1 MAAGCLLALTTLFOSLLIGSPSEPPFSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60  
QY 61 YEKYQDLTYVEPNNAQQLVEAARDIEKLLSNRSKALVSLALEAKVQAAHQRWEDFASN 120  
DB 61 YEKYQDLTYVEPNNAQQLVEAARDIEKLLSNRSKALVSLALEAKVQAAHQRWEDFASN 120  
QY 121 EYVYNNAKDDLPKNDSEPGSQRIKPVFIEDANFGROIYSOHAHVHIPTDIYEGSTIVL 180  
DB 121 EYVYNNAKDDLPKNDSEPGSQRIKPVFIEDANFGROIYSOHAHVHIPTDIYEGSTIVL 180  
QY 181 NELNWTLSALDEVFKKNREDDPSLLMQVFGSATGLARYYPASPWVDNSRTPNKKIDLYVRR 240  
DB 181 NELNWTLSALDEVFKKNREDDPSLLMQVFGSATGLARYYPASPWVDNSRTPNKKIDLYVRR 240  
QY 241 RPWYTOGAASPKDMLILVDVSGVSGSLTLKLRITSVSEMLEFTLSDDDFVNVASFNSNAQD 300  
DB 241 RPWYTOGAASPKDMLILVDVSGVSGSLTLKLRITSVSEMLEFTLSDDDFVNVASFNSNAQD 300  
QY 301 VSCFQHLVQVNRNKKVLKDAVNNITAKGIDYKKGFSFAFEQLLNLYNVRANCKIIML 360  
DB 301 VSCFQHLVQVNRNKKVLKDAVNNITAKGIDYKKGFSFAFEQLLNLYNVRANCKIIML 360  
QY 361 FTDGGEERAQEIFNKNYKDKKVRVRFVSGQHNRYERGPIQWMACENKGYEYIPISIGAIR 420  
DB 361 FTDGGEERAQEIFNKNYKDKKVRVRFVSGQHNRYERGPIQWMACENKGYEYIPISIGAIR 420  
QY 421 INTQEYLDVLGRPMVLGADKAKQVQWTVNYLDALGLVITGTLVPFNITGOFENKTNLK 480  
DB 421 INTQEYLDVLGRPMVLGADKAKQVQWTVNYLDALGLVITGTLVPFNITGOFENKTNLK 480  
QY 481 NQILGVMGVDSLEDIKRLTRPTLCPNGYVFAIDPNGYVLLHPNLQPKNPQSEPTVL 540  
DB 481 NQILGVMGVDSLEDIKRLTRPTLCPNGYVFAIDPNGYVLLHPNLQPKNPQSEPTVL 540  
QY 541 DELDAELENDIKVEIRNKMIDGESGEKFTRLVKSDERYIDKGNRTYTWTVPNGTDYSL 600  
DB 541 DELDAELENDIKVEIRNKMIDGESGEKFTRLVKSDERYIDKGNRTYTWTVPNGTDYSL 600  
QY 601 ALVLPYSPYIYKAKLEETITQARKSKGKMDSETLKPDPNPESEGYTFIAPRDYCNLDKI 660  
DB 601 ALVLPYSPYIYKAKLEETITQARKSKGKMDSETLKPDPNPESEGYTFIAPRDYCNLDKI 660  
QY 661 SDNTEFLNNEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQYNSKQNIKGVKAR 720  
DB 661 SDNTEFLNNEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQYNSKQNIKGVKAR 720  
QY 721 FVYTDGGITRVYPKEAGENQENPETYEDSFYKRLSDNDNYYFTAPYFNKSGPGAYESGI 780  
DB 721 FVYTDGGITRVYPKEAGENQENPETYEDSFYKRLSDNDNYYFTAPYFNKSGPGAYESGI 780  
QY 781 MYSKAVEIYIQGLKPAVVGIKIDVNSWIEFTKTSIRDPGAGPVCDCRNSDVMDCVI 840  
DB 781 MYSKAVEIYIQGLKPAVVGIKIDVNSWIEFTKTSIRDPGAGPVCDCRNSDVMDCVI 840  
QY 841 LDGDFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNIYSYAFNKSVDYQSVCEPAAAPKQ 900  
DB 841 LDGDFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNIYSYAFNKSVDYQSVCEPAAAPKQ 900  
QY 901 GAGHRSAVPSVADILQIGWATAAAMWSILQQFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960  
DB 901 GAGHRSAVPSVADILQIGWATAAAMWSILQQFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960

Db 901 GAGHRSAVPSVADILQIGWATAAAMWSILQQFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960  
QY 961 SCITEQTYQFFDNDKSKFSGLDGCNCSRIHFHGEKLMNTNLIFITMVESKGTCPCDTRL 1018  
DB 961 SCITEQTYQFFDNDKSKFSGLDGCNCSRIHFHGEKLMNTNLIFITMVESKGTCPCDTRL 1018

RESULT 3  
AAU01033  
ID AAU01033 standard; Protein; 1036 AA.

XX AAU01033;  
AC AAU01033;  
XX 04-JUL-2001 (first entry)  
DT 04-JUL-2001 (first entry)  
XX Human secreted soluble alpha2delta calcium channel subunit #13 protein.  
DE Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;  
XX alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;  
KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;  
KW filter binding assay; wheat germ lectin flashplate assay.  
XX Homo sapiens.  
OS Homo sapiens.  
XX WO200119870-A2.  
PN 22-MAR-2001.  
XX 18-SEP-2000; 2000WO-EP09137.  
PF 16-SEP-1999; 99US-0397550.  
XX (WARN ) WARNER LAMBERT CO.  
PA Brown JP, Bertelli F;  
PI WPI; 2001-235262/24.  
DR N-PSDB; AAS01424.

XX Calcium channel alpha2delta subunits, useful in e.g. SPA assays,  
PT Flashplate assays, Nickel Flashplate assays, Filter binding assays or  
PT Wheat Germ Lectin Flashplate assays -  
XX Claim 31; Page 134-137; 160pp; English.

XX The present sequence represents human secreted calcium channel  
CC alpha2delta subunit #13 which is soluble and retains the functional  
CC characteristics of the full length or wild type alpha2delta subunit  
CC (AAU01025) from which it is derived. The invention relates to truncated  
CC alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins  
CC which retain their affinity for radioactively labelled gabapentin. The  
CC alpha2delta subunit is 1 of the components of the heteromultimeric  
CC voltage-dependent calcium channel (VDCC) complexes present in neuronal  
CC and non-neuronal tissues including heart and skeletal muscle. Numerous  
CC soluble forms of the human calcium channel alpha2delta subunits  
CC (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the  
CC porcine calcium channel alpha2delta subunits (AAU01027-AAU01031) are  
CC described. The secreted soluble alpha2delta subunit may be used in assays  
CC e.g. scintillation proximity assay (SPA), flashplate, nickel flashplate,  
CC filter binding or wheat germ lectin flashplate assays to detect or  
CC measure the binding or interaction of a ligand (e.g. gabapentin,  
CC L-Norleucine, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Isoleucine,  
CC L-Valine, Spermine and/or L-Phenylalanine) of a calcium channel  
CC alpha2delta subunit.

XX Sequence 1036 AA;  
SQ Query Match 100.0%; Score 5346; DB 22; Length 1036;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAAGCLLALTTLFOSLLIGSPSEPPFSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60  
DB 1 MAAGCLLALTTLFOSLLIGSPSEPPFSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60

Db 1 MAAGCLLALTLTLFQSLLLIGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60  
 QY 61 YEKYQDLYTVEPNARQVLEIAARDIEKLLSNRSKALVSLALEAKVQAAHQWRDFASN 120  
 Db 61 YEKYQDLYTVEPNARQVLEIAARDIEKLLSNRSKALVSLALEAKVQAAHQWRDFASN 120  
 QY 121 EVVYNAKDDLPKNDSPGSGRIKPVIEDANFGRIQISYQHAHVHIPTDIYEGSTIVL 180  
 Db 121 EVVYNAKDDLPKNDSPGSGRIKPVIEDANFGRIQISYQHAHVHIPTDIYEGSTIVL 180  
 QY 181 NELNWTLSALDEVFKKKNREEDPSLLMQVFGSATGLARYYPASPDVNSRTPNKIDLYDVR 240  
 Db 181 NELNWTLSALDEVFKKKNREEDPSLLMQVFGSATGLARYYPASPDVNSRTPNKIDLYDVR 240  
 QY 241 RPWYIQGAASPKDMLILVDVSGVSGLTLLKLRISVSEMLETLDSDDFVNVASFNNAQD 300  
 Db 241 RPWYIQGAASPKDMLILVDVSGVSGLTLLKLRISVSEMLETLDSDDFVNVASFNNAQD 300  
 QY 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGIDTYKKGFSFAFQELLNLYNVRANCKNIIML 360  
 Db 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGIDTYKKGFSFAFQELLNLYNVRANCKNIIML 360  
 QY 361 FTDGGERAEQEIFNKYNDKKVRFRFVSQGHNYERGPQIWMACENKGYEYIEPSIGAIR 420  
 Db 361 FTDGGERAEQEIFNKYNDKKVRFRFVSQGHNYERGPQIWMACENKGYEYIEPSIGAIR 420  
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 QY 541 DFLDAELNDIKVEIRNKMIDGSEKTFRLVKQSODERYIDKGNRTYVTFPVNGTDSL 600  
 Db 541 DFLDAELNDIKVEIRNKMIDGSEKTFRLVKQSODERYIDKGNRTYVTFPVNGTDSL 600  
 QY 601 ALVLPYTFYIIKALEETITQARKSKKMKDSETLKPDNFEESGYTFIAPRDYCNLDKI 660  
 Db 601 ALVLPYTFYIIKALEETITQARKSKKMKDSETLKPDNFEESGYTFIAPRDYCNLDKI 660  
 QY 661 SDNTEFLINFEFIDRTKTPNPNCSNADLINRVLLDAGFTNELVQNYWSKOKNKGVKAR 720  
 Db 661 SDNTEFLINFEFIDRTKTPNPNCSNADLINRVLLDAGFTNELVQNYWSKOKNKGVKAR 720  
 QY 721 FVYTDGGITRVYPKEAGENWQENPTYEDSYFKRSLDNDNTVFTAPYFNKSGPGAYESGI 780  
 Db 721 FVYTDGGITRVYPKEAGENWQENPTYEDSYFKRSLDNDNTVFTAPYFNKSGPGAYESGI 780  
 QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIEFTKTSIRDPGAGVDCCKRNSDVMDCVI 840  
 Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIEFTKTSIRDPGAGVDCCKRNSDVMDCVI 840  
 QY 841 LDGCGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNSVYAFNKSVDYQSYCEPGAAPKQ 900  
 Db 841 LDGCGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNSVYAFNKSVDYQSYCEPGAAPKQ 900  
 QY 901 GAGHSATVPSVADILQIGWATAAANSILOQFLLSLTFFPRLLEAVEMEDDDFTASLSKQ 960  
 Db 901 GAGHSATVPSVADILQIGWATAAANSILOQFLLSLTFFPRLLEAVEMEDDDFTASLSKQ 960  
 QY 961 SCITBOTQYFFDNDKSPSGVLDGNCGRIPFGKLMNTNLIIFTWBSKGTCPDTRL 1018  
 Db 961 SCITBOTQYFFDNDKSPSGVLDGNCGRIPFGKLMNTNLIIFTWBSKGTCPDTRL 1018

RESULT 4

AAB62257

ID AAB62257 standard; Protein; 1036 AA.

XX

AC AAB62257;

XX

11-JUN-2001 (first entry)  
 Porcine calcium channel alpha2delta subunit.  
 Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;  
 nervous system disorder; pain; epilepsy; anxiety; pig.  
 Sus scrofa.

W0200120336-A2.

22-MAR-2001.

18-SEP-2000; 2000WO-EP09136.

16-SEP-1999; 99US-0397549.

(WARN ) WARNER LAMBERT CO.

Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;

WPI; 2001-257902/26.

N-PSDB; AAF57561.

Competitive binding assay for screening ligands which bind a cerebral  
 cortical voltage-dependent calcium channel alpha2-delta-1 subunit,  
 where the ligands identified are useful for treating disorders of the  
 nervous system, including pain -

Claim 8; Page 132-135; 158pp; English.

The invention relates to a new method for screening ligands which bind a  
 cerebral cortical voltage-dependent calcium channel alpha2delta subunit,  
 preferably alpha2delta-1 subunit. The method comprises contacting a  
 secreted soluble recombinant alpha2delta-1 subunit with a ligand of  
 interest and a labelled compound which binds the subunit, followed by  
 measuring the level of binding of the labelled compound to alpha2delta-1  
 subunit. The method is useful for screening ligands, preferably  
 biologically active products that modulate a nervous system function,  
 which bind a cerebral cortical voltage-dependent calcium channel  
 alpha2delta-1 subunit. The ligands identified by the method are useful  
 for treating disorders of the nervous system, including pain, epilepsy  
 and anxiety. The present sequence represents a porcine calcium channel  
 alpha2delta subunit.

Sequence 1036 AA;

Query Match 100.0%; Score 5346; DB 22; Length 1036;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLTLFQSLLLIGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60

Db 1 MAAGCLLALTLTLFQSLLLIGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60

QY 61 YEKYQDLYTVEPNARQVLEIAARDIEKLLSNRSKALVSLALEAKVQAAHQWRDFASN 120

Db 61 YEKYQDLYTVEPNARQVLEIAARDIEKLLSNRSKALVSLALEAKVQAAHQWRDFASN 120

QY 121 EVVYNAKDDLPKNDSPGSGRIKPVIEDANFGRIQISYQHAHVHIPTDIYEGSTIVL 180

Db 121 EVVYNAKDDLPKNDSPGSGRIKPVIEDANFGRIQISYQHAHVHIPTDIYEGSTIVL 180

QY 181 NELNWTLSALDEVFKKKNREEDPSLLMQVFGSATGLARYYPASPDVNSRTPNKIDLYDVR 240

Db 181 NELNWTLSALDEVFKKKNREEDPSLLMQVFGSATGLARYYPASPDVNSRTPNKIDLYDVR 240

QY 241 RPWYIQGAASPKDMLILVDVSGVSGLTLLKLRISVSEMLETLDSDDFVNVASFNNAQD 300

Db 241 RPWYIQGAASPKDMLILVDVSGVSGLTLLKLRISVSEMLETLDSDDFVNVASFNNAQD 300

QY 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGIDTYKKGFSFAFQELLNLYNVRANCKNIIML 360

Db 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGIDTYKKGFSFAFQELLNLYNVRANCKNIIML 360

Db 301 VSCFOHLYQANVRNKKVLLKDAVNNTAKGTDYKKGFSFAFEQOLLNINVSFRANCKIIML 360  
 QY 361 FTDGGEERAQAEIFNKYNKDKKVRFRFVSQGHNYERGPQIOWMACENKGGYIYEPSICAIR 420  
 Db 361 FTDGGEERAQAEIFNKYNKDKKVRFRFVSQGHNYERGPQIOWMACENKGGYIYEPSICAIR 420  
 QY 421 INTQEYLDVLRPMVLAGDKAKQVQWTVNYLDALGLVITGTLVPVFNITGQFENKTNLK 480  
 Db 421 INTQEYLDVLRPMVLAGDKAKQVQWTVNYLDALGLVITGTLVPVFNITGQFENKTNLK 480  
 QY 481 NOLILGVMGVDVSLDIKRLTPRETLCPCNGYIYFAIDPQGVLLHLPNLPKNPKSQBPVTL 540  
 Db 481 NOLILGVMGVDVSLDIKRLTPRETLCPCNGYIYFAIDPQGVLLHLPNLPKNPKSQBPVTL 540  
 QY 541 DFLDAELNDIKVIRKMKIDGSGEKTFTLVKSODERYDKGNRTYTWTPVNGTDYSL 600  
 Db 541 DFLDAELNDIKVIRKMKIDGSGEKTFTLVKSODERYDKGNRTYTWTPVNGTDYSL 600  
 QY 601 ALVLPYTSFYIYAKLEETITQARSKKGMKDSKSETLKPONFESGYTFIAPRDYCNLDKI 660  
 Db 601 ALVLPYTSFYIYAKLEETITQARSKKGMKDSKSETLKPONFESGYTFIAPRDYCNLDKI 660  
 QY 661 SDNTEFLNPNFIDRKTPNPNPCNADLINRVLLDAGFTNELVQWYSKOKNIKGVKAR 720  
 Db 661 SDNTEFLNPNFIDRKTPNPNPCNADLINRVLLDAGFTNELVQWYSKOKNIKGVKAR 720  
 QY 721 FVVTDDGTRVYKPEAGENKQENPEYEDSFYKRSKLDNDNYFTAPYFNKSGPGAYESGI 780  
 Db 721 FVVTDDGTRVYKPEAGENKQENPEYEDSFYKRSKLDNDNYFTAPYFNKSGPGAYESGI 780  
 QY 781 MVSXAVEIYIQGKLLPAVVGKIDVNSWIENTFTKTSIRDPKAGVPCDCKRNSDVMDCVI 840  
 Db 781 MVSXAVEIYIQGKLLPAVVGKIDVNSWIENTFTKTSIRDPKAGVPCDCKRNSDVMDCVI 840  
 QY 841 LDGGFLLMANHDDYTNQIGRFGELDPSLMRHLNVSIVYAFNPKSYDYOSVCEPAAAPK 900  
 Db 841 LDGGFLLMANHDDYTNQIGRFGELDPSLMRHLNVSIVYAFNPKSYDYOSVCEPAAAPK 900  
 QY 901 GAGHSAYVPSVADIIQIGWATAAAWSILOQFLLSLTFPRLLEAVEMEDDDFTASLSK 960  
 Db 901 GAGHSAYVPSVADIIQIGWATAAAWSILOQFLLSLTFPRLLEAVEMEDDDFTASLSK 960  
 QY 961 SCITEQOTYFFDNDSKFSFGLDCGNCRSRIFHGEKLMNTNLIIFIMVESKGTCPDTRL 1018  
 Db 961 SCITEQOTYFFDNDSKFSFGLDCGNCRSRIFHGEKLMNTNLIIFIMVESKGTCPDTRL 1018

RESULT 5  
 AAU01034  
 ID AAU01034 standard; Protein; 1063 AA.  
 AC AAU01034;  
 XX AAU01034;  
 DT 04-JUL-2001 (first entry)  
 XX Human secreted soluble alpha2delta calcium channel subunit #14 protein.  
 DE Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;  
 KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;  
 KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;  
 XX filter binding assay; wheat germ lectin flashplate assay.  
 OS Homo sapiens.  
 XX WO200119870-A2.  
 PN 22-MAR-2001.  
 XX 18-SEP-2000; 2000WO-EP09137.  
 XX 16-SEP-1999; 99US-0397550.  
 XX (WARN ) WARNER LAMBERT CO.

XX Brown JP, Bertelli F;  
 PI WPI; 2001-235262/24.  
 XX N-PSDB; AAS01425.  
 XX Calcium channel alpha2delta subunits, useful in e.g. SPA assays,  
 PT Flashplate assays, Nickel Flashplate assays, Filter binding assays or  
 PT Wheat Germ Lectin Flashplate assays -  
 XX Claim 31; Page 137-140; 160pp; English.  
 XX The present sequence represents human secreted calcium channel  
 CC alpha2delta subunit #14, which is soluble and retains the functional  
 CC characteristics of the full length or wild type alpha2delta subunit  
 CC (AAU01025) from which it is derived. The invention relates to truncated  
 CC alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins  
 CC which retain their affinity for radioactively labelled gabapentin. The  
 CC alpha2delta subunit is 1 of the components of the heteromultimeric  
 CC voltage-dependent calcium channel (VDCC) complexes present in neuronal  
 CC and non-neuronal tissues including heart and skeletal muscle. Numerous  
 CC soluble forms of the human calcium channel alpha2delta subunits  
 CC (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the  
 CC porcine calcium channel alpha2delta subunits (AAU01027-AAU01031) are  
 CC described. The secreted soluble alpha2delta subunit may be used in assays  
 CC e.g. scintillation proximity assay (SPA), flashplate, nickel flashplate,  
 CC filter binding or wheat germ lectin flashplate assays to detect or  
 CC measure the binding or interaction of a ligand (e.g. gabapentin,  
 CC L-Norleucine, L-Allo-isoleucine, L-methionine, L-Leucine, L-Isoleucine,  
 CC L-Valine, Spermine and/or L-phenylalanine) of a calcium channel  
 CC alpha2delta subunit.  
 XX Sequence 1063 AA;

Query Match 100.0%; Score 5346; DB 22; Length 1063;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAAGCLLALTTLTFLQSLILIGSPSEPPFSAVTIKSWDKMOEDLVTLAKTAGSYNQLVDI 60  
 Db 1 MAAGCLLALTTLTFLQSLILIGSPSEPPFSAVTIKSWDKMOEDLVTLAKTAGSYNQLVDI 60  
 QY 61 YEKYQDLYTVENPNARQOLVEIAARDIEKLLSNRSKALVSLAEKVAQAQHWREDFASN 120  
 Db 61 YEKYQDLYTVENPNARQOLVEIAARDIEKLLSNRSKALVSLAEKVAQAQHWREDFASN 120  
 QY 121 EVVYNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROISTQHAHVHIPTDIYEGSTIVL 180  
 Db 121 EVVYNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROISTQHAHVHIPTDIYEGSTIVL 180  
 QY 181 NELNMTSALDEVFKKNREDEPSLLMQVFGSATGLARYYPASPDVNSRTPNKIDLYDVR 240  
 Db 181 NELNMTSALDEVFKKNREDEPSLLMQVFGSATGLARYYPASPDVNSRTPNKIDLYDVR 240  
 QY 241 RPYITOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETLSDDDDFVNVASFNSNAQD 300  
 Db 241 RPYITOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETLSDDDDFVNVASFNSNAQD 300  
 QY 301 VSCFOHLYQANVRNKKVLLKDAVNNTAKGTDYKKGFSFAFEQOLLNINVSFRANCKIIML 360  
 Db 301 VSCFOHLYQANVRNKKVLLKDAVNNTAKGTDYKKGFSFAFEQOLLNINVSFRANCKIIML 360  
 QY 361 FTDGGEERAQAEIFNKYNKDKKVRFRFVSQGHNYERGPQIOWMACENKGGYIYEPSICAIR 420  
 Db 361 FTDGGEERAQAEIFNKYNKDKKVRFRFVSQGHNYERGPQIOWMACENKGGYIYEPSICAIR 420  
 QY 421 INTQEYLDVLRPMVLAGDKAKQVQWTVNYLDALGLVITGTLVPVFNITGQFENKTNLK 480  
 Db 421 INTQEYLDVLRPMVLAGDKAKQVQWTVNYLDALGLVITGTLVPVFNITGQFENKTNLK 480  
 QY 481 NOLILGVMGVDVSLDIKRLTPRETLCPCNGYIYFAIDPQGVLLHLPNLPKNPKSQBPVTL 540  
 Db 481 NOLILGVMGVDVSLDIKRLTPRETLCPCNGYIYFAIDPQGVLLHLPNLPKNPKSQBPVTL 540

541 DFLDAELENKIVEIRNKIMIDGESGKFTFTLVKSODERYIDKGNRTYTWTPVNGTDYSL 600  
 541 DFLDAELENKIVEIRNKIMIDGESGKFTFTLVKSODERYIDKGNRTYTWTPVNGTDYSL 600  
 601 ALVLPYTSFYIIKAKLEETITQARSKKGMKDSKSETLKPONFEESGYTFIAPRDYCNLDKI 660  
 601 ALVLPYTSFYIIKAKLEETITQARSKKGMKDSKSETLKPONFEESGYTFIAPRDYCNLDKI 660  
 661 SDNTEFLNFEIDRKTTPNPNPCNADLINRVLLDAGFTNELVQNSKQNIKGKVKAR 720  
 661 SDNTEFLNFEIDRKTTPNPNPCNADLINRVLLDAGFTNELVQNSKQNIKGKVKAR 720  
 721 FVVTGGITRVYPKEAGENQENPETEYDSFYKRSKLDNDNYFTAPYFNKSGPGAYESGI 780  
 721 FVVTGGITRVYPKEAGENQENPETEYDSFYKRSKLDNDNYFTAPYFNKSGPGAYESGI 780  
 781 MYSKAVEIYIOGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPACGVCDCRNSDVMDCVI 840  
 781 MYSKAVEIYIOGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPACGVCDCRNSDVMDCVI 840  
 841 LDGCGFLMANHDDYTNOIGRFFGEIDPSLMRLHLNLSVYAFNKSXYDSVCEPGAAPKQ 900  
 841 LDGCGFLMANHDDYTNOIGRFFGEIDPSLMRLHLNLSVYAFNKSXYDSVCEPGAAPKQ 900  
 901 GAGHSAYVPSVADILQIGWATAAASIIQQFLLSLTFFPRLLLEAVEMEDDDFTASLSKQ 960  
 901 GAGHSAYVPSVADILQIGWATAAASIIQQFLLSLTFFPRLLLEAVEMEDDDFTASLSKQ 960  
 961 SCITETQYFFDNDSKSPSGVLDGCGNCSRIPIHGEKLMNTNLIIFIMVSKGTCPCDTRL 1018  
 961 SCITETQYFFDNDSKSPSGVLDGCGNCSRIPIHGEKLMNTNLIIFIMVSKGTCPCDTRL 1018

RESULT 6  
 AAB62258  
 ID AAB62258 standard; Protein; 1063 AA.  
 AC AAB62258;  
 DT 11-JUN-2001 (first entry)  
 DE Porcine calcium channel alpha2delta subunit.  
 KW Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;  
 KW nervous system disorder; pain; epilepsy; anxiety; pig.  
 OS Sus scrofa.  
 PN WO200120336-A2.  
 PD 22-MAR-2001.  
 PF 18-SEP-2000; 2000WO-EP09136.  
 PR 16-SEP-1999; 99US-0397549.  
 XX (WARN ) WARNER LAMBERT CO.  
 XX Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;  
 WPI; 2001-257902/26.  
 DR N-PSDB; AAF57562.  
 XX Competitive binding assay for screening ligands which bind a cerebral  
 XX cortical voltage-dependent calcium channel alpha2delta-1 subunit,  
 XX where the ligands identified are useful for treating disorders of the  
 XX nervous system, including pain -  
 XX Claim 8; Page 135-139; 158pp; English.  
 XX The invention relates to a new method for screening ligands which bind a  
 XX cerebral cortical voltage-dependent calcium channel alpha2delta subunit,  
 CC

CC preferably alpha2delta-1 subunit. The method comprises contacting a  
 CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of  
 CC interest and a labelled compound which binds the subunit, followed by  
 CC measuring the level of binding of the labelled compound to alpha2delta-1  
 CC subunit. The method is useful for screening ligands, preferably  
 CC biologically active products that modulate a nervous system function,  
 CC which bind a cerebral cortical voltage-dependent calcium channel  
 CC alpha2delta-1 subunit. The ligands identified by the method are useful  
 CC for treating disorders of the nervous system, including pain, epilepsy  
 CC and anxiety. The present sequence represents a porcine calcium channel  
 CC alpha2delta subunit.  
 XX  
 XX Sequence 1063 AA;  
 SQ  
 Query Match 100.0%; Score 5346; DB 22; Length 1063;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAACGLLALTLTLPQSLLIGPSSSEPPPSAVTIKSWDKMDEDLVTLAKTASGVNQLVDI 60  
 DB 1 MAACGLLALTLTLPQSLLIGPSSSEPPPSAVTIKSWDKMDEDLVTLAKTASGVNQLVDI 60  
 QY 61 YEKYODLYTVEPNARQVLAARDIEKLLSNRSKALVSLAEAEKVQAAHQWREDFASN 120  
 DB 61 YEKYODLYTVEPNARQVLAARDIEKLLSNRSKALVSLAEAEKVQAAHQWREDFASN 120  
 QY 121 EVVYNAKDDLDPKNDSEPGSORIKPVFTEDANFRQISYQHAHVHIPTDIYEGSTIVL 180  
 DB 121 EVVYNAKDDLDPKNDSEPGSORIKPVFTEDANFRQISYQHAHVHIPTDIYEGSTIVL 180  
 QY 181 NELNWTSAIDVFKKNEEDPSLLQVFGSATGLARYYPASPWVDSNRPNKIDLYDVR 240  
 DB 181 NELNWTSAIDVFKKNEEDPSLLQVFGSATGLARYYPASPWVDSNRPNKIDLYDVR 240  
 QY 241 RPWYIQGAASPKDMLILVDVSGSVGLTLKLRITSVSEMLETISDDDFNVNASFNSNAOD 300  
 DB 241 RPWYIQGAASPKDMLILVDVSGSVGLTLKLRITSVSEMLETISDDDFNVNASFNSNAOD 300  
 QY 301 VSCFOHLVQANVRNKKVLDKAVNNITAGITDYKKGFSFAFEOALLNYSRANCNKIIML 360  
 DB 301 VSCFOHLVQANVRNKKVLDKAVNNITAGITDYKKGFSFAFEOALLNYSRANCNKIIML 360  
 QY 361 FTDGGEERAQEIFNKYKDKKRVFRFVSQGHNYERGPIONMACENKGYIYIIPSGAIR 420  
 DB 361 FTDGGEERAQEIFNKYKDKKRVFRFVSQGHNYERGPIONMACENKGYIYIIPSGAIR 420  
 QY 421 INTQYLDVLRGPMVLADGKAKQVQWNTNYLDLELGLVITGTLPVFNITQGFENKINL 480  
 DB 421 INTQYLDVLRGPMVLADGKAKQVQWNTNYLDLELGLVITGTLPVFNITQGFENKINL 480  
 QY 481 NOLILGVMGVDVSLIEDIKRLTPRTLCPNGYIYFAIDPNGYVLLHPNLQPKNSQEPVTL 540  
 DB 481 NOLILGVMGVDVSLIEDIKRLTPRTLCPNGYIYFAIDPNGYVLLHPNLQPKNSQEPVTL 540  
 QY 541 DFLDAELENKIVEIRNKIMIDGESGKFTFTLVKSODERYIDKGNRTYTWTPVNGTDYSL 600  
 DB 541 DFLDAELENKIVEIRNKIMIDGESGKFTFTLVKSODERYIDKGNRTYTWTPVNGTDYSL 600  
 QY 601 ALVLPYTSFYIIKAKLEETITQARSKKGMKDSKSETLKPONFEESGYTFIAPRDYCNLDKI 660  
 DB 601 ALVLPYTSFYIIKAKLEETITQARSKKGMKDSKSETLKPONFEESGYTFIAPRDYCNLDKI 660  
 QY 661 SDNTEFLNFEIDRKTTPNPNPCNADLINRVLLDAGFTNELVQNSKQNIKGKVKAR 720  
 DB 661 SDNTEFLNFEIDRKTTPNPNPCNADLINRVLLDAGFTNELVQNSKQNIKGKVKAR 720  
 QY 721 FVVTGGITRVYPKEAGENQENPETEYDSFYKRSKLDNDNYFTAPYFNKSGPGAYESGI 780  
 DB 721 FVVTGGITRVYPKEAGENQENPETEYDSFYKRSKLDNDNYFTAPYFNKSGPGAYESGI 780  
 QY 781 MYSKAVEIYIOGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPACGVCDCRNSDVMDCVI 840  
 DB 781 MYSKAVEIYIOGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPACGVCDCRNSDVMDCVI 840

QY 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNISVYAFNKSVDYQSVCEPAAAPKQ 900  
 DB 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNISVYAFNKSVDYQSVCEPAAAPKQ 900  
 QY 901 GAGHRSAYVPSVADILQIGWATAAASILQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
 DB 901 GAGHRSAYVPSVADILQIGWATAAASILQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
 QY 961 SCITEQTOYFFDNDKSKFSGLDCGNCRSRIFPHGKLMNTNLIFIMVSKGTCPCDTRL 1018  
 DB 961 SCITEQTOYFFDNDKSKFSGLDCGNCRSRIFPHGKLMNTNLIFIMVSKGTCPCDTRL 1018

## RESULT 7

AAR71011  
 ID AAR71011 standard; Protein: 1091 AA.

AC AAR71011;

DT 01-DEC-1995 (first entry)

DE Human neuronal calcium channel subunit alpha 2b.

KW Calcium channel subunit; antagonist; agonist; diagnosis;  
 KW Lambert Eaton Syndrome.

XX Homo sapiens.

OS W09504822-A.

PN 16-FEB-1995.

XX 11-AUG-1994; 94WO-US09230.

PR 11-AUG-1993; 93US-0105536.

PR 05-NOV-1993; 93US-0149097.

PA (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.

PI Ellis SB, Gillespie A, Harpold MM, Mccue AF, Williams ME;

DR WPI: 1995-090900/12.

DR N-PSDB; AAQ84664.

PT DNA encoding human calcium channel sub-unit(s) - used for  
 PT developing prods. for studying calcium channels, e.g. for  
 PT obtaining agonists and antagonists

PS Disclosure; Page 166-171; 285pp; English.

XX Human neuronal alpha 2 coding sequence (AAQ84664) transcript is  
 CC differentially processed in skeletal muscle, aorta, and CNS in  
 CC the region corresp. to nt 1595-1942 of AAQ84664 in each of the  
 CC tissues. Five alternatively spliced variant transcripts that differ  
 CC in the presence or absence of one to three different portions of  
 CC this region. There are three sequences involved (see AAQ84664 FT  
 CC alpha 2 encoding transcripts from the different tissues include  
 CC different combinations of the three sequences, except for one of  
 CC the alpha 2 transcripts expressed in aorta which lacks all three  
 CC sequences. The five alpha 2 forms identified are (1) a form that  
 CC lacks sequence 3 called alpha 2a, expressed in skeletal muscle  
 CC (2) one that lacks sequence 1 called alpha 2b, expressed in CNS  
 CC (3) one that lacks sequences 1 and 2 called alpha 2c, expressed in  
 CC aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,  
 CC expressed in aorta and (5) one that lacks sequences 1 and 3  
 CC called alpha 2e.

XX Sequence 1091 AA;

Query Match

Best Local Similarity 100.0%; Score 5346; DB 16; Length 1091;

Pred. No. 0;

Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLTLFOSLLIGPSSSEEPSPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60  
 DB 1 MAAGCLLALTLTLFOSLLIGPSSSEEPSPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60  
 QY 61 YEKYQDLTYTEPNNAKQLVEIAARDIEKLSNRSKALVSLALEAEKVQAQAHQWREDFASN 120  
 DB 61 YEKYQDLTYTEPNNAKQLVEIAARDIEKLSNRSKALVSLALEAEKVQAQAHQWREDFASN 120  
 QY 121 EVVYNAKDDLDPEKNDSEPGSORIKPVFTEDANFGQISYQHAHVHPDIYEGSTIVL 180  
 DB 121 EVVYNAKDDLDPEKNDSEPGSORIKPVFTEDANFGQISYQHAHVHPDIYEGSTIVL 180  
 QY 181 NELNWT SALDEVEFKKNREEDPSLLWQVFGSATGLARYYPASPMVDNSRTPNKIDLYDVR 240  
 DB 181 NELNWT SALDEVEFKKNREEDPSLLWQVFGSATGLARYYPASPMVDNSRTPNKIDLYDVR 240  
 QY 241 RPWYIQGAASPDKMLILVDVSGVSGLTCLKIRTSYSEMLETLSDDDDFNVASFNSNAQD 300  
 DB 241 RPWYIQGAASPDKMLILVDVSGVSGLTCLKIRTSYSEMLETLSDDDDFNVASFNSNAQD 300  
 QY 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNYNVSRANCKIIML 360  
 DB 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNYNVSRANCKIIML 360  
 QY 361 FTDGGEERAQEIFNKYKDKKVRVFRFSYGOHNYERGPQIOWMACENKGYEYIETPSIGAIR 420  
 DB 361 FTDGGEERAQEIFNKYKDKKVRVFRFSYGOHNYERGPQIOWMACENKGYEYIETPSIGAIR 420  
 QY 421 INTQEVLDVLRPMVLGADKAKQVQWNTVYLDALGLVITGTLPVFNITGTFENKTNLK 480  
 DB 421 INTQEVLDVLRPMVLGADKAKQVQWNTVYLDALGLVITGTLPVFNITGTFENKTNLK 480  
 QY 481 NQILGVMGVDVSLSDIKRLTPRFLCPNGYTFADPNQYVLLHNPQPKNSQEPVTL 540  
 DB 481 NQILGVMGVDVSLSDIKRLTPRFLCPNGYTFADPNQYVLLHNPQPKNSQEPVTL 540  
 QY 541 DFLDAELENDIKVEIRNKMIDGESGKFTRTLVKSODERYIDKGNRTYTWTPVNGTDSL 600  
 DB 541 DFLDAELENDIKVEIRNKMIDGESGKFTRTLVKSODERYIDKGNRTYTWTPVNGTDSL 600  
 QY 601 ALVLPYTFYIKAKLEETITQARSKKGMKDSSETLKPONFEESGYTFIAPRDYCNLDKI 660  
 DB 601 ALVLPYTFYIKAKLEETITQARSKKGMKDSSETLKPONFEESGYTFIAPRDYCNLDKI 660  
 QY 661 SONNTEFLLNFNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQYWSKQKNIKVKAR 720  
 DB 661 SONNTEFLLNFNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQYWSKQKNIKVKAR 720  
 QY 721 FVVTGGGITRVYPKEAGENQENPETYEDSFYKRSILDNDNYVFTAPYFNKSGPGAYESGI 780  
 DB 721 FVVTGGGITRVYPKEAGENQENPETYEDSFYKRSILDNDNYVFTAPYFNKSGPGAYESGI 780  
 QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPCCAGPVCDCKRNSDVMDCVI 840  
 DB 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPCCAGPVCDCKRNSDVMDCVI 840  
 QY 841 LDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNISVYAFNKSVDYQSVCEPAAAPKQ 900  
 DB 841 LDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNISVYAFNKSVDYQSVCEPAAAPKQ 900  
 QY 901 GAGHRSAYVPSVADILQIGWATAAASILQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
 DB 901 GAGHRSAYVPSVADILQIGWATAAASILQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
 QY 961 SCITEQTOYFFDNDKSKFSGLDCGNCRSRIFPHGKLMNTNLIFIMVSKGTCPCDTRL 1018  
 DB 961 SCITEQTOYFFDNDKSKFSGLDCGNCRSRIFPHGKLMNTNLIFIMVSKGTCPCDTRL 1018

RESULT 8  
 AAW63145

ID AAW63145 standard; Protein; 1091 AA.  
 AC AAW63145;  
 XX  
 DT 12-OCT-1998 (first entry)  
 DE Human calcium channel alpha-2 subunit.  
 XX  
 KW Alpha-2 subunit; human; calcium channel; assay; detection;  
 KW characterisation; Lambert Eaton Syndrome; LES; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US5792846-A.  
 XX  
 PD 11-AUG-1998.  
 XX  
 PF 31-MAY-1995; 95US-0455543.  
 XX  
 PR 04-APR-1994; 94US-0223305.  
 PR 04-APR-1988; 88US-0176899.  
 PR 04-APR-1989; 89US-0603751.  
 PR 04-APR-1989; 89WO-US01408.  
 PR 20-FEB-1990; 90US-0482384.  
 PR 30-NOV-1990; 90US-0620250.  
 PR 15-AUG-1991; 91US-0745206.  
 PR 31-MAY-1995; 95US-0455543.  
 XX  
 PA (SIBI-) SIBIA NEUROSCIENCES INC.  
 XX  
 PI Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;  
 PI Williams ME;  
 XX  
 DR WPI; 1998-456192/39.  
 DR N-PSDB; AAV42689.  
 XX  
 PT DNA encoding human calcium channel alpha 1B subunit protein -  
 PT useful for recombinant production of the channel for screening of  
 PT its modulators, and diagnosis of Lambert Eaton Syndrome  
 XX  
 PS Claim 4; Columns 283-288; 166pp; English.  
 XX  
 CC The present sequence represents the alpha-2 subunit of a human calcium  
 CC channel. Calcium channels are membrane-spanning, multi-subunit proteins  
 CC that allow controlled entry of calcium ions into cells. This leads  
 CC to depolarisation events required for muscle contraction. The recombinant  
 CC subunit, when expressed with nucleic acids encoding the complete calcium  
 CC channel, can be used in assays for the detection and characterisation of  
 CC compounds that modulate the channel. The DNA encoding the subunits can  
 CC be alternatively spliced when transcribed, giving more than one form of  
 CC the protein from the same transcript, each having slightly different  
 CC properties. In addition, the reactivity of the alpha 1 subunit with IgG  
 CC molecules from the serum of an individual with Lambert Eaton Syndrome  
 CC (LES) can be used as a diagnostic for the disease.  
 XX  
 SQ Sequence 1091 AA;

Query Match 100.0%; Score 5346; DB 19; Length 1091;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAAGCLLALTTLFOSLLIGSPSEPPFSAVTIKSWDKMQEDLVTLAKTAGVGNQLVDI 60  
 DB 1 MAAGCLLALTTLFOSLLIGSPSEPPFSAVTIKSWDKMQEDLVTLAKTAGVGNQLVDI 60  
 QY 61 YEKYQDLYTVEPNNAQLVEIARIEKLLSNRSKALVSLALEKVKQAAHQWREDFASN 120  
 DB 61 YEKYQDLYTVEPNNAQLVEIARIEKLLSNRSKALVSLALEKVKQAAHQWREDFASN 120  
 QY 121 EVVYNNAKDDLDPKNDSEPGSQRIKPVIEDANFGROIQSYQHAHVHIPTDIYEGSTIVL 180  
 DB 121 EVVYNNAKDDLDPKNDSEPGSQRIKPVIEDANFGROIQSYQHAHVHIPTDIYEGSTIVL 180

QY 181 NELNWTSALEDVEFKKNREEDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240  
 DB 181 NELNWTSALEDVEFKKNREEDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240  
 QY 241 RPWYIQGAASPKDMLILVDVSGVSGLTLLKLRISVSEMLETSLSDDDDFVNVASFNSNAQ 300  
 DB 241 RPWYIQGAASPKDMLILVDVSGVSGLTLLKLRISVSEMLETSLSDDDDFVNVASFNSNAQ 300  
 QY 301 VSCFQHLVQANVRNKKVLDVANNITAKGIDYKKGFSAFQQLLNYNVSRANCKIIML 360  
 DB 301 VSCFQHLVQANVRNKKVLDVANNITAKGIDYKKGFSAFQQLLNYNVSRANCKIIML 360  
 QY 361 FTDGGEERAQEIFNKYKDKKVRVFRFVSGQHNRYERGPQWACENKGYGYYEIPISGAIR 420  
 DB 361 FTDGGEERAQEIFNKYKDKKVRVFRFVSGQHNRYERGPQWACENKGYGYYEIPISGAIR 420  
 QY 421 INTQEYLDVLGRPMVLGAKAKOVQNTVYLDALGLGLVITGLPVFNITGOFENKTNLK 480  
 DB 421 INTQEYLDVLGRPMVLGAKAKOVQNTVYLDALGLGLVITGLPVFNITGOFENKTNLK 480  
 QY 481 NQLILGVMGVDSLEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHPLNLPKNPKSQEPVTL 540  
 DB 481 NQLILGVMGVDSLEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHPLNLPKNPKSQEPVTL 540  
 QY 541 DFLDAELENDIKVEIRNKIMIDGESGEKTRTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
 DB 541 DFLDAELENDIKVEIRNKIMIDGESGEKTRTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
 QY 601 ALVLPYTSFYIKAKLEETITQARSKKGMKDSSETLKPNFEEGYTFIAPRDYCNLDKI 660  
 DB 601 ALVLPYTSFYIKAKLEETITQARSKKGMKDSSETLKPNFEEGYTFIAPRDYCNLDKI 660  
 QY 661 SDNTEFLNNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQVWSKQKNIKGVKAR 720  
 DB 661 SDNTEFLNNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQVWSKQKNIKGVKAR 720  
 QY 721 FVYTDGGITRVYPKEAGENQWENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
 DB 721 FVYTDGGITRVYPKEAGENQWENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
 QY 781 MVSKAVERIYIQGLKLPVAVGIGKIDVNSWIENFTKTSIRDPGAGPVCDCKRNSDVMDCVI 840  
 DB 781 MVSKAVERIYIQGLKLPVAVGIGKIDVNSWIENFTKTSIRDPGAGPVCDCKRNSDVMDCVI 840  
 QY 841 LDGGLFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYOSVCEPGAAPKQ 900  
 DB 841 LDGGLFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYOSVCEPGAAPKQ 900  
 QY 901 GAGHRSAYVPSVADILQIGWATAAAWSILQQFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960  
 DB 901 GAGHRSAYVPSVADILQIGWATAAAWSILQQFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960  
 QY 961 SCITEQTQYFFFDNDKSFSGVLDCGNCSTRIFHGEKLMNTNLIFIMVESKGTCPDTRL 1018  
 DB 961 SCITEQTQYFFFDNDKSFSGVLDCGNCSTRIFHGEKLMNTNLIFIMVESKGTCPDTRL 1018  
 RESULT 9  
 AAB10576  
 ID AAB10576 standard; Protein; 1091 AA.  
 XX  
 AC AAB10576;  
 XX  
 DT 22-DEC-2000 (first entry)  
 XX  
 DE Human calcium channel alpha-2 subunit protein.  
 XX  
 KW Human; calcium channel; calcium channel subunit; diagnosis;  
 KW Lambert Eaton Syndrome; calcium channel subunit alpha-2.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6096514-A.



XX 01-AUG-2000.  
 PD 25-MAY-1995; 95US-0450562.  
 XX 04-APR-1988; 88US-0176899.  
 XX 02-FEB-1990; 90US-0482384.  
 PR 08-NOV-1990; 90US-0603751.  
 PR 30-NOV-1990; 90US-0620250.  
 PR 15-AUG-1991; 91US-0745206.  
 PR 10-APR-1992; 92US-0868354.  
 PR 13-JUL-1992; 92US-0914231.  
 PR 11-AUG-1993; 93US-0105536.  
 PR 05-NOV-1993; 93US-0149097.  
 PR 07-FEB-1994; 94US-0193078.  
 PR 04-APR-1994; 94US-0223305.  
 PR 11-AUG-1994; 94US-0290012.  
 PR 23-SEP-1994; 94US-0311363.  
 PR 28-SEP-1994; 94US-0314083.  
 PR 07-NOV-1994; 94US-0336257.  
 PR 13-MAR-1995; 95US-0404950.  
 XX (SIBI-) SIBIA NEUROSCIENCES INC.  
 PA Ellis SB, Williams ME, McCue AF, Harpold MW;  
 XX WPI: 2000-548230/50.  
 XX N-PSDB; AAA71707.  
 XX Human calcium channel beta subunit polynucleotides, useful for  
 XX producing recombinant eukaryotic cells and for diagnosing Lambert Eaton  
 XX Syndrome -  
 XX Example IV; Column 135-144; 153pp; English.  
 XX This invention describes a novel isolated DNA molecule (I) comprising a  
 CC sequence encoding a beta3-1 subunit of a human calcium channel.  
 CC Nucleic acid probes comprising 14-30 contiguous nucleotides of  
 CC beta3 subunit encoding DNA are useful for isolation and cloning of  
 CC calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that  
 CC express heterologous calcium channel are useful for identifying compounds  
 CC that modulate calcium channel activity and in assays for identifying  
 CC agonists and antagonists of calcium channel activity in humans. Human  
 CC calcium channel subunit or eukaryotic cells expressing the channel are  
 CC useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This  
 CC sequence represents the human calcium channel alpha-2 subunit which is  
 CC described in the method of the invention.  
 XX Sequence 1091 AA;  
 SQ Query Match 100.0%; Score 5346; DB 21; Length 1091;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAAGCLLALTLFOSLLIGSPSEPPPSAVTIKSWDKMQEDLVTLAKTAGSYNQLVDI 60  
 DB 1 MAAGCLLALTLFOSLLIGSPSEPPPSAVTIKSWDKMQEDLVTLAKTAGSYNQLVDI 60  
 QY 61 YEKYODLVTVPENNARQLVETAAARDIEKLLNSRKALVSLALEAEKVQAAHQRDEFASN 120  
 DB 61 YEKYODLVTVPENNARQLVETAAARDIEKLLNSRKALVSLALEAEKVQAAHQRDEFASN 120  
 QY 121 EVVYVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIYSOHAHVHPTDIYEGSTIVL 180  
 DB 121 EVVYVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIYSOHAHVHPTDIYEGSTIVL 180  
 QY 181 NELNWTLSALDEVFKKNREDDPSLLNQVFGSATGLARYYPASPWVDNSETPNKIDLYDVR 240  
 DB 181 NELNWTLSALDEVFKKNREDDPSLLNQVFGSATGLARYYPASPWVDNSETPNKIDLYDVR 240  
 QY 241 RPWYIQGAASPKDMLILVDVSGVSGSLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
 DB 241 RPWYIQGAASPKDMLILVDVSGVSGSLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300

301 VSCFOHLVQANVRNKKVLKDAVNNTAKGIDYKKGFSAFEQLLNYNVSRANCNKIIML 360  
 DB 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGIDYKKGFSAFEQLLNYNVSRANCNKIIML 360  
 QY 361 FTDGGEERAQEIFNKYNKDKKVRVFRFVSGQHNRYERGPQIOMACENKGYEIPISGAIR 420  
 DB 361 FTDGGEERAQEIFNKYNKDKKVRVFRFVSGQHNRYERGPQIOMACENKGYEIPISGAIR 420  
 QY 421 INTQEYLDVLGRPMVLADKAKOVQWNTVYLDALGLVITGLTPVFNITGOFENKTNLK 480  
 DB 421 INTQEYLDVLGRPMVLADKAKOVQWNTVYLDALGLVITGLTPVFNITGOFENKTNLK 480  
 QY 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPCNGYYFAIDPNGYVLLHLPNLPKPKSQEPVTL 540  
 DB 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPCNGYYFAIDPNGYVLLHLPNLPKPKSQEPVTL 540  
 QY 541 DFLDAELNDIKVEIRNKMIDGESGEKTRTLVKQSDERYIDKGNRTYTWTPVNGTDYSL 600  
 DB 541 DFLDAELNDIKVEIRNKMIDGESGEKTRTLVKQSDERYIDKGNRTYTWTPVNGTDYSL 600  
 QY 601 ALVLPITYSFYITKALEETITQARSKKGMKDSITLKPDPNFESGYTFIAPRDYCNDLKI 660  
 DB 601 ALVLPITYSFYITKALEETITQARSKKGMKDSITLKPDPNFESGYTFIAPRDYCNDLKI 660  
 QY 661 SDNTEFLNFEFIDRKTPNNPSCNADLINRVLLDAGFTNELVQVWSKQNIKGVKAR 720  
 DB 661 SDNTEFLNFEFIDRKTPNNPSCNADLINRVLLDAGFTNELVQVWSKQNIKGVKAR 720  
 QY 721 FVYTDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
 DB 721 FVYTDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
 QY 781 MVS KAVEIYTOGKLLKPAVVGKIDVNSWIENFTKTSIRDPCAGPVCDCKRNSDMVDCVI 840  
 DB 781 MVS KAVEIYTOGKLLKPAVVGKIDVNSWIENFTKTSIRDPCAGPVCDCKRNSDMVDCVI 840  
 QY 841 LDGDFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNIYSVAFNKSVDYOSVCEPGAAPKQ 900  
 DB 841 LDGDFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNIYSVAFNKSVDYOSVCEPGAAPKQ 900  
 QY 901 GAGHRSAVPSVADILQIGWATAAAWSILQOFLLSLTPRLLAEVEMEDDDFTASLSKQ 960  
 DB 901 GAGHRSAVPSVADILQIGWATAAAWSILQOFLLSLTPRLLAEVEMEDDDFTASLSKQ 960  
 QY 961 SCITEQTQVFFDNDKSFSGVLDGCGNCSRIHFHGEKLMNTNLIPIFIMVESKGTCPDTRL 1018  
 DB 961 SCITEQTQVFFDNDKSFSGVLDGCGNCSRIHFHGEKLMNTNLIPIFIMVESKGTCPDTRL 1018  
 RESULT 10  
 AAU01035  
 ID AAU01035 standard; Protein; 1091 AA.  
 XX AC AAU01035;  
 XX AC AAU01035;  
 DT 04-JUL-2001 (first entry)  
 XX Human secreted soluble alpha2delta calcium channel subunit #15 protein.  
 XX Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;  
 KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;  
 KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;  
 KW filter binding assay; wheat germ lectin flashplate assay.  
 XX Homo sapiens.  
 OS WO200119870-A2.  
 PN 22-MAR-2001.  
 XX 18-SEP-2000; 2000MO-EP09137.  
 XX

PR 16-SEP-1999; 99US-0397550.  
 PA (WARN ) WARNER LAMBERT CO.  
 XX Brown JP, Bertelli F;  
 XX WPI; 2001-235262/24.  
 DR N-PSDB; AAS01426.  
 XX  
 XX Calcium channel alpha2delta subunits, useful in e.g. SPA assays,  
 PT Flashplate assays, Nickel flashplate assays, Filter binding assays or  
 PT Wheat Germ Lectin Flashplate assays -  
 XX Claim 30; Page 141-144; 160pp; English.  
 XX  
 CC The present sequence represents human secreted calcium channel  
 CC alpha2delta subunit #15 which is soluble and retains the functional  
 CC characteristics of the full length or wild type alpha2delta subunit  
 CC (AAU01025) from which it is derived. The invention relates to truncated  
 CC alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins  
 CC which retain their affinity for radioactively labelled gabapentin. The  
 CC alpha2delta subunit is 1 of the components of the heteromultimeric  
 CC voltage-dependent calcium channel (VCC) complexes present in neuronal  
 CC and non-neuronal tissues including heart and skeletal muscle. Numerous  
 CC soluble forms of the human calcium channel alpha2delta subunits  
 CC (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the  
 CC porcine calcium channel alpha2delta subunits (AAU01027-AAU01031) are  
 CC described. The secreted soluble alpha2delta subunit may be used in assays  
 CC e.g. scintillation proximity assay (SPA), flashplate, nickel flashplate,  
 CC filter binding or wheat germ lectin flashplate assays to detect or  
 CC measure the binding or interaction of a ligand (e.g. gabapentin,  
 CC L-Norleucine, L-Allo-Isoleucine, L-methionine, L-leucine, L-Isoleucine,  
 CC L-Valine, Spermine and/or L-Phenylalanine) of a calcium channel  
 CC alpha2delta subunit.  
 XX Sequence 1091 AA;

Query Match 100.08; Score 5346; DB 22; Length 1091;  
 Best Local Similarity 100.08; Pred. No. 0;  
 Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCILLALTLFQSLILIGSPSEPPFPFSAVTIKSWVDKMOEDLVTLAKTAGVGNQLVDI 60  
 DB 1 MAAGCILLALTLFQSLILIGSPSEPPFPFSAVTIKSWVDKMOEDLVTLAKTAGVGNQLVDI 60

QY 61 YEKYQDLTYTVEPNARQIVLAEARIEKLLSNRSKALVSLAEAEKQAAHQWREDFASN 120  
 DB 61 YEKYQDLTYTVEPNARQIVLAEARIEKLLSNRSKALVSLAEAEKQAAHQWREDFASN 120

QY 121 EVVYNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROIQSYOHAHVHIPTDIYEGSTIVL 180  
 DB 121 EVVYNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROIQSYOHAHVHIPTDIYEGSTIVL 180

QY 181 NELNWTSSALDEVFKKRNEDPSLLQVFGSGATGLARYYPASPWDNSRTPNPKIDLYDVR 240  
 DB 181 NELNWTSSALDEVFKKRNEDPSLLQVFGSGATGLARYYPASPWDNSRTPNPKIDLYDVR 240

QY 241 RPWYIQGAASPKDMLILVDVSGVSGLTGLKIRTSVSEMLETLSDDDFVNVSFNSNAQD 300  
 DB 241 RPWYIQGAASPKDMLILVDVSGVSGLTGLKIRTSVSEMLETLSDDDFVNVSFNSNAQD 300

QY 301 VSCFHLVQANVRNKKVLDKAVNNITAKITDYKKGFSAFEQLLLNVSRANCNKIIML 360  
 DB 301 VSCFHLVQANVRNKKVLDKAVNNITAKITDYKKGFSAFEQLLLNVSRANCNKIIML 360

QY 361 FTDGGEERAQEIFNKNKDKVRFRFSVGOHNYERGPQIWMACENKGYIYEIPSGAIR 420  
 DB 361 FTDGGEERAQEIFNKNKDKVRFRFSVGOHNYERGPQIWMACENKGYIYEIPSGAIR 420

QY 421 INTQFYLDVLRPMVLAGDKAKQVQWNTNVLDLLEGLVITGLTPVNTITGQFENKTNLK 480  
 DB 421 INTQFYLDVLRPMVLAGDKAKQVQWNTNVLDLLEGLVITGLTPVNTITGQFENKTNLK 480

QY 481 NQLILGVMGVDVSLIEDIKRLTPRETLCPCNGYYFAIDPNGYVLLHPNLPKNPKSQEPVTL 540  
 DB 481 NQLILGVMGVDVSLIEDIKRLTPRETLCPCNGYYFAIDPNGYVLLHPNLPKNPKSQEPVTL 540

QY 541 DFLDAELENDIKVEIRNKMIDGESGEKTFRTLVSQDERYIDKGNRTYTTWTPVNGTDSL 600  
 DB 541 DFLDAELENDIKVEIRNKMIDGESGEKTFRTLVSQDERYIDKGNRTYTTWTPVNGTDSL 600

QY 601 ALVLPYTSFYIYKAKLEETITQARSKKGMKDSSTLKPDNFEESGYTFIAPRDYCNLDKI 660  
 DB 601 ALVLPYTSFYIYKAKLEETITQARSKKGMKDSSTLKPDNFEESGYTFIAPRDYCNLDKI 660

QY 661 SDNTEFLLNENEFIDRKTNNPNSCNADLNRVLLDAGFTNELVQNVWSKOKNIKGKAR 720  
 DB 661 SDNTEFLLNENEFIDRKTNNPNSCNADLNRVLLDAGFTNELVQNVWSKOKNIKGKAR 720

QY 721 FVVTDDGGITRVYPKEAGENWQENPETEYDSFYKRSKLDNDNYVFTAPYFNKSGPGAYESGI 780  
 DB 721 FVVTDDGGITRVYPKEAGENWQENPETEYDSFYKRSKLDNDNYVFTAPYFNKSGPGAYESGI 780

QY 781 MYSKAVEIYIOGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPGAGVDCCKRNSDVMDCVI 840  
 DB 781 MYSKAVEIYIOGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPGAGVDCCKRNSDVMDCVI 840

QY 841 LDDGCFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 900  
 DB 841 LDDGCFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 900

QY 901 GAGHRSAYVSVADIIQIGWATAAAMSIIQOFLLSITFPRLLEAVEMEDDDFTASLSKQ 960  
 DB 901 GAGHRSAYVSVADIIQIGWATAAAMSIIQOFLLSITFPRLLEAVEMEDDDFTASLSKQ 960

QY 961 SCITEQIYFFDNDKSFSGVLDGCGNCSRIFFHGEKLMNTNLIIFIMVESKGTCPDTRL 1018  
 DB 961 SCITEQIYFFDNDKSFSGVLDGCGNCSRIFFHGEKLMNTNLIIFIMVESKGTCPDTRL 1018

RESULT 11  
 AAB62259

ID AAB62259 standard; Protein; 1091 AA.

AC AAB62259;

XX 11-JUN-2001 (first entry)

XX Porcine calcium channel alpha2delta subunit.

XX Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;  
 KW nervous system disorder; pain; epilepsy; anxiety; pig.  
 XX Sus scrofa.

XX WO200120336-A2.

XX 22-MAR-2001.

XX 18-SEP-2000; 2000WO-EP09136.

XX 16-SEP-1999; 99US-0397549.

XX (WARN ) WARNER LAMBERT CO.

XX Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;

XX WPI; 2001-257902/26.

XX N-PSDB; AAF57563.

XX Competitive binding assay for screening ligands which bind a cerebral  
 PT cortical voltage-dependent calcium channel alpha2-delta-1 subunit,  
 PT where the ligands identified are useful for treating disorders of the  
 PT nervous system, including pain -  
 XX Claim 7; Page 139-142; 158pp; English.

XX The invention relates to a new method for screening ligands which bind a  
 CC cerebral cortical voltage-dependent calcium channel alpha2delta subunit,  
 CC preferably alpha2delta-1 subunit. The method comprises contacting a  
 CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of  
 CC interest and a labelled compound which binds the subunit, followed by  
 CC measuring the level of binding of the labelled compound to alpha2delta-1  
 CC subunit. The method is useful for screening ligands, preferably  
 CC biologically active products that modulate a nervous system function,  
 CC which bind a cerebral cortical voltage-dependent calcium channel  
 CC alpha2delta-1 subunit. The ligands identified by the method are useful  
 CC for treating disorders of the nervous system, including pain, epilepsy  
 CC and anxiety. The present sequence represents a porcine calcium channel  
 CC alpha2delta subunit.  
 XX  
 SQ Sequence 1091 AA;

Query Match 100.0%; Score 5346; DB 22; Length 1091;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLTFOILLIGPSEEPFSAVTIKSWDKMQEDLVTLAKTAGSVNQLVDI 60  
 Db 1 MAAGCLLALTTLTFOILLIGPSEEPFSAVTIKSWDKMQEDLVTLAKTAGSVNQLVDI 60

QY 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSALAEAKVQAAHQWREDFASN 120  
 Db 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSALAEAKVQAAHQWREDFASN 120

QY 121 EYVYNAKDDLPKNDSEPGSORIKPVFIEDANFORQISYQHAHVHPTDIYEGSTIVL 180  
 Db 121 EYVYNAKDDLPKNDSEPGSORIKPVFIEDANFORQISYQHAHVHPTDIYEGSTIVL 180

QY 181 NELNWTSALEDEVFKKNEEDPSLLWVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240  
 Db 181 NELNWTSALEDEVFKKNEEDPSLLWVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240

QY 241 RPWYIOGAASPKDMLILVDVSGVSGILTKLIRTSVSEMLETLSDDDDFNVASFNSNAQD 300  
 Db 241 RPWYIOGAASPKDMLILVDVSGVSGILTKLIRTSVSEMLETLSDDDDFNVASFNSNAQD 300

QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSFAFOLLNPNKNSRANCKIIML 360  
 Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSFAFOLLNPNKNSRANCKIIML 360

QY 361 FTDGGEERAQEIFNKYKDKKVRFRFVSQGHNYERGPQIOWMACENKGYIYEIPSGAIR 420  
 Db 361 FTDGGEERAQEIFNKYKDKKVRFRFVSQGHNYERGPQIOWMACENKGYIYEIPSGAIR 420

QY 421 INTQEYLDVLGRPMVLGADKAKQVQNTNVDLDALEGLVITGTLPVFNITQGFENKTNLK 480  
 Db 421 INTQEYLDVLGRPMVLGADKAKQVQNTNVDLDALEGLVITGTLPVFNITQGFENKTNLK 480

QY 481 NQLILGVGVDSVLEDIKRLTPRTLCPCNGYYFAIDPVGVLHPNLQPNKPSQEPVTL 540  
 Db 481 NQLILGVGVDSVLEDIKRLTPRTLCPCNGYYFAIDPVGVLHPNLQPNKPSQEPVTL 540

QY 541 DFLDAELENKIKVIRKMDIGESGKFTFTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
 Db 541 DFLDAELENKIKVIRKMDIGESGKFTFTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600

QY 601 ALVLPTSYFYIKAKLEETITQARKSKGKMKDSETLKPDPNFEESGYFTIAPRDCNDLKI 660  
 Db 601 ALVLPTSYFYIKAKLEETITQARKSKGKMKDSETLKPDPNFEESGYFTIAPRDCNDLKI 660

QY 661 SDNNTFELLNNEFTDRKTPNPNPCNADLNRLVLLDAGFTNELVQNSKQNKIKGVKAR 720  
 Db 661 SDNNTFELLNNEFTDRKTPNPNPCNADLNRLVLLDAGFTNELVQNSKQNKIKGVKAR 720

QY 721 FWVTDGGITRVYPKAGENWQENPETVEDSFYKRSLDNDNVYFTAPYFNKSGPAGESGI 780  
 Db 721 FWVTDGGITRVYPKAGENWQENPETVEDSFYKRSLDNDNVYFTAPYFNKSGPAGESGI 780

QY 781 MVSKAVEIYIQGKLLKPAVVGVGIKIDVNSWIENFTKTSIRDPGAGPVCDCRNSDVMDCVI 840  
 Db 781 MVSKAVEIYIQGKLLKPAVVGVGIKIDVNSWIENFTKTSIRDPGAGPVCDCRNSDVMDCVI 840

QY 841 LDDGGFLLMANHDDYTQOIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 900  
 Db 841 LDDGGFLLMANHDDYTQOIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 900

QY 901 GAGHRSAYVPSVADILQIGMWATAAAMSILQOQFLLSLTFPRLLAEVEMEDDDFTASLSKQ 960  
 Db 901 GAGHRSAYVPSVADILQIGMWATAAAMSILQOQFLLSLTFPRLLAEVEMEDDDFTASLSKQ 960

QY 961 SCITEQTYQFPDNDKSFSGVLDGCGNSRIPHGKLMNTNLIFIMVSKGTCTPCDTRL 1018  
 Db 961 SCITEQTYQFPDNDKSFSGVLDGCGNSRIPHGKLMNTNLIFIMVSKGTCTPCDTRL 1018

## RESULT 12

AAW37879 standard; Protein; 1091 AA.

XX AAW37879;  
 XX AC  
 XX 28-AUG-1998 (first entry)  
 XX DE Human calcium channel a2d subunit.  
 XX KW Calcium channel; human; central nervous system disorder;  
 XX KW Lambert-Eaton syndrome; diagnosis; therapy.  
 XX OS Homo sapiens.  
 XX PN WO9811131-A2.  
 XX 19-MAR-1998.  
 XX PD  
 XX PF 11-SEP-1997; 97WO-US16146.  
 XX PR 16-SEP-1996; 96US-0713118.  
 XX PA (AMHP ) AMERICAN HOME PROD CORP.  
 XX PI Chen ARS, Franco R, Shuey DJ;  
 XX WPI; 1998-207325/18.  
 XX N-PSDB; AAV29060.

DNA encoding human neuronal calcium channel subunit(s) - useful for diagnosis of and treatment of central nervous system disorders, e.g. Lambert-Eaton syndrome

Disclosure: Fig 2; 89pp; English.

This polypeptide comprises the a2d subunit of the human neuronal calcium channel. cDNA clones (see AAV29059-61) encoding the a1b subunit (see AAW37878), the a2d subunit and a b3 subunit (see AAW37880) have been isolated. These have been inserted into expression vectors and are stably expressed in transformed cell lines. The transformed cells show omega-conotoxin GVIA binding activity, and omega-conotoxin GVIA toxin sensitive potassium-stimulated calcium uptake, indicating that the proteins expressed by the clones are capable of forming a functioning calcium channel. Nucleic acids encoding the 3 subunits, as well as vectors, host cells and methods of isolating nucleic acids encoding related calcium channels are disclosed. Fusion proteins incorporating the subunit proteins, antibodies, and assays for identifying agents that modulate calcium channel activity are also provided. Such agents can be used to treat certain central nervous system disorders by altering calcium channel activity. Methods of diagnosing diseases associated with particular calcium channels, such as Lambert-Eaton syndrome, are disclosed.

Sequence 1091 AA;

Query Match 99.9%; Score 5342; DB 19; Length 1091;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1017; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLTFLQSLLIGPSSSEPPPSAVTIKSWDKMOEDLVTLAKTAGSVNQLVDI 60  
DB 1 MAAGCLLALTTLTFLQSLLIGPSSSEPPPSAVTIKSWDKMOEDLVTLAKTAGSVNQLVDI 60

QY 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDEFASN 120  
DB 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDEFASN 120

QY 121 EVVYVNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIYSQHAHVHIPTDIYEGSTIVL 180  
DB 121 EVVYVNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIYSQHAHVHIPTDIYEGSTIVL 180

QY 181 NELNWTSAALDEVEFKNREDEPSLLMQVFGSATGLARYYPASPWDNSRTPNKIDLYDVR 240  
DB 181 NELNWTSAALDEVEFKNREDEPSLLMQVFGSATGLARYYPASPWDNSRTPNKIDLYDVR 240

QY 241 RPWYIQGAASPKDMLILVDVSGVSGSLTKLIRTSVSEMLETSLDDDFNVVASFNSNAQD 300  
DB 241 RPWYIQGAASPKDMLILVDVSGVSGSLTKLIRTSVSEMLETSLDDDFNVVASFNSNAQD 300

QY 301 VSCFQHLVQANVRNKKVLKDVANNITAKGIDTDYKKGFSFAFEQLLNVNVRANCNKIIML 360  
DB 301 VSCFQHLVQANVRNKKVLKDVANNITAKGIDTDYKKGFSFAFEQLLNVNVRANCNKIIML 360

QY 361 FTDGGEERAQETIFNKNYKDKVRVFRFVSGVGHNYERGPQIOMACENKGYIYEISGAIR 420  
DB 361 FTDGGEERAQETIFNKNYKDKVRVFRFVSGVGHNYERGPQIOMACENKGYIYEISGAIR 420

QY 421 INTQBYLDVLRPMVLAGDKAQVQWNTVYLDLLEGLVITGTLVPFNITGQFENKTNLK 480  
DB 421 INTQBYLDVLRPMVLAGDKAQVQWNTVYLDLLEGLVITGTLVPFNITGQFENKTNLK 480

QY 481 NQLILGVMGVDVLEDIKRLTPRETLCNPGYFFAIDPNGYVLLHPNLQPNKPSQEPVTL 540  
DB 481 NQLILGVMGVDVLEDIKRLTPRETLCNPGYFFAIDPNGYVLLHPNLQPNKPSQEPVTL 540

QY 541 DFLDAELNDIKVEIRNKMIDGSEKTFRTLKVSQDERYIDKGNRTYTWTPVNGTDYSL 600  
DB 541 DFLDAELNDIKVEIRNKMIDGSEKTFRTLKVSQDERYIDKGNRTYTWTPVNGTDYSL 600

QY 601 ALVLTPTSYFYIKAKLETTIQAARKKGMKDSKTLKPDNFEESGYTFIAPROYCNDLKI 660  
DB 601 ALVLTPTSYFYIKAKLETTIQAARKKGMKDSKTLKPDNFEESGYTFIAPROYCNDLKI 660

QY 661 SDNNTFELLNFEITDRKTPNPNPCNADLINRVLLDAGFTNELVQNYWSKQKNIKVYAR 720  
DB 661 SDNNTFELLNFEITDRKTPNPNPCNADLINRVLLDAGFTNELVQNYWSKQKNIKVYAR 720

QY 721 FVVTDDGTRIVYPKEAGENQENPETEYDSFYKRSIDNDNYVFTAPYFNKSGPGAYESGI 780  
DB 721 FVVTDDGTRIVYPKEAGENQENPETEYDSFYKRSIDNDNYVFTAPYFNKSGPGAYESGI 780

QY 781 MYSKAVEIYIOGKLLKPAVVGIIKIDVNSWIENTKTSIRDPACAGVCDCKRNSDVMDCVI 840  
DB 781 MYSKAVEIYIOGKLLKPAVVGIIKIDVNSWIENTKTSIRDPACAGVCDCKRNSDVMDCVI 840

QY 841 LDGCGFLMANHDDYTNOIGRFTGEIDPSLMRHLVNIISVYAFNKSVDYQSVCEPGAAPKQ 900  
DB 841 LDGCGFLMANHDDYTNOIGRFTGEIDPSLMRHLVNIISVYAFNKSVDYQSVCEPGAAPKQ 900

QY 901 GAGHRSAYVPSVADILQIGWATAAAMSILQOFLLSITFPRLLLEAVEMEDDDFTASLSQ 960  
DB 901 GAGHRSAYVPSVADILQIGWATAAAMSILQOFLLSITFPRLLLEAVEMEDDDFTASLSQ 960

QY 961 SCITEQTYEFDNDKSFSGVLDCGNCSTRIFHGEKLMNTNLFIMVYESKGTCPCDTRL 1018  
DB 961 SCITEQTYEFDNDKSFSGVLDCGNCSTRIFHGEKLMNTNLFIMVYESKGTCPCDTRL 1018

RESULT 13  
AAR33553  
ID AAR33553 standard; Protein; 1091 AA.  
XX  
AC AAR33553;  
XX  
DT 30-JUN-1993 (first entry)  
XX  
DE Sequence of the alpha 2 human calcium channel subunit.  
XX  
KW Human calcium channel subunit; diagnosis; agonist; antagonist;  
KW Lambert Eaton syndrome.  
XX  
OS Homo sapiens.  
XX  
PN W09304083-A.  
XX  
PD 04-MAR-1993.  
XX  
PF 14-AUG-1992; 92WO-US06903.  
XX  
PR 15-AUG-1991; 91DS-0745206.  
PR 10-APR-1992; 92US-0868354.  
XX  
PA (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.  
XX  
PI Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;  
PI Williams ME;  
XX  
DR WPI; 1993-093936/11.  
DR N-PSDB; AAQ37821.  
XX  
PT DNA encoding specific human calcium channel sub-units - used for  
PT identifying calcium channel agonists and antagonists and  
PT diagnosing Lambert Eaton syndrome  
XX  
PS Disclosure; Page 134-138; 150pp; English.  
XX  
CC DNA encoding a human neuronal calcium channel alpha 2 subunit was  
CC isolated from a human genomic DNA library probed under low and high  
CC stringency conditions with a fragment of DNA encoding the rabbit  
CC skeletal muscle calcium channel alpha 2 subunit. The fragment  
CC included nucleotides having a sequence corresponding to the  
CC nucleotide sequence between nucleotides 43 and 272 inclusive of  
CC rabbit back skeletal muscle calcium channel alpha 2 subunit cDNA.  
CC PCR analysis identified splice variants of the human calcium alpha  
CC 2 subunit transcript. In particularly preferred embodiments, the  
CC DNA encoding the alpha 2 subunit is produced by alternative  
CC processing of a primary transcript that includes DNA encoding the  
CC amino acids set forth in AAR33553 and the DNA of AAQ37823 inserted  
CC between nucleotides 1624 and 1625 of AAQ37821.  
XX  
SQ Sequence 1091 AA;

Query Match 99.9%; Score 5340; DB 14; Length 1091;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1017; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLTFLQSLLIGPSSSEPPPSAVTIKSWDKMOEDLVTLAKTAGSVNQLVDI 60  
DB 1 MAAGCLLALTTLTFLQSLLIGPSSSEPPPSAVTIKSWDKMOEDLVTLAKTAGSVNQLVDI 60

QY 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDEFASN 120  
DB 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDEFASN 120

QY 121 EVVYVNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIYSQHAHVHIPTDIYEGSTIVL 180  
DB 121 EVVYVNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIYSQHAHVHIPTDIYEGSTIVL 180

QY 181 NELNWTSAALDEVEFKNREDEPSLLMQVFGSATGLARYYPASPWDNSRTPNKIDLYDVR 240  
DB 181 NELNWTSAALDEVEFKNREDEPSLLMQVFGSATGLARYYPASPWDNSRTPNKIDLYDVR 240

Db 181 NELNWTSSALDEVFKNREEDPSLLMQVFGSATGLARYYPASVPWVNSRTPNKIDLYDVR 240  
 Qy 241 RPWYIOGAASPKDMLILVDVSGVSGTLKLRITVSSEMLETLSDDDFVNVASFNSNAQD 300  
 Db 241 RPWYIOGAASPKDMLILVDVSGVSGTLKLRITVSSEMLETLSDDDFVNVASFNSNAQD 300  
 Qy 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFQOLLNVNVRANCNKIIML 360  
 Db 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFQOLLNVNVRANCNKIIML 360  
 Qy 361 FTGGEERAQEIFNKYKNDKVRVRFVSQOHNYERGPQIOWMACENKGYIYEIPISGAIR 420  
 Db 361 FTGGEERAQEIFNKYKNDKVRVRFVSQOHNYERGPQIOWMACENKGYIYEIPISGAIR 420  
 Qy 421 INTQYLDVLRPMVLAGDKAKQVQWNTVYLDLLEGLVITGTPVFNITGQFENKTNLK 480  
 Db 421 INTQYLDVLRPMVLAGDKAKQVQWNTVYLDLLEGLVITGTPVFNITGQFENKTNLK 480  
 Qy 481 NQILGVMGVDVSLIEDIKRTPRTICPNGYIFAIDPNGVYLLHPNLOPKNPKSQEPVTL 540  
 Db 481 NQILGVMGVDVSLIEDIKRTPRTICPNGYIFAIDPNGVYLLHPNLOPKNPKSQEPVTL 540  
 Qy 541 DFLDAELNDIKVEIRNKMIDGESGKFTFLYKSDQERYIDKGNRTYTWTPVNGTDYSL 600  
 Db 541 DFLDAELNDIKVEIRNKMIDGESGKFTFLYKSDQERYIDKGNRTYTWTPVNGTDYSL 600  
 Qy 601 ALVLPYTFYIKAKLEETITQARKKGMKDSKTLKPDNFEESGYTFTAPRYCNDLKI 660  
 Db 601 ALVLPYTFYIKAKLEETITQARKKGMKDSKTLKPDNFEESGYTFTAPRYCNDLKI 660  
 Qy 661 SONNTEFLNFEFIDRTKTPNPNCSNADLINRVLLDAGFTNELVONYSKOKNIKGVKAR 720  
 Db 661 SONNTEFLNFEFIDRTKTPNPNCSNADLINRVLLDAGFTNELVONYSKOKNIKGVKAR 720  
 Qy 721 FVVTGDIITRVYKKEAGENWQENPETYEDSFYKRSNDNDNTVFTAPYFNKSGPGAYESGI 780  
 Db 721 FVVTGDIITRVYKKEAGENWQENPETYEDSFYKRSNDNDNTVFTAPYFNKSGPGAYESGI 780  
 Qy 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWENFTKTSIRDPACGVPDCDKRNSDVMDCVI 840  
 Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWENFTKTSIRDPACGVPDCDKRNSDVMDCVI 840  
 Qy 841 LDGGLMANHDDYTNQIGREFGEIDPSLMRHLVNIISVYAFNKSIDYQSVCEPGAAPKQ 900  
 Db 841 LDGGLMANHDDYTNQIGREFGEIDPSLMRHLVNIISVYAFNKSIDYQSVCEPGAAPKQ 900  
 Qy 901 GAGHSAYVPSVADILQIGWATAAASWILQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
 Db 901 GAGHSAYVPSVADILQIGWATAAASWILQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
 Qy 961 SCITEQYQFFDNDKSFSGVLDGNCRIIFHGEKLMNTNLIIFIMVESKGTCPDTRL 1018  
 Db 961 SCITEQYQFFDNDKSFSGVLDGNCRIIFHGEKLMNTNLIIFIMVESKGTCPDTRL 1018  
 RESULT 14  
 AA63148  
 ID AA63148 standard; Protein; 1110 AA.  
 XX  
 AC AA63148;  
 XX  
 DT 12-OCT-1998 (first entry)  
 XX  
 DE Human calcium channel alpha-2 subunit.  
 XX  
 KW Alpha-2 subunit; human; calcium channel; assay; detection;  
 KW Characterisation; Lambert Eaton Syndrome; LES; diagnosis.  
 XX  
 OS Homo sapiens.  
 PN US5792846-A.  
 XX  
 PD 11-AUG-1998.

31-MAY-1995; 95US-0455543.  
 04-APR-1994; 94US-0223305.  
 04-APR-1988; 88US-0176899.  
 04-APR-1989; 89US-0603751.  
 04-APR-1989; 89WO-US01408.  
 20-FEB-1990; 90US-0482384.  
 30-NOV-1990; 90US-0620250.  
 15-AUG-1991; 91US-0745206.  
 31-MAY-1995; 95US-0455543.  
 (SIBI-) SIBIA NEUROSCIENCES INC.  
 Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;  
 Williams ME;  
 WPI; 1998-456192/39.  
 N-PSDB; AAV42694.  
 DNA encoding human calcium channel alpha 1B subunit protein -  
 useful for recombinant production of the channel for screening of  
 its modulators, and diagnosis of Lambert Eaton Syndrome  
 Disclosure; Columns 131-138; 166pp; English.  
 The present sequence represents the alpha-2 subunit of a human calcium  
 channel. Calcium channels are membrane-spanning, multi-subunit proteins  
 that allow controlled entry of calcium ions into cells. This leads  
 to depolarisation events required for muscle contraction. The recombinant  
 subunit, when expressed with nucleic acids encoding the complete calcium  
 channel, can be used in assays for the detection and characterisation of  
 compounds that modulate the channel. The DNA encoding the subunits can  
 be alternatively spliced when transcribed, giving more than one form of  
 the protein from the same transcript, each having slightly different  
 properties. In addition, the reactivity of the alpha 1 subunit with IgG  
 molecules from the serum of an individual with Lambert Eaton Syndrome  
 (LES) can be used as a diagnostic for the disease.

Query Match 99.6%; Score 5326.5; DB 19; Length 1110;  
 Best Local Similarity 98.2%; Pred. No. 0;  
 Matches 1018; Conservative 0; Mismatches 0; Indels 19; Gaps 1;  
 QY 1 MAAGCLLALTLFQSLILIGSPSEPPSAVTIKSWDKMOEDLVTLAKTAGSYNQLVDI 60  
 Db 1 MAAGCLLALTLFQSLILIGSPSEPPSAVTIKSWDKMOEDLVTLAKTAGSYNQLVDI 60  
 QY 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSLVSLAEAEKVQAAHQRDEDFASN 120  
 Db 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSLVSLAEAEKVQAAHQRDEDFASN 120  
 QY 121 EVVYNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROIYQOHAHVHPTDIYEGSTIVL 180  
 Db 121 EVVYNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROIYQOHAHVHPTDIYEGSTIVL 180  
 QY 181 NELNWTSSALDEVFKNREEDPSLLMQVFGSATGLARYYPASVPWVNSRTPNKIDLYDVR 240  
 Db 181 NELNWTSSALDEVFKNREEDPSLLMQVFGSATGLARYYPASVPWVNSRTPNKIDLYDVR 240  
 QY 241 RPWYIOGAASPKDMLILVDVSGVSGTLKLRITVSSEMLETLSDDDFVNVASFNSNAQD 300  
 Db 241 RPWYIOGAASPKDMLILVDVSGVSGTLKLRITVSSEMLETLSDDDFVNVASFNSNAQD 300  
 QY 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFQOLLNVNVRANCNKIIML 360  
 Db 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFQOLLNVNVRANCNKIIML 360  
 QY 361 FTGGEERAQEIFNKYKNDKVRVRFVSQOHNYERGPQIOWMACENKGYIYEIPISGAIR 420  
 Db 361 FTGGEERAQEIFNKYKNDKVRVRFVSQOHNYERGPQIOWMACENKGYIYEIPISGAIR 420

QY 421 INTQYLDVLRPMVLGACAKAQVQWNTNVLDALELGLVITGTLPVFNITGQFENKTNLK 480  
 Db 421 INTQYLDVLRPMVLGACAKAQVQWNTNVLDALELGLVITGTLPVFNITGQFENKTNLK 480  
 QY 481 NQILGVMGVDVSLIEDIKRLTPRETLCPCNGYFFAIDPNGVYLLHPNLPK 530  
 Db 481 NQILGVMGVDVSLIEDIKRLTPRETLCPCNGYFFAIDPNGVYLLHPNLPK 530  
 QY 531 -----NPKSQEPVTLDFDALENDIKVEIRNKMIDGESGKTFRTLVKSQDERY 581  
 Db 541 LKRRPNIQNPKSQEPVTLDFDALENDIKVEIRNKMIDGESGKTFRTLVKSQDERY 600  
 QY 582 DKGRTYTWTPVNGTDYSLALVPTYSFYIKAKLEETIQOARSKGKMDSETLKPDNF 641  
 Db 601 DKGRTYTWTPVNGTDYSLALVPTYSFYIKAKLEETIQOARSKGKMDSETLKPDNF 660  
 QY 642 EESGYTFTAPDYCNLDKISDNNTTEFLNFEFIDRKTNNPNSCNADLNRLVLDAGFTN 701  
 Db 661 EESGYTFTAPDYCNLDKISDNNTTEFLNFEFIDRKTNNPNSCNADLNRLVLDAGFTN 720  
 QY 702 ELVONYWSKOKNIGVKARFVVDGGITRVYPKEAGENWOENPETYEDSFYKRSLDNDY 761  
 Db 721 ELVONYWSKOKNIGVKARFVVDGGITRVYPKEAGENWOENPETYEDSFYKRSLDNDY 780  
 QY 762 VFTAPYFNKSGPAYESGIMVSKAVIYIOGKLLKPAVVGIIKIDVNSWLENFTKTSIRDP 821  
 Db 781 VFTAPYFNKSGPAYESGIMVSKAVIYIOGKLLKPAVVGIIKIDVNSWLENFTKTSIRDP 840  
 QY 822 CAGPVCDCCKRNSDVMDCVILDDGGFLMANHDDYTNIQIRFGEIDPSLMRLNLSVYA 881  
 Db 841 CAGPVCDCCKRNSDVMDCVILDDGGFLMANHDDYTNIQIRFGEIDPSLMRLNLSVYA 900  
 QY 882 FNKSYDQSYCEPAGAPKOGAGHRSAYVPSVADIIQIGWATAAAWSILOQFLLSLTFPR 941  
 Db 901 FNKSYDQSYCEPAGAPKOGAGHRSAYVPSVADIIQIGWATAAAWSILOQFLLSLTFPR 960  
 QY 942 LLEAVEMEDDDFTASLSKOSCTEQTYFFDNDSKFSFSGVLDGCGNCRIFHGEKLMNTNL 1001  
 Db 961 LLEAVEMEDDDFTASLSKOSCTEQTYFFDNDSKFSFSGVLDGCGNCRIFHGEKLMNTNL 1020  
 QY 1002 IFIMVESKGTCTCDTRL 1018  
 Db 1021 IFIMVESKGTCTCDTRL 1037  
 RESULT 15  
 AAR71013  
 ID AAR71013 standard; Protein; 1086 AA.  
 AC AAR71013;  
 XX AAR71013;  
 DT 01-DEC-1995 (first entry)  
 DE Human neuronal calcium channel subunit alpha 2c.  
 XX Calcium channel subunit; antagonist; agonist; diagnosis;  
 KW Lambert Eaton Syndrome.  
 XX Homo sapiens.  
 OS W09504822-A.  
 PN 16-FEB-1995.  
 PD 11-AUG-1994; 94WO-0509230.  
 PF 11-AUG-1993; 93US-0105536.  
 PR 05-NOV-1993; 93US-0149097.  
 XX (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.  
 PA Ellis SB, Gillespie A, Harpold MM, McCue AF, Williams ME;  
 -PI

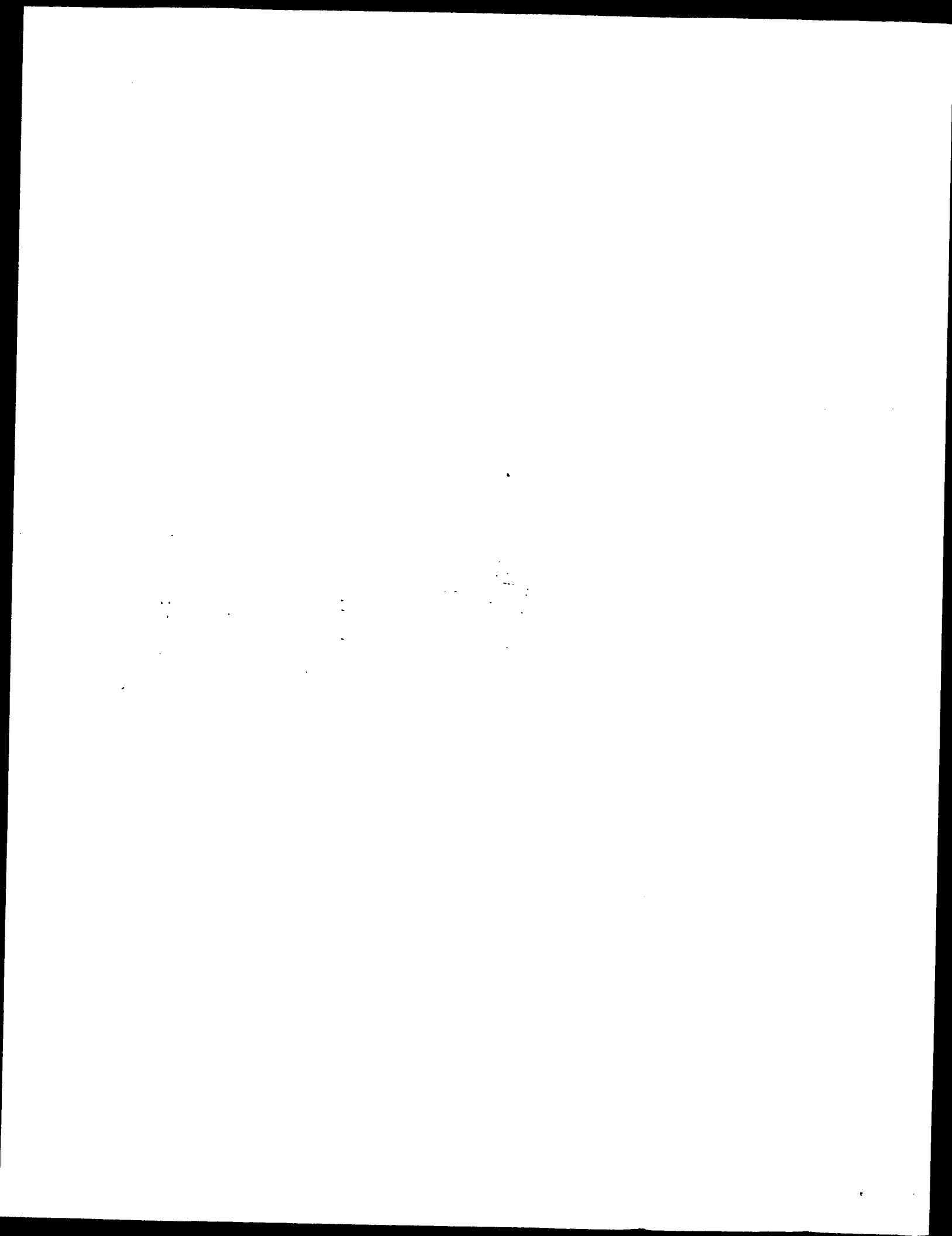
DR WPI; 1995-090900/12.  
 DR N-PSDB; AAQ84667.  
 PT DNA encoding human calcium channel sub-unit(s) - used for  
 PT developing prods. for studying calcium channels, e.g. for  
 PT obtaining agonists and antagonists  
 XX Disclosure; Page 237-242; 285pp; English.  
 PS Human neuronal alpha 2 coding sequence (AAQ84664) transcript is  
 XX differentially processed in skeletal muscle, aorta, and CNS in  
 CC the region corresp. to nt 1595-1942 of AAQ84664 in each of the  
 CC tissues. Five alternatively spliced variant transcripts that differ  
 CC in the presence or absence of one to three different portions of  
 CC this region. There are three sequences involved (see AAQ84664 FT  
 CC and AAQ84665 FT), sequence 1, sequence 2 and sequence 3. The five  
 CC alpha 2 encoding transcripts from the different tissues include  
 CC different combinations of the three sequences, except for one of  
 CC the alpha 2 transcripts expressed in aorta which lacks all three  
 CC sequences. The five alpha 2 forms identified are (1) a form that  
 CC lacks sequence 3 called alpha 2a, expressed in skeletal muscle  
 CC (2) one that lacks sequence 1 called alpha 2b, expressed in CNS  
 CC (3) one that lacks sequences 1 and 2 called alpha 2c, expressed in  
 CC aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,  
 CC expressed in aorta and (5) one that lacks sequences 1 and 3  
 CC called alpha 2e. The DNA and AA sequences of alpha 2a - alpha 2e  
 CC are set forth in AAQ84666-Q84669 and AAR71012-R71015 respectively.  
 XX SQ Sequence 1086 AA;

Query Match 99.3%; Score 5306.5; DB 16; Length 1086;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 1013; Conservative 0; Mismatches 0; Indels 5; Gaps 1;  
 QY 1 MAAGCLLALTITLFOSLLIGPSSEPPFPSPVATIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
 Db 1 MAAGCLLALTITLFOSLLIGPSSEPPFPSPVATIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
 QY 61 YEKYQDLYTVPEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDFASN 120  
 Db 61 YEKYQDLYTVPEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDFASN 120  
 QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGQISVQAAHAIPTDIYEGSTIVL 180  
 Db 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGQISVQAAHAIPTDIYEGSTIVL 180  
 QY 181 NELNWTALDEVEFKNREEDPSLLWQVFGSATGLARYYPASPVWDSRTPNKIDLYDVR 240  
 Db 181 NELNWTALDEVEFKNREEDPSLLWQVFGSATGLARYYPASPVWDSRTPNKIDLYDVR 240  
 QY 241 RPWYIOGAASPKDMLILVDYSGVSGLTLLIRTSVSEMLETSLDDDFNVASFNSAQD 300  
 Db 241 RPWYIOGAASPKDMLILVDYSGVSGLTLLIRTSVSEMLETSLDDDFNVASFNSAQD 300  
 QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSFAFQQLLNYSRANCNKIIML 360  
 Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSFAFQQLLNYSRANCNKIIML 360  
 QY 361 FTDGGEERAQEIFKNYKNDKKVRFVFSVQHNRYERGPIONWACENKGYEIPISGAIR 420  
 Db 361 FTDGGEERAQEIFKNYKNDKKVRFVFSVQHNRYERGPIONWACENKGYEIPISGAIR 420  
 QY 421 INTQYLDVLRPMVLGACAKAQVQWNTNVLDALELGLVITGTLPVFNITGQFENKTNLK 480  
 Db 421 INTQYLDVLRPMVLGACAKAQVQWNTNVLDALELGLVITGTLPVFNITGQFENKTNLK 480  
 QY 481 NQILGVMGVDVSLIEDIKRLTPRETLCPCNGYFFAIDPNGVYLLHPNLPK 540  
 Db 481 NQILGVMGVDVSLIEDIKRLTPRETLCPCNGYFFAIDPNGVYLLHPNLPK 540  
 QY 541 DFLDALENDIKVEIRNKMIDGESGKTFRTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
 Db 536 DFLDALENDIKVEIRNKMIDGESGKTFRTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 595

Tue Feb 11 13:47:49 2003

QY	601	ALVLPYTSFYIKAKLEETITQARSKGKMKDSETLKPDNFESGYTFIAPRDYCNDLKI	660
Db	596	ALVLPYTSFYIKAKLEETITQARSKGKMKDSETLKPDNFESGYTFIAPRDYCNDLKI	655
QY	661	SDNTEFLNFEFIDRKTNNPSCNADLINRVLLDAGFTNELVQYWSKQKNIKGVKAR	720
Db	656	SDNTEFLNFEFIDRKTNNPSCNADLINRVLLDAGFTNELVQYWSKQKNIKGVKAR	715
QY	721	FVVDGGITRVYPKEAGENWOENPETVEDSYKRSNDNDNYVFTAPYFNKSGPGAYESGI	780
Db	716	FVVDGGITRVYPKEAGENWOENPETVEDSYKRSNDNDNYVFTAPYFNKSGPGAYESGI	775
QY	781	MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPCAGPVCDCRNSDVMDCVI	840
Db	776	MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPCAGPVCDCRNSDVMDCVI	835
QY	841	LDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNIISVYAFNKSXDYQSVCEPGAAPKQ	900
Db	836	LDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNIISVYAFNKSXDYQSVCEPGAAPKQ	895
QY	901	GAGHSAYVPSVADILQIGWATAAASILQOFLLSLTFPRLLLEAVEMEDDDFTASLSKQ	960
Db	896	GAGHSAYVPSVADILQIGWATAAASILQOFLLSLTFPRLLLEAVEMEDDDFTASLSKQ	955
QY	961	SCITEQTYFFDNDKSFSGVLDGNCGRIFHGEKLMNTNLIFIMVESKGTCPDTRL	1018
Db	956	SCITEQTYFFDNDKSFSGVLDGNCGRIFHGEKLMNTNLIFIMVESKGTCPDTRL	1013

Search completed: February 10, 2003, 14:18:18  
Job time : 37.0366 secs





GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run On: February 10, 2003, 14:13:50 ; Search time 33.6207 Seconds  
(without alignments)  
4106.031 Million cell updates/sec

Title: US-10-090-827-14

Perfect score: 5443

Sequence: 1 MAAGCLLALTLTFLQSLLIG.....RLLIQAERTSDGNPCDMVK 1036

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_101002.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5443	100.0	1036	22 AAU01033	Human secreted sol
2	5443	100.0	1036	22 AAB62257	Porcine calcium ch
3	5443	100.0	1063	22 AAU01034	Human secreted sol
4	5443	100.0	1063	22 AAB62258	Porcine calcium ch
5	5443	100.0	1091	16 AAR71011	Human neuronal cal
6	5443	100.0	1091	19 AAW63145	Human calcium chan
7	5443	100.0	1091	21 AAB10576	Human calcium chan
8	5443	100.0	1091	22 AAU01035	Human secreted sol
9	5443	100.0	1091	22 AAB62259	Porcine calcium ch
10	5439	99.9	1091	19 AAW37879	Human calcium chan

11	5437	99.9	1091	14 AAR33553	Sequence of the al
12	5423.5	99.6	1110	19 AAW63148	Human calcium chan
13	5403.5	99.3	1086	16 AAR71013	Human neuronal cal
14	5403.5	99.3	1086	19 AAW63153	Human calcium chan
15	5403.5	99.3	1086	21 AAB10587	Human calcium chan
16	5386.5	99.0	1084	16 AAR71015	Human neuronal cal
17	5386.5	99.0	1084	19 AAW63155	Human calcium chan
18	5386.5	99.0	1084	21 AAB10589	Human calcium chan
19	5380	98.8	1036	22 AAU01029	Pig secreted solub
20	5380	98.8	1036	22 AAB62253	Porcine calcium ch
21	5380	98.8	1063	22 AAU01030	Pig secreted solub
22	5380	98.8	1063	22 AAB62254	Porcine calcium ch
23	5380	98.8	1069	22 AAU01031	Pig secreted solub
24	5380	98.8	1069	22 AAB62255	Porcine calcium ch
25	5380	98.8	1091	22 AAU01027	Pig secreted solub
26	5380	98.8	1091	22 AAB62251	Porcine calcium ch
27	5367	98.6	1103	16 AAR71012	Human neuronal cal
28	5367	98.6	1103	19 AAW63151	Human calcium chan
29	5367	98.6	1103	21 AAB10586	Human calcium chan
30	5347	98.2	1079	19 AAW63154	Human calcium chan
31	5347	98.2	1079	21 AAB10588	Human calcium chan
32	5346	98.2	1018	22 AAU01032	Human secreted sol
33	5346	98.2	1018	22 AAB62256	Porcine calcium ch
34	5341	98.1	1079	16 AAR71014	Human neuronal cal
35	5288	97.2	1018	22 AAU01028	Pig secreted solub
36	5288	97.2	1018	22 AAB62252	Porcine calcium ch
37	5229.5	96.1	1106	18 AAW37712	Rabbit skeletal ca
38	5229.5	96.1	1106	18 AAW18389	Rabbit calcium cha
39	5229.5	96.1	1106	21 AAY77545	Rabbit skeletal ca
40	5208.5	95.7	1106	16 AAR73056	Rabbit skeletal ca
41	5101.5	93.7	1100	10 AAF95844	Rabbit skeletal mus
42	2907.5	53.4	1082	22 AAU01015	Human secreted sol
43	2907.5	53.4	1082	22 AAB62239	Human calcium chan
44	2907.5	53.4	1109	22 AAU01016	Human secreted sol
45	2907.5	53.4	1109	22 AAB62240	Human calcium chan

#### ALIGNMENTS

##### RESULT 1

AAU01033  
ID AAU01033 standard; Protein; 1036 AA.

XX AAU01033;

XX 04-JUL-2001 (first entry)

DT Human secreted soluble alpha2delta calcium channel subunit #13 protein.

DE Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;  
XX alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;  
KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;  
KW filter binding assay; wheat germ lectin flashplate assay.

XX Homo sapiens.

OS WO200119870-A2.

PN 22-MAR-2001.

XX 18-SEP-2000; 2000WO-EP09137.

XX 16-SEP-1999; 99US-0397550.

XX (WARN ) WARNER LAMBERT CO.

XX Brown JP, Bertelli F;

XX WPI; 2001-235262/24.

XX N-PSDB; AAS01424.

XX Calcium channel alpha2delta subunits, useful in e.g. SPA assays,

Flashplate assays, Nickel Flashplate assays, Filter binding assays or Wheat Germ Lactin Flashplate assays -  
 Claim 31; Page 134-137; 160pp; English.

The present sequence represents human secreted calcium channel alpha2delta subunit #13 which is soluble and retains the functional characteristics of the full length or wild type alpha2delta subunit (AAU01025) from which it is derived. The invention relates to truncated alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins which retain their affinity for radioactively labelled gabapentin. The alpha2delta subunit is 1 of the components of the heteromultimeric voltage-dependent calcium channel (VDC) complexes present in neuronal and non-neuronal tissues including heart and skeletal muscle. Numerous soluble forms of the human calcium channel alpha2delta subunits (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the porcine calcium channel alpha2delta subunits (AAU01027-AAU01031) are described. The secreted soluble alpha2delta subunit may be used in assays e.g. scintillation proximity assay (SPA), flashplate, nickel flashplate, filter binding or wheat germ lectin flashplate assays to detect or measure the binding or interaction of a ligand (e.g. gabapentin, L-Norleucine, L-Allo-Isoleucine, L-methionine, L-leucine, L-isoleucine, L-Valine, Spermine and/or L-Phenylalanine) of a calcium channel alpha2delta subunit.

Sequence 1036 AA;

Query Match 100.0%; Score 5443; DB 22; Length 1036;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCILLATLTLFOSLLIGSPSEPPFSAVTIKSWDKMOEDLVTLAKTAGVGNQLVDI 60  
 DB 1 MAAGCILLATLTLFOSLLIGSPSEPPFSAVTIKSWDKMOEDLVTLAKTAGVGNQLVDI 60  
 QY 61 YEKYODLYTVEPNARQVLVEAARDEIKLLNSRKALVSLALEAEKVQAAHQWREDFASN 120  
 DB 61 YEKYODLYTVEPNARQVLVEAARDEIKLLNSRKALVSLALEAEKVQAAHQWREDFASN 120  
 QY 121 EYVYNAKDDLDPEKNDESPQSQRKPVFIEDANFGROIYQHAHAVHIPTDIYEGSTIVL 180  
 DB 121 EYVYNAKDDLDPEKNDESPQSQRKPVFIEDANFGROIYQHAHAVHIPTDIYEGSTIVL 180  
 QY 181 NELNWTSSALDEVFKKNREEDPSLWQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVR 240  
 DB 181 NELNWTSSALDEVFKKNREEDPSLWQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVR 240  
 QY 241 RPWYIQGAASPKDMLILVDVSGVSGLTCLKIRTSVSEMLETLSDDDFVNVASFNSNAQD 300  
 DB 241 RPWYIQGAASPKDMLILVDVSGVSGLTCLKIRTSVSEMLETLSDDDFVNVASFNSNAQD 300  
 QY 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEQLLNYNVSRANCKLI 360  
 DB 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEQLLNYNVSRANCKLI 360  
 QY 361 FTDGGEERAQEIFNKYKNDKKVRVFRFSVGOHNYTERGPIOWMACENKGYIYIPISGAIR 420  
 DB 361 FTDGGEERAQEIFNKYKNDKKVRVFRFSVGOHNYTERGPIOWMACENKGYIYIPISGAIR 420  
 QY 421 INTOEYLDLVGRPMVLADGAKQVQWNTNVLDALEGLVITGILPVNITGQFENKTNLK 480  
 DB 421 INTOEYLDLVGRPMVLADGAKQVQWNTNVLDALEGLVITGILPVNITGQFENKTNLK 480  
 QY 481 NQLILGVNGVDVSLDIKRLTPFTLCNPGYIYFAIDPNGVYLLHPNLQPNKPSQBPVTL 540  
 DB 481 NQLILGVNGVDVSLDIKRLTPFTLCNPGYIYFAIDPNGVYLLHPNLQPNKPSQBPVTL 540  
 QY 541 DFLDAELNDIKVIRNKMIDGSGEKTFTLVKSDQERYIDKGNRTYTWTPVNGTDYSL 600  
 DB 541 DFLDAELNDIKVIRNKMIDGSGEKTFTLVKSDQERYIDKGNRTYTWTPVNGTDYSL 600  
 QY 601 ALVLPITYSFYIYKAKLEETITQARSKKGMKMDSETLKPDPNFEESGYTFTAPRYCNDLKI 660  
 DB 601 ALVLPITYSFYIYKAKLEETITQARSKKGMKMDSETLKPDPNFEESGYTFTAPRYCNDLKI 660

DB 601 ALVLPITYSFYIYKAKLEETITQARSKKGMKMDSETLKPDPNFEESGYTFTAPRYCNDLKI 660  
 QY 661 SDNTEFLLNFEFTDRKTPNNPSCNADLINRVLLIDAGFTNELVQYWSKOKNKGVKAR 720  
 DB 661 SDNTEFLLNFEFTDRKTPNNPSCNADLINRVLLIDAGFTNELVQYWSKOKNKGVKAR 720  
 QY 721 FVWTDGGTTRYVPKAEAGENWQENPETEDSFYKRSKLDNDNVFTAPYFNKSGPGAYESGI 780  
 DB 721 FVWTDGGTTRYVPKAEAGENWQENPETEDSFYKRSKLDNDNVFTAPYFNKSGPGAYESGI 780  
 QY 781 MYSKAVEIYIQGKLLKPAVVGIIKIDVNSWTFNFKTSIRDPACGVCDCCKRNSDVMDCVI 840  
 DB 781 MYSKAVEIYIQGKLLKPAVVGIIKIDVNSWTFNFKTSIRDPACGVCDCCKRNSDVMDCVI 840  
 QY 841 LDDGGFLMANHDDYTQIGRFFGEIDPSLMRHLVNI SVTAFNKS YDYSQVCEPFGAAPKQ 900  
 DB 841 LDDGGFLMANHDDYTQIGRFFGEIDPSLMRHLVNI SVTAFNKS YDYSQVCEPFGAAPKQ 900  
 QY 901 GAGHRSAYVPSVADILQIGWMTAAAWSIIQQFLLSTFFPRLLLEAVEMEDDDFTASLSKQ 960  
 DB 901 GAGHRSAYVPSVADILQIGWMTAAAWSIIQQFLLSTFFPRLLLEAVEMEDDDFTASLSKQ 960  
 QY 961 SCITEQTQYFEDNDSKFSFVLDGCGNCSRIFFHGEKLMNTNLIETIMVESKGTCPCDTRLII 1020  
 DB 961 SCITEQTQYFEDNDSKFSFVLDGCGNCSRIFFHGEKLMNTNLIETIMVESKGTCPCDTRLII 1020  
 QY 1021 QAEQTSQDGNPCDMVK 1036  
 DB 1021 QAEQTSQDGNPCDMVK 1036

# RESULT 2

AA62257 standard; Protein; 1036 AA.

AA62257;

11-JUN-2001 (first entry)

Porcine calcium channel alpha2delta subunit.

Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex; nervous system disorder; pain; epilepsy; anxiety; pig.

Sus scrofa.

WO200120336-A2.

22-MAR-2001.

18-SEP-2000; 2000WO-EP09136.

16-SEP-1999; 99US-0397549.

(WARN) WARNER LAMBERT CO.

Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;

WPI; 2001-257902/26.

N-PSDB; AAF57561.

Competitive binding assay for screening ligands which bind a cerebral cortical voltage-dependent calcium channel alpha2delta-1 subunit, where the ligands identified are useful for treating disorders of the nervous system, including pain -

Claim 8; Page 132-135; 158pp; English.

The invention relates to a new method for screening ligands which bind a cerebral cortical voltage-dependent calcium channel alpha2delta subunit, preferably alpha2delta-1 subunit. The method comprises contacting a secreted soluble recombinant alpha2delta-1 subunit with a ligand of interest and a labelled compound which binds the subunit, followed by

CC measuring the level of binding of the labelled compound to alpha2delta-1 subunit. The method is useful for screening ligands, preferably biologically active products that modulate a nervous system function, which bind a cerebral cortical voltage-dependent calcium channel alpha2delta-1 subunit. The ligands identified by the method are useful for treating disorders of the nervous system, including pain, epilepsy and anxiety. The present sequence represents a porcine calcium channel alpha2delta subunit.		CC 841 LDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLNINISYAFNKSVDYQSVCEPGAAPKQ 900	
CC	XX	QY	901 GAGHRGAYPSVADIIQIGWATAAAWSILOQFLLSLTFPRLEAVEMEDDDFTASLSKQ 960
CC	DB	DB	901 GAGHRGAYPSVADIIQIGWATAAAWSILOQFLLSLTFPRLEAVEMEDDDFTASLSKQ 960
CC	QY	QY	961 SCITEQTQYFFDNDKSFSGVLDGCGNCSRFHGEKLMNTNLFIMVESKGTGCPDTRLLI 1020
CC	DB	DB	961 SCITEQTQYFFDNDKSFSGVLDGCGNCSRFHGEKLMNTNLFIMVESKGTGCPDTRLLI 1020
QY	QY	QY	1021 QAEQTSQDGNPCDMVK 1036
DB	DB	DB	1021 QAEQTSQDGNPCDMVK 1036
RESULT 3			
AAU01034			
ID	AAU01034	standard; Protein; 1063 AA.	
XX	AC	AAU01034;	
XX	XX	04-JUL-2001 (first entry)	
DT	XX	Human secreted soluble alpha2delta calcium channel subunit #14 protein.	
XX	DE	Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;	
XX	KW	alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;	
KW	KW	gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;	
KW	XX	filter binding assay; wheat germ lectin flashplate assay.	
OS	XX	Homo sapiens.	
XX	PN	WO200119870-A2.	
XX	XX	22-MAR-2001.	
XX	PF	18-SEP-2000; 2000WO-EP09137.	
XX	XX	16-SEP-1999; 99US-0397550.	
XX	PA	(WARN ) WARNER LAMBERT CO.	
XX	PI	Brown JP, Bertelli F;	
XX	XX	WPI: 2001-235262/24.	
DR	DR	N-PSDB; AAS01425.	
XX	PT	Calcium channel alpha2delta subunits, useful in e.g. SPA assays,	
PT	PT	Flashplate assays, Nickel Flashplate assays, Filter binding assays or	
XX	XX	Wheat Germ Lectin Flashplate assays.	
PS	PS	Claim 31; Page 137-140; 160pp; English.	
XX	XX	The present sequence represents human secreted calcium channel	
CC	CC	alpha2delta subunit #14 which is soluble and retains the functional	
CC	CC	characteristics of the full length or wild type alpha2delta subunit	
CC	CC	(AAU01025) from which it is derived. The invention relates to truncated	
CC	CC	alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins	
CC	CC	which retain their affinity for the components of the heteromultimeric	
CC	CC	alpha2delta subunit is 1 of the components of a ligand (e.g. gabapentin,	
CC	CC	voltage-dependent calcium channel (VDCC) complexes present in neuronal	
CC	CC	and non-neuronal tissues including heart and skeletal muscle. Numerous	
CC	CC	soluble forms of the human calcium channel alpha2delta subunits	
CC	CC	(AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the	
CC	CC	porcine calcium channel alpha2delta subunits (AAU01027-AAU01031) are	
CC	CC	described. The secreted soluble alpha2delta subunit may be used in assays	
CC	CC	e.g. scintillation proximity assay (SPA), flashplate, nickel flashplate,	
CC	CC	filter binding or wheat germ lectin flashplate assays to detect or	
CC	CC	measure the binding or interaction of a ligand (e.g. gabapentin,	
CC	CC	L-Norleucine, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Isoleucine,	
CC	CC	L-valine, Spermine and/or L-Phenylalanine) of a calcium channel	
CC	XX	alpha2delta subunit.	

SQ Sequence 1063 AA;

Query Match 100.0%; Score 5443; DB 22; Length 1063;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLTFLQSLLLIGPSSEEPFPPSAVTIKSWDKMQEDLVTLAKTAGSGVNLVDI 60  
 DB 1 MAAGCLLALTLTFLQSLLLIGPSSEEPFPPSAVTIKSWDKMQEDLVTLAKTAGSGVNLVDI 60

QY 61 YEKYQDLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRREDFASN 120  
 DB 61 YEKYQDLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRREDFASN 120

QY 121 EVVYNAKDDLDPEKNDESPGSGRIKPVFIEDANFGROIYSQHAHVHPTDIYEGSTIVL 180  
 DB 121 EVVYNAKDDLDPEKNDESPGSGRIKPVFIEDANFGROIYSQHAHVHPTDIYEGSTIVL 180

QY 181 NELNNTSALDEVFKKNEEDPSLLWQVFGSATGLARYYPASPVWDSNRTPNKIDLYVRR 240  
 DB 181 NELNNTSALDEVFKKNEEDPSLLWQVFGSATGLARYYPASPVWDSNRTPNKIDLYVRR 240

QY 241 RPWYIQAASPKDMLILVDVSGVSGTLKLIIRTSVSSEMLTSLDDDFVNVASFNSAQD 300  
 DB 241 RPWYIQAASPKDMLILVDVSGVSGTLKLIIRTSVSSEMLTSLDDDFVNVASFNSAQD 300

QY 301 VSCFOHLVQAVNRNKKVLKDAVNNITAKITDYKKGFSFAPEQLLNVNVRANCNKIIML 360  
 DB 301 VSCFOHLVQAVNRNKKVLKDAVNNITAKITDYKKGFSFAPEQLLNVNVRANCNKIIML 360

QY 361 FTDGGEERAQIFNKYKDKKVRVFRFSVGHNYERGPQIMACENKGYEYIETPSIGAIR 420  
 DB 361 FTDGGEERAQIFNKYKDKKVRVFRFSVGHNYERGPQIMACENKGYEYIETPSIGAIR 420

QY 421 INTQYILDVLCRPMVLAGDAKAKOVNVLDALELGLVITGILPVNITGQFENKTNLK 480  
 DB 421 INTQYILDVLCRPMVLAGDAKAKOVNVLDALELGLVITGILPVNITGQFENKTNLK 480

QY 481 NOLLGVGVGVDSLEDIKRLTPRTFLCPNGYFPAIDPNGVYLLHPNLQPNKPKSQBPVTL 540  
 DB 481 NOLLGVGVGVDSLEDIKRLTPRTFLCPNGYFPAIDPNGVYLLHPNLQPNKPKSQBPVTL 540

QY 541 DFLDAELENKIKVEIRNKMIDGESGKFTFLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
 DB 541 DFLDAELENKIKVEIRNKMIDGESGKFTFLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600

QY 601 ALVLPYTFYIIKAKLEETITQARSKKGMKDSITLKPDPNFESGYTFTAPRDYCNLDKI 660  
 DB 601 ALVLPYTFYIIKAKLEETITQARSKKGMKDSITLKPDPNFESGYTFTAPRDYCNLDKI 660

QY 661 SDNNTFELNFEIDRKTNPNSCNADILNRVLDDAGFTNVLQVNSKQNKIKGVKAR 720  
 DB 661 SDNNTFELNFEIDRKTNPNSCNADILNRVLDDAGFTNVLQVNSKQNKIKGVKAR 720

QY 721 FVYTDGGITRVYPKEAGENQENPETYEDSFYKRSIDNDNYVFTAPYFNKSPGAYESGI 780  
 DB 721 FVYTDGGITRVYPKEAGENQENPETYEDSFYKRSIDNDNYVFTAPYFNKSPGAYESGI 780

QY 781 MYSKAVEIYIOGKLKPAVVGKIDVNSWIENTFTKTSIRDPKAGPVCDCKRNSDVMDCVI 840  
 DB 781 MYSKAVEIYIOGKLKPAVVGKIDVNSWIENTFTKTSIRDPKAGPVCDCKRNSDVMDCVI 840

QY 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLNIVSYAFNKSIDYQVCEPGAAPKQ 900  
 DB 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLNIVSYAFNKSIDYQVCEPGAAPKQ 900

QY 901 GAGHSAYVPSVADILQIGWATAAASILQOFLSLTFFPRLLEAVEMDDDFETASLSKQ 960  
 DB 901 GAGHSAYVPSVADILQIGWATAAASILQOFLSLTFFPRLLEAVEMDDDFETASLSKQ 960

QY 961 SCITEQTOYFFDNDKSFSGVLDGNCNRSRIFHGEKLMNTNLIIFTWBSKGTCPCDTRLLI 1020  
 DB 961 SCITEQTOYFFDNDKSFSGVLDGNCNRSRIFHGEKLMNTNLIIFTWBSKGTCPCDTRLLI 1020

QY 1021 QAEQTSDBGPNPCDMVK 1036  
 DB 1021 QAEQTSDBGPNPCDMVK 1036

RESULT 4  
 AAB62258  
 ID AAB62258 standard; Protein; 1063 AA.  
 AC AAB62258;  
 XX  
 DT 11-JUN-2001 (first entry)  
 XX Porcine calcium channel alpha2delta subunit.  
 DE  
 XX Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;  
 KW nervous system disorder; pain; epilepsy; anxiety; pig.  
 XX  
 OS Sus scrofa.  
 PN WO200120336-A2.  
 XX  
 PD 22-MAR-2001.  
 PF 18-SEP-2000; 2000WO-EP09136.  
 XX  
 PR 16-SEP-1999; 99US-0397549.  
 XX  
 PA (WARN ) WARNER LAMBERT CO.  
 XX  
 PI Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;  
 XX  
 DR WPI; 2001-257902/26.  
 N-PSDB; AAF57562.  
 XX  
 PT Competitive binding assay for screening ligands which bind a cerebral  
 cortical voltage-dependent calcium channel alpha2delta-1 subunit,  
 where the ligands identified are useful for treating disorders of the  
 nervous system, including pain -  
 XX  
 PS Claim 8; Page 135-139; 158pp; English.  
 XX  
 CC The invention relates to a new method for screening ligands which bind a  
 cerebral cortical voltage-dependent calcium channel alpha2delta subunit,  
 preferably alpha2delta-1 subunit. The method comprises contacting a  
 secreted soluble recombinant alpha2delta-1 subunit with a ligand of  
 interest and a labelled compound which binds the subunit, followed by  
 measuring the level of binding of the labelled compound to alpha2delta-1  
 subunit. The method is useful for screening ligands, preferably  
 biologically active products that modulate a nervous system function,  
 which bind a cerebral cortical voltage-dependent calcium channel  
 alpha2delta-1 subunit. The ligands identified by the method are useful  
 for treating disorders of the nervous system, including pain, epilepsy  
 and anxiety. The present sequence represents a porcine calcium channel  
 alpha2delta subunit.  
 CC  
 SQ Sequence 1063 AA;

Query Match 100.0%; Score 5443; DB 22; Length 1063;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLTFLQSLLLIGPSSEEPFPPSAVTIKSWDKMQEDLVTLAKTAGSGVNLVDI 60  
 DB 1 MAAGCLLALTLTFLQSLLLIGPSSEEPFPPSAVTIKSWDKMQEDLVTLAKTAGSGVNLVDI 60

QY 61 YEKYQDLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRREDFASN 120  
 DB 61 YEKYQDLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRREDFASN 120

QY 121 EVVYNAKDDLDPEKNDESPGSGRIKPVFIEDANFGROIYSQHAHVHPTDIYEGSTIVL 180  
 DB 121 EVVYNAKDDLDPEKNDESPGSGRIKPVFIEDANFGROIYSQHAHVHPTDIYEGSTIVL 180

```
Db 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGQISYQHAHVHPDIIYEGSTIVL 180
Qy 181 NELNWTSSALDEVEFKKNREDDPSLLMQVFGSATGLARYYPASPWDNSRTPNKKIDLYDVR 240
Db 181 NELNWTSSALDEVEFKKNREDDPSLLMQVFGSATGLARYYPASPWDNSRTPNKKIDLYDVR 240
Qy 241 RPWYIQAASPKDMLILVDVSGVSGLTCLKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
Db 241 RPWYIQAASPKDMLILVDVSGVSGLTCLKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
Qy 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEOHLLNYSRANCKIIML 360
Db 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEOHLLNYSRANCKIIML 360
Qy 361 FTDGGEERAQEIFNKYNDKKVRFVRSYVGHYERGPQIOWMACENKGYEYIIPSIGAIR 420
Db 361 FTDGGEERAQEIFNKYNDKKVRFVRSYVGHYERGPQIOWMACENKGYEYIIPSIGAIR 420
Qy 421 INTQEYLDVLGRPMVLGADKAKOVQWNTVYLDALGLVITGTLVPVNIITQFENKTNLK 480
Db 421 INTQEYLDVLGRPMVLGADKAKOVQWNTVYLDALGLVITGTLVPVNIITQFENKTNLK 480
Qy 481 NOLILGVMSVDVSLDIIKRLTFRFTLCPNGYYFAIDPNGYVLLHPNLOPKPKSQEPVTL 540
Db 481 NOLILGVMSVDVSLDIIKRLTFRFTLCPNGYYFAIDPNGYVLLHPNLOPKPKSQEPVTL 540
Qy 541 DFLDAELNDIKVEIRNKNMIDGESGKFTRTLKVSQDERYIDKGNRTYTWTVPNGTDYSL 600
Db 541 DFLDAELNDIKVEIRNKNMIDGESGKFTRTLKVSQDERYIDKGNRTYTWTVPNGTDYSL 600
Qy 601 ALVLPYISYYIAKLEETITQARSKGKMKDSEITLKPDPFESGYTFIAPRDYCNLDKI 660
Db 601 ALVLPYISYYIAKLEETITQARSKGKMKDSEITLKPDPFESGYTFIAPRDYCNLDKI 660
Qy 661 SDNTEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNVLVONYSKOKNIKGVAR 720
Db 661 SDNTEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNVLVONYSKOKNIKGVAR 720
Qy 721 FVYTDGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPAYESGI 780
Db 721 FVYTDGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPAYESGI 780
Qy 781 MYSKAVEIYIOGKLLKPAVVGLIKIDVNSWIEFTKTSIRDPGAGVCDCKRNSDVMDCVI 840
Db 781 MYSKAVEIYIOGKLLKPAVVGLIKIDVNSWIEFTKTSIRDPGAGVCDCKRNSDVMDCVI 840
Qy 841 LDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNSIVYAFNKSVDYOSVCEPAAAPQ 900
Db 841 LDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNSIVYAFNKSVDYOSVCEPAAAPQ 900
Qy 901 GAGHSAYVPSVADILQIGWATAAWSILOQFLLSLTFPRLEAVEMEDDDFTASLSQ 960
Db 901 GAGHSAYVPSVADILQIGWATAAWSILOQFLLSLTFPRLEAVEMEDDDFTASLSQ 960
Qy 961 SCITEGTOYFFONDSKSFSGVLDGNCSPHFHGEKLMNTNLIFINVESKGTCPDTRLLI 1020
Db 961 SCITEGTOYFFONDSKSFSGVLDGNCSPHFHGEKLMNTNLIFINVESKGTCPDTRLLI 1020
Qy 1021 QABQTSIDGPNPCDMVK 1036
Db 1021 QABQTSIDGPNPCDMVK 1036

RESULT 5
ID AAR71011
XX AAR71011 standard; Protein; 1091 AA.
AC AAR71011;
XX
DT 01-DEC-1995 (first entry)
XX
DE Human neuronal calcium channel subunit alpha 2b.
XX
```

```
Kw Calcium channel subunit; antagonist; agonist; diagnosis;
KX Lambert Eaton Syndrome.
OS Homo sapiens.
PN W09504822-A.
XX
PD 16-FEB-1995.
XX
PF 11-AUG-1994; 94WO-US09230.
XX
PR 11-AUG-1993; 93US-0105536.
PR 05-NOV-1993; 93US-0149097.
XX
PA (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
XX
PI Ellis SB, Gillespie A, Harpold MM, Mccue AF, Williams ME;
XX WPI; 1995-090900/12.
DR N-PSDB; AAQ84664.
XX
PT DNA encoding human calcium channel sub-unit(s) - used for
PT developing prods. for studying calcium channels, e.g. for
XX obtaining agonists and antagonists
PS Disclosure; Page 166-171; 285pp; English.
XX
CC Human neuronal alpha 2 coding sequence (AAQ84664) transcript is
CC differentially processed in skeletal muscle, aorta, and CNS in
CC the region corresp. to nt 1595-1942 of AAQ84664 in each of the
CC tissues. Five alternatively spliced variant transcripts that differ
CC in the presence or absence of one to three different portions of
CC this region. There are three sequences involved (see AAQ84664 FT
CC and AAQ84665 FT), sequence 1, sequence 2 and sequence 3. The five
CC alpha 2 encoding transcripts from the different tissues include
CC different combinations of the three sequences, except for one of
CC the alpha 2 transcripts expressed in aorta which lacks all three
CC sequences. The five alpha 2 forms identified are (1) a form that
CC lacks sequence 3 called alpha 2a, expressed in skeletal muscle
CC (2) one that lacks sequence 1 called alpha 2b, expressed in CNS
CC (3) one that lacks sequences 1 and 2 called alpha 2c, expressed in
CC aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,
CC expressed in aorta and (5) one that lacks sequences 1 and 3
CC called alpha 2e.
XX
SQ Sequence 1091 AA;
```

Query Match 100.0%; Score 5443; DB 16; Length 1091;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 MAAGCLLALTTLFQSLIGSPSEPPPSAVTIKSWDKMOEDLVTLAKTASGVNQLVDI 60
Db 1 MAAGCLLALTTLFQSLIGSPSEPPPSAVTIKSWDKMOEDLVTLAKTASGVNQLVDI 60
Qy 61 YEKYQDLYTVEPNARQIVEAARDIEKLSNRKALVSLALEAEKQVAAHQWREDFASN 120
Db 61 YEKYQDLYTVEPNARQIVEAARDIEKLSNRKALVSLALEAEKQVAAHQWREDFASN 120
Qy 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGQISYQHAHVHPDIIYEGSTIVL 180
Db 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGQISYQHAHVHPDIIYEGSTIVL 180
Qy 181 NELNWTSSALDEVEFKKNREDDPSLLMQVFGSATGLARYYPASPWDNSRTPNKKIDLYDVR 240
Db 181 NELNWTSSALDEVEFKKNREDDPSLLMQVFGSATGLARYYPASPWDNSRTPNKKIDLYDVR 240
Qy 241 RPWYIQAASPKDMLILVDVSGVSGLTCLKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
Db 241 RPWYIQAASPKDMLILVDVSGVSGLTCLKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
Qy 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEOHLLNYSRANCKIIML 360
Db 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEOHLLNYSRANCKIIML 360
```

Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSEAFQQLLNVNVRANCNKIIML 360  
 QY 361 FTDGGERAQEIEFNKYNKDKKVRFRFSVQOHNYERGPQIOWMACENKGYIIEIPISGAIR 420  
 Db 361 FTDGGERAQEIEFNKYNKDKKVRFRFSVQOHNYERGPQIOWMACENKGYIIEIPISGAIR 420  
 QY 421 INTQEYLDVLRPMVLGADKAKQVQWNTVYLDALGLGLVITGTLPVFNITGOFENKTNLK 480  
 Db 421 INTQEYLDVLRPMVLGADKAKQVQWNTVYLDALGLGLVITGTLPVFNITGOFENKTNLK 480  
 QY 481 NQLILGVMGVDSLEIDIKRLTFRFTLCPCNGYFAIDPNCYVLLHPNLPKPKSQEPVTL 540  
 Db 481 NQLILGVMGVDSLEIDIKRLTFRFTLCPCNGYFAIDPNCYVLLHPNLPKPKSQEPVTL 540  
 QY 541 DFLDAELENDIKVEIRNKMIDGESGKFTTLVKSDODERYIDKGNRTYTWTPVNGTDSL 600  
 Db 541 DFLDAELENDIKVEIRNKMIDGESGKFTTLVKSDODERYIDKGNRTYTWTPVNGTDSL 600  
 QY 601 ALVLPYTFYIIKAKLEETITQARSKKMKDSETLKPDNFESGYTFIAPRDYCNLKI 660  
 Db 601 ALVLPYTFYIIKAKLEETITQARSKKMKDSETLKPDNFESGYTFIAPRDYCNLKI 660  
 QY 661 SDNTEFLNFNEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQYWSKQKNIKGVKAR 720  
 Db 661 SDNTEFLNFNEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQYWSKQKNIKGVKAR 720  
 QY 721 FVYTDGGITRVYPKEAGENQENPETYEDSFYKRSIDNDNVYFTAPYFNKSGPGAYESGI 780  
 Db 721 FVYTDGGITRVYPKEAGENQENPETYEDSFYKRSIDNDNVYFTAPYFNKSGPGAYESGI 780  
 QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIEFTKTSIRDPKAGPVCDCRNSDVMDCVI 840  
 Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIEFTKTSIRDPKAGPVCDCRNSDVMDCVI 840  
 QY 841 LDGCGFLLMANHDDYTNOIGRFFGEIDPSLMRHLNIVSYAFNKSIDYQSVCEPGAAPKQ 900  
 Db 841 LDGCGFLLMANHDDYTNOIGRFFGEIDPSLMRHLNIVSYAFNKSIDYQSVCEPGAAPKQ 900  
 QY 901 GAGHSAYVPSVADILQIGWATAAASWTLQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
 Db 901 GAGHSAYVPSVADILQIGWATAAASWTLQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
 QY 961 SCITQTOYFFDNDKSFSGVLDGNCNCRIFHGEKIMNTNLIIFIMVESKGTCPDTRLLI 1020  
 Db 961 SCITQTOYFFDNDKSFSGVLDGNCNCRIFHGEKIMNTNLIIFIMVESKGTCPDTRLLI 1020  
 QY 1021 QAEQTSQGNPCDMVK 1036  
 Db 1021 QAEQTSQGNPCDMVK 1036

## RESULT 6

AAW63145  
 ID AAW63145 standard; Protein; 1091 AA.

XX AC AAW63145;

XX DF 12-OCT-1998 (first entry)

XX DE Human calcium channel alpha-2 subunit.

XX KW Alpha-2 subunit; human; calcium channel; assay; detection;  
 characterisation; Lambert Eaton Syndrome; LES; diagnosis.

XX OS Homo sapiens.

XX PN US5792846-A.

XX PD 11-AUG-1998.

XX PF 31-MAY-1995; 95US-0455543.

XX PR 04-APR-1994; 94US-0223305.

PR 04-APR-1988; 88US-0176899.  
 PR 04-APR-1989; 89US-0603751.  
 PR 04-APR-1989; 89WO-US01408.  
 PR 20-FEB-1990; 90US-0482384.  
 PR 30-NOV-1990; 90US-0620250.  
 PR 15-AUG-1991; 91US-0745206.  
 PR 31-MAY-1995; 95US-0455543.  
 XX (SIBI-) SIBIA NEUROSCIENCES INC.

XX Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;  
 Williams ME;

DR WPT; 1998-456192/39.  
 DR N-PSDB; AAV42689.

PT DNA encoding human calcium channel alpha 1B subunit protein -  
 useful for recombinant production of the channel for screening of  
 its modulators, and diagnosis of Lambert Eaton Syndrome  
 XX Claim 4; Columns 283-288; 166pp; English.

CC The present sequence represents the alpha-2 subunit of a human calcium  
 channel. Calcium channels are membrane-spanning, multi-subunit proteins  
 that allow controlled entry of calcium ions into cells. This leads  
 to depolarisation events required for muscle contraction. The recombinant  
 subunit, when expressed with nucleic acids encoding the complete calcium  
 channel, can be used in assays for the detection and characterisation of  
 compounds that modulate the channel. The DNA encoding the subunits can  
 be alternatively spliced when transcribed, giving more than one form of  
 the protein from the same transcript, each having slightly different  
 properties. In addition, the reactivity of the alpha 1 subunit with IgG  
 molecules from the serum of an individual with Lambert Eaton Syndrome  
 (LES) can be used as a diagnostic for the disease.

XX Sequence 1091 AA;

Query Match 100.0%; Score 5443; DB 19; Length 1091;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLTFLQSLIGPSEEPFPPSAVTIKSWDKMQEDLVTLAKTASGVNOLVDI 60  
 Db 1 MAAGCLLALTLTFLQSLIGPSEEPFPPSAVTIKSWDKMQEDLVTLAKTASGVNOLVDI 60

QY 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLAEAKVQAAHQWREDFASN 120  
 Db 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLAEAKVQAAHQWREDFASN 120

QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISYQHAHVHPTDIYEGSTIVL 180  
 Db 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISYQHAHVHPTDIYEGSTIVL 180

QY 181 NELNWT SALDVEFKNREEDPSLLQVFGSATGLARYYPASPMWDSRTPNKIDLYDVR 240  
 Db 181 NELNWT SALDVEFKNREEDPSLLQVFGSATGLARYYPASPMWDSRTPNKIDLYDVR 240

QY 241 RPWYIQGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETISDDDFVNVASFNSNAQD 300  
 Db 241 RPWYIQGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETISDDDFVNVASFNSNAQD 300

QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSEAFQQLLNVNVRANCNKIIML 360  
 Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSEAFQQLLNVNVRANCNKIIML 360

QY 361 FTDGGERAQEIEFNKYNKDKKVRFRFSVQOHNYERGPQIOWMACENKGYIIEIPISGAIR 420  
 Db 361 FTDGGERAQEIEFNKYNKDKKVRFRFSVQOHNYERGPQIOWMACENKGYIIEIPISGAIR 420

QY 421 INTQEYLDVLRPMVLGADKAKQVQWNTVYLDALGLGLVITGTLPVFNITGOFENKTNLK 480  
 Db 421 INTQEYLDVLRPMVLGADKAKQVQWNTVYLDALGLGLVITGTLPVFNITGOFENKTNLK 480

QY 481 NOLLGVMGVDVSLDIKRLTPRFTLCPNGYFFAIDPNGYVLLHPLNPKSPQEPVTL 540  
 DB 481 NOLLGVMGVDVSLDIKRLTPRFTLCPNGYFFAIDPNGYVLLHPLNPKSPQEPVTL 540  
 QY 541 DFLDAELENDIKVEIRKMKIDGSGEKTFTLVKSODERYIDKGNRTYTWTVPVNGDYSL 600  
 DB 541 DFLDAELENDIKVEIRKMKIDGSGEKTFTLVKSODERYIDKGNRTYTWTVPVNGDYSL 600  
 QY 601 ALVLPYTFYFIKAKLEETITOARSKKGMKDSKSETLKPONFEESGYTFIAPRDYCNLDKI 660  
 DB 601 ALVLPYTFYFIKAKLEETITOARSKKGMKDSKSETLKPONFEESGYTFIAPRDYCNLDKI 660  
 QY 661 SDNTEFLNFEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQYWSKQKNIKGVKAR 720  
 DB 661 SDNTEFLNFEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQYWSKQKNIKGVKAR 720  
 QY 721 FVYTDGGITRVYKPEAGENQENPEYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
 DB 721 FVYTDGGITRVYKPEAGENQENPEYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
 QY 781 MVS KAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPACAGPVCDCKRNSDVMDCVI 840  
 DB 781 MVS KAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPACAGPVCDCKRNSDVMDCVI 840  
 QY 841 LDGGLFLMANHDDYINQIGRFFGEIDPSLMRHLVNIYAFNKSVDYOSVCEPGAAPKQ 900  
 DB 841 LDGGLFLMANHDDYINQIGRFFGEIDPSLMRHLVNIYAFNKSVDYOSVCEPGAAPKQ 900  
 QY 901 GAGHSAYVPSVADILQIGHWATAAASILQOFLLSLTPRLLAEVEMEDDDFTASLSKQ 960  
 DB 901 GAGHSAYVPSVADILQIGHWATAAASILQOFLLSLTPRLLAEVEMEDDDFTASLSKQ 960  
 QY 961 SCITEQTYFFDNDKSFSGVLDCGNCRSIFHGEKLMNTNLIFIMVESKGTCPDPRLLI 1020  
 DB 961 SCITEQTYFFDNDKSFSGVLDCGNCRSIFHGEKLMNTNLIFIMVESKGTCPDPRLLI 1020  
 QY 1021 QAEQTS DGPNC DMVK 1036  
 DB 1021 QAEQTS DGPNC DMVK 1036

RESULT 7  
 AAB10576  
 ID AAB10576 standard; Protein; 1091 AA.  
 AC AAB10576;  
 XX  
 XX  
 XX 22-DEC-2000 (first entry)  
 XX  
 DE Human calcium channel alpha-2 subunit protein.  
 XX  
 KW Human; calcium channel; calcium channel subunit; diagnosis;  
 KW Lambert Eaton Syndrome; calcium channel subunit alpha-2.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6096514-A.  
 XX  
 PD 01-AUG-2000.  
 XX  
 PF 25-MAY-1995; 95US-0450562.  
 XX  
 PR 04-APR-1988; 88US-0176899.  
 PR 02-FEB-1990; 90US-0482384.  
 PR 08-NOV-1990; 90US-0603751.  
 PR 30-NOV-1990; 90US-0620250.  
 PR 15-AUG-1991; 91US-0745206.  
 PR 10-APR-1992; 92US-0868354.  
 PR 13-JUL-1992; 92US-0914231.  
 PR 11-AUG-1993; 93US-0105536.  
 PR 05-NOV-1993; 93US-0149097.  
 PR 07-FEB-1994; 94US-0193078.  
 PR 04-APR-1994; 94US-0223305.

PR 11-AUG-1994; 94US-0290012.  
 PR 23-SEP-1994; 94US-0311363.  
 PR 28-SEP-1994; 94US-0314083.  
 PR 07-NOV-1994; 94US-0336257.  
 PR 13-MAR-1995; 95US-0404950.  
 XX (SIBI-) SIBIA NEUROSCIENCES INC.  
 XX  
 PI Ellis SB, Williams ME, McCue AF, Harpold MM;  
 XX  
 DR WPI; 2000-548230/50.  
 DR N-PSDB; AAA71707.  
 XX  
 PT Human calcium channel beta subunit polynucleotides, useful for  
 PT producing recombinant eukaryotic cells and for diagnosing Lambert Eaton  
 PT Syndrome -  
 XX  
 PS Example IV; Column 135-144; 153pp; English.  
 XX  
 CC This invention describes a novel isolated DNA molecule (I) comprising a  
 CC sequence encoding a beta3-1 subunit of a human calcium channel.  
 CC Nucleic acid probes comprising 14-30 contiguous nucleotides of  
 CC beta3 subunit encoding DNA are useful for isolation and cloning of  
 CC calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that  
 CC express heterologous calcium channel are useful for identifying compounds  
 CC that modulate calcium channel activity and in assays for identifying  
 CC agonists and antagonists of calcium channel activity in humans. Human  
 CC calcium channel subunit or eukaryotic cells expressing the channel are  
 CC useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This  
 CC sequence represents the human calcium channel alpha-2 subunit which is  
 CC described in the method of the invention.  
 XX  
 SQ Sequence 1091 AA;  
 Query Match 100.0%; Score 5443; DB 21; Length 1091;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAAGCLLALTTLFQSLIGPSSEPPFSAVTIKSWDKMQEDLVTLAKTAGVGNQLYDI 60  
 DB 1 MAAGCLLALTTLFQSLIGPSSEPPFSAVTIKSWDKMQEDLVTLAKTAGVGNQLYDI 60  
 QY 61 YEKYQDLYTVEPNNAQQLVETAAARDIEKLLNSRKALVSLALEAEKVQAAHQWREDFASN 120  
 DB 61 YEKYQDLYTVEPNNAQQLVETAAARDIEKLLNSRKALVSLALEAEKVQAAHQWREDFASN 120  
 QY 121 EVVYTNAKDDLDPKNDSEPGSQRIKPVFIEDANFGROISYOHAAVHIPTDIYEGSTIVL 180  
 DB 121 EVVYTNAKDDLDPKNDSEPGSQRIKPVFIEDANFGROISYOHAAVHIPTDIYEGSTIVL 180  
 QY 181 NELNWTSAIDDEVFKKNREEDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240  
 DB 181 NELNWTSAIDDEVFKKNREEDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240  
 QY 241 RPWYIQAASPKDMLILVDVSGSVSGLTKLIRTSVSEMLETLSDDDFVNVASFNSNAQD 300  
 DB 241 RPWYIQAASPKDMLILVDVSGSVSGLTKLIRTSVSEMLETLSDDDFVNVASFNSNAQD 300  
 QY 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFEQLLNYSRANCNKIIML 360  
 DB 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFEQLLNYSRANCNKIIML 360  
 QY 361 FTDGGEERAQAEIFNKYKDKKVRVFRFSGVGHNYERGFQIWMACENKGYEIEFSIGAIR 420  
 DB 361 FTDGGEERAQAEIFNKYKDKKVRVFRFSGVGHNYERGFQIWMACENKGYEIEFSIGAIR 420  
 QY 421 INTQEYLDVLGRPMVLADGAKAQVQWNTVYLDALGLVITGTLPVFNITQGFENKTNLK 480  
 DB 421 INTQEYLDVLGRPMVLADGAKAQVQWNTVYLDALGLVITGTLPVFNITQGFENKTNLK 480  
 QY 481 NOLIILGVMGVDVSLDIKRLTPRFTLCPNGYFFAIDPNGYVLLHPLNPKSPQEPVTL 540  
 DB 481 NOLIILGVMGVDVSLDIKRLTPRFTLCPNGYFFAIDPNGYVLLHPLNPKSPQEPVTL 540





QY 661 SDNTEFLNNEFIDRKTNNPNSNADLINRVLLDAGFTNELVQYWSKQKNIKGVKAR 720  
 DB 661 SDNTEFLNNEFIDRKTNNPNSNADLINRVLLDAGFTNELVQYWSKQKNIKGVKAR 720  
 QY 721 FVVTGGITRVYPKEAGENWQENPETEYDSFYKRSLDNDNVFTAPYFNKSGPGAYESGI 780  
 DB 721 FVVTGGITRVYPKEAGENWQENPETEYDSFYKRSLDNDNVFTAPYFNKSGPGAYESGI 780  
 QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWNIENFTKTSIRDPKAGVPCDCKRNSDVMDCVI 840  
 DB 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWNIENFTKTSIRDPKAGVPCDCKRNSDVMDCVI 840  
 QY 841 LDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNIISYAFNKSIDYQSCVCEPGAAPKQ 900  
 DB 841 LDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNIISYAFNKSIDYQSCVCEPGAAPKQ 900  
 QY 901 GAGHSAYVPSVADILQIGWATAAASWTLQOFLLSLTFPRLLAEVEMEDDDFTASLSKQ 960  
 DB 901 GAGHSAYVPSVADILQIGWATAAASWTLQOFLLSLTFPRLLAEVEMEDDDFTASLSKQ 960  
 QY 961 SCITTEQTOYFFNDKSFSGVLDGNCNSRIFPHGEKLMNTNLIIFINVESKGTCPDTRLLI 1020  
 DB 961 SCITTEQTOYFFNDKSFSGVLDGNCNSRIFPHGEKLMNTNLIIFINVESKGTCPDTRLLI 1020  
 QY 1021 QAEQTSDBGPNPCDMVK 1036  
 DB 1021 QAEQTSDBGPNPCDMVK 1036

## RESULT 9

AAB62259  
 ID AAB62259 standard; Protein: 1091 AA.

AC AAB62259;  
 XX 11-JUN-2001 (first entry)

XX Porcine calcium channel alpha2delta subunit.  
 XX Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;  
 KW nervous system disorder; pain; epilepsy; anxiety; pig.  
 XX  
 OS Sus scrofa.  
 XX WO200120336-A2.  
 XX 22-MAR-2001.  
 XX 18-SEP-2000; 2000WO-EP09136.  
 XX 16-SEP-1999; 99US-0397549.  
 XX (WARN ) WARNER LAMBERT CO.  
 XX Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;  
 PI N-PSDB; AAF57563.  
 DR WPI; 2001-257902/26.  
 XX Competitive binding assay for screening ligands which bind a cerebral  
 PT cortical voltage-dependent calcium channel alpha2delta-1 subunit,  
 PT where the ligands identified are useful for treating disorders of the  
 PT nervous system, including pain -  
 XX Claim 7; Page 139-142; 158pp; English.  
 XX The invention relates to a new method for screening ligands which bind a  
 CC cerebral cortical voltage-dependent calcium channel alpha2delta subunit,  
 CC preferably alpha2delta-1 subunit. The method comprises contacting a  
 CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of  
 CC interest and a labelled compound which binds the subunit, followed by  
 CC measuring the level of binding of the labelled compound to alpha2delta-1  
 CC subunit. The method is useful for screening ligands, preferably

CC biologically active products that modulate a nervous system function,  
 CC which bind a cerebral cortical voltage-dependent calcium channel  
 CC alpha2delta-1 subunit. The ligands identified by the method are useful  
 CC for treating disorders of the nervous system, including pain, epilepsy  
 CC and anxiety. The present sequence represents a porcine calcium channel  
 CC alpha2delta subunit.  
 XX  
 SQ Sequence 1091 AA;

Query Match 100.0%; Score 5443; DB 22; Length 1091;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLTLFQSLIGSPSEPPSAVTIKSWYDKMOEDLVTAKTASGVNQLVDI 60  
 DB 1 MAAGCLLALTLTLFQSLIGSPSEPPSAVTIKSWYDKMOEDLVTAKTASGVNQLVDI 60  
 QY 61 YEKQDLYTTPNNARQIVETAAARDIEKLLSNRSKALVSLALEAEKQVAAHQRREDFASN 120  
 DB 61 YEKQDLYTTPNNARQIVETAAARDIEKLLSNRSKALVSLALEAEKQVAAHQRREDFASN 120  
 QY 121 EVYVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRIQISYQHAHVHIPTDIYEGSTIVL 180  
 DB 121 EVYVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRIQISYQHAHVHIPTDIYEGSTIVL 180  
 QY 181 NELNMTSALDEVFKKREEDPSLLQVFGSATGLARYYPASPPWVDSNRTPNKIDLYDVR 240  
 DB 181 NELNMTSALDEVFKKREEDPSLLQVFGSATGLARYYPASPPWVDSNRTPNKIDLYDVR 240  
 QY 241 RPWYIOGAASPKDMLLDVDSGVSGLTLKLI RTSVSEMLETSDDDDFVNVASFNSNAQD 300  
 DB 241 RPWYIOGAASPKDMLLDVDSGVSGLTLKLI RTSVSEMLETSDDDDFVNVASFNSNAQD 300  
 QY 301 VSCFQHLVQANVRNKVKLDVNNITAKGIDYKGFSAFEQLLNYSRANCNKIIML 360  
 DB 301 VSCFQHLVQANVRNKVKLDVNNITAKGIDYKGFSAFEQLLNYSRANCNKIIML 360  
 QY 361 FTDGGEERAQEIFNKNKDKKVRFRFVSQGHNYERGPIONMACENKGYEIPESIGAIR 420  
 DB 361 FTDGGEERAQEIFNKNKDKKVRFRFVSQGHNYERGPIONMACENKGYEIPESIGAIR 420  
 QY 421 INTOEYLDVLRPMVLGADKAKQVQWNTNYLDLELGLVITGTLPVENITGQFENKTNLK 480  
 DB 421 INTOEYLDVLRPMVLGADKAKQVQWNTNYLDLELGLVITGTLPVENITGQFENKTNLK 480  
 QY 481 NQLILGVMGVDVSLIEDIKRLTPRETLCPNGYFFAIDPNGYVLLHPNLPKPKSQEPVTL 540  
 DB 481 NQLILGVMGVDVSLIEDIKRLTPRETLCPNGYFFAIDPNGYVLLHPNLPKPKSQEPVTL 540  
 QY 541 DFLDAELENDIKVEIRNKMIDGESGEKTRFLVKSQDERYIDKGNRTYTTWTPVNGTDYSL 600  
 DB 541 DFLDAELENDIKVEIRNKMIDGESGEKTRFLVKSQDERYIDKGNRTYTTWTPVNGTDYSL 600  
 QY 601 ALVLPYTSFYIYKAKLEETITQARKSKGKMDSETLKPDNFEESGYTFIAPRDCNDLKI 660  
 DB 601 ALVLPYTSFYIYKAKLEETITQARKSKGKMDSETLKPDNFEESGYTFIAPRDCNDLKI 660  
 QY 661 SDNTEFLNNEFIDRKTNNPNSNADLINRVLLDAGFTNELVQYWSKQKNIKGVKAR 720  
 DB 661 SDNTEFLNNEFIDRKTNNPNSNADLINRVLLDAGFTNELVQYWSKQKNIKGVKAR 720  
 QY 721 FVVTGGITRVYPKEAGENWQENPETEYDSFYKRSLDNDNVFTAPYFNKSGPGAYESGI 780  
 DB 721 FVVTGGITRVYPKEAGENWQENPETEYDSFYKRSLDNDNVFTAPYFNKSGPGAYESGI 780  
 QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWNIENFTKTSIRDPKAGVPCDCKRNSDVMDCVI 840  
 DB 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWNIENFTKTSIRDPKAGVPCDCKRNSDVMDCVI 840  
 QY 841 LDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNIISYAFNKSIDYQSCVCEPGAAPKQ 900  
 DB 841 LDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNIISYAFNKSIDYQSCVCEPGAAPKQ 900

QY 901 GAGHSAYVPSVADILQIGWATAAASWILQOFLLSLTPRLLLEAVEMEDDDFTASLSKQ 960  
 DB 901 GAGHSAYVPSVADILQIGWATAAASWILQOFLLSLTPRLLLEAVEMEDDDFTASLSKQ 960  
 QY 961 SCITEQTOFFNDKSKFSVGLDCCGNSRIFHGEKLMNTNLFIMVESKGTCPDTRLII 1020  
 DB 961 SCITEQTOFFNDKSKFSVGLDCCGNSRIFHGEKLMNTNLFIMVESKGTCPDTRLII 1020  
 QY 1021 QAEQTSQDGNPCDMVK 1036  
 DB 1021 QAEQTSQDGNPCDMVK 1036

RESULT 10  
 AAW37879  
 ID AAW37879 standard; Protein; 1091 AA.  
 XX  
 AC AAW37879;  
 XX  
 DT 28-AUG-1998 (first entry)  
 DE Human calcium channel a2d subunit.  
 DE  
 XX Calcium channel; human; central nervous system disorder;  
 KW Lambert-Eaton syndrome; diagnosis; therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9811131-A2.  
 XX  
 XX 19-MAR-1998.  
 PD  
 XX  
 PF 11-SEP-1997; 97WO-US16146.  
 XX  
 XX 16-SEP-1996; 96US-0713118.  
 XX  
 PA (AMHP ) AMERICAN HOME PROD CORP.  
 XX  
 PI Chen ARS, Franco R, Shuey DJ;  
 XX  
 DR WPI; 1998-207325/18.  
 DR N-PSDB; AAV29060.  
 XX  
 PT DNA encoding human neuronal calcium channel subunit(s) - useful for  
 PT diagnosis of and treatment of central nervous system disorders, e.g.  
 PT Lambert-Eaton syndrome  
 XX  
 PS Disclosure; Fig 2; 89pp; English.  
 XX  
 CC This polypeptide comprises the a2d subunit of the human neuronal  
 CC calcium channel. cDNA clones (see AAY29059-61) encoding the a1b  
 CC subunit (see AAW37878), the a2d subunit and a b3 subunit (see AAW37880)  
 CC have been isolated. These have been inserted into expression  
 CC vectors and are stably expressed in transformed cell lines. The  
 CC transformed cells show omega-conotoxin GVIA binding activity,  
 CC and omega-conotoxin GVIA toxin sensitive potassium-stimulated  
 CC calcium uptake, indicating that the proteins expressed by the  
 CC clones are capable of forming a functioning calcium channel.  
 CC Nucleic acids encoding the 3 subunits, as well as vectors, host  
 CC cells and methods of isolating nucleic acids encoding related  
 CC calcium channels are disclosed. Fusion proteins incorporating the  
 CC subunit proteins, antibodies, and assays for identifying agents  
 CC that modulate calcium channel activity are also provided. Such  
 CC agents can be used to treat certain central nervous system  
 CC disorders by altering calcium channel activity. Methods of  
 CC diagnosing diseases associated with particular calcium channels,  
 CC such as Lambert-Eaton syndrome, are disclosed.  
 XX  
 SQ Sequence 1091 AA;

Query Match 99.9%; Score 5439; DB 19; Length 1091;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1035; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLTLFQSLIGPSSPEPPSAVTIKSWDKMQEDLVLTKTASGVNOLVDI 60  
 DB 1 MAAGCLLALTLTLFQSLIGPSSPEPPSAVTIKSWDKMQEDLVLTKTASGVNOLVDI 60  
 QY 61 YEKYQDLYTVEPNARQLVEIAAARDIEKLLSNRSKALVSLALEAEKVAQAAHOWREDFASN 120  
 DB 61 YEKYQDLYTVEPNARQLVEIAAARDIEKLLSNRSKALVSLALEAEKVAQAAHOWREDFASN 120  
 QY 121 EVVYVNAKDDLDPEKNDSEPGSQRIKPVFIEDANFRGQISYQHAHVHPTDIYEGSTIVL 180  
 DB 121 EVVYVNAKDDLDPEKNDSEPGSQRIKPVFIEDANFRGQISYQHAHVHPTDIYEGSTIVL 180  
 QY 181 NELNWTSALEDEVEFKKNEEDPSLLWQVFGSATGLARYYPASPMVDNSRTPNKIDLDVDRR 240  
 DB 181 NELNWTSALEDEVEFKKNEEDPSLLWQVFGSATGLARYYPASPMVDNSRTPNKIDLDVDRR 240  
 QY 241 RPWYIOGAASPKDMLILVDVSGSVGLTLKLI RTSVSEMLETSLDDDFVNVASFNSNAQD 300  
 DB 241 RPWYIOGAASPKDMLILVDVSGSVGLTLKLI RTSVSEMLETSLDDDFVNVASFNSNAQD 300  
 QY 301 VSCFOHLVQANVRNKKVLDKDAVNNTAKGITYDKKGFSAFAEQLLNNVSRANCNKIIML 360  
 DB 301 VSCFOHLVQANVRNKKVLDKDAVNNTAKGITYDKKGFSAFAEQLLNNVSRANCNKIIML 360  
 QY 361 FTDGGERAQEIEFNKYNKDKKVRFRFSVGOHNYERGPIQWMACENKGYEYIEPSIGAIR 420  
 DB 361 FTDGGERAQEIEFNKYNKDKKVRFRFSVGOHNYERGPIQWMACENKGYEYIEPSIGAIR 420  
 QY 421 INTQEYLDVLGRPMVLADKAKOVQNTNYLDALGLVITGTPVFNITGQFENKTNLK 480  
 DB 421 INTQEYLDVLGRPMVLADKAKOVQNTNYLDALGLVITGTPVFNITGQFENKTNLK 480  
 QY 481 NQILGVMGVDVSLDIEDIKRLTPRETLCPNGYIFAIDPNGVYLLHPNLQPNKPSQEPVTL 540  
 DB 481 NQILGVMGVDVSLDIEDIKRLTPRETLCPNGYIFAIDPNGVYLLHPNLQPNKPSQEPVTL 540  
 QY 541 DFLDAELENDIKVEIRNKMIDGESGKFTLTKVKSODERYIDKGNRTYTWTPVNGTDYSL 600  
 DB 541 DFLDAELENDIKVEIRNKMIDGESGKFTLTKVKSODERYIDKGNRTYTWTPVNGTDYSL 600  
 QY 601 ALVLPYTFYVIKAKLEETITQARSKKKMKDSETLKPNFESGYTFIAPRDYCNLDKI 660  
 DB 601 ALVLPYTFYVIKAKLEETITQARSKKKMKDSETLKPNFESGYTFIAPRDYCNLDKI 660  
 QY 661 SDNTEFLNFEFFIDRKTNPNSCNADLINRVLLDAGFTNELVQYWSKQNKIKGVKAR 720  
 DB 661 SDNTEFLNFEFFIDRKTNPNSCNADLINRVLLDAGFTNELVQYWSKQNKIKGVKAR 720  
 QY 721 FVYTDGGITRVYPKEAGENWQENPETEYDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
 DB 721 FVYTDGGITRVYPKEAGENWQENPETEYDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
 QY 781 MVSKAVEIYIQGLLPAVVGITKIDVNSTENFTKTSIRDPGAGPVCDCKRNSDVMDCVI 840  
 DB 781 MVSKAVEIYIQGLLPAVVGITKIDVNSTENFTKTSIRDPGAGPVCDCKRNSDVMDCVI 840  
 QY 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRLNINISYAFNKNISYDYSVCEPGAAPKQ 900  
 DB 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRLNINISYAFNKNISYDYSVCEPGAAPKQ 900  
 QY 901 GAGHSAYVPSVADILQIGWATAAASWILQOFLLSLTPRLLLEAVEMEDDDFTASLSKQ 960  
 DB 901 GAGHSAYVPSVADILQIGWATAAASWILQOFLLSLTPRLLLEAVEMEDDDFTASLSKQ 960  
 QY 961 SCITEQTOFFNDKSKFSVGLDCCGNSRIFHGEKLMNTNLFIMVESKGTCPDTRLII 1020  
 DB 961 SCITEQTOFFNDKSKFSVGLDCCGNSRIFHGEKLMNTNLFIMVESKGTCPDTRLII 1020  
 QY 1021 QAEQTSQDGNPCDMVK 1036  
 DB 1021 QAEQTSQDGNPCDMVK 1036

## RESULT 11

AAAR33553  
ID AAR33553 standard; Protein; 1091 AA.

XX AC AAR33553;

XX DT 30-JUN-1993 (first entry)

XX DE Sequence of the alpha 2 human calcium channel subunit.

XX KW Human calcium channel subunit; diagnosis; agonist; antagonist;

XX KW Lambert Eaton syndrome.

XX OS Homo sapiens.

XX PN W09304083-A.

XX PD 04-MAR-1993.

XX PF 14-AUG-1992; 92WO-US06903.

XX PR 15-AUG-1991; 91US-0745206.

XX PR 10-APR-1992; 92US-0868354.

XX PA (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.

XX PI Brenner R, Ellis SB, Feldman DH, Harpold MM, Mccue AF;

XX PI Williams MB;

XX DR WPI; 1993-093936/11.

XX DR N-PSDB; AAQ37821.

XX PT DNA encoding specific human calcium channel sub-units - used for  
PT identifying calcium channel agonists and antagonists and  
PT diagnosing Lambert Eaton syndrome

XX PS Disclosure; Page 134-138; 150pp; English.

XX CC DNA encoding a human neuronal calcium channel alpha 2 subunit was  
CC isolated from a human genomic DNA library probed under low and high  
CC stringency conditions with a fragment of DNA encoding the rabbit  
CC skeletal muscle calcium channel alpha 2 subunit. The fragment  
CC included nucleotides having a sequence corresponding to the  
CC nucleotide sequence between nucleotides 43 and 272 inclusive of  
CC rabbit back skeletal muscle calcium channel alpha 2 subunit cDNA.  
CC PCR analysis identified splice variants of the human calcium alpha  
CC 2 subunit transcript. In particularly preferred embodiments, the  
CC DNA encoding the alpha 2 subunit is produced by alternative  
CC processing of a primary transcript that includes DNA encoding the  
CC amino acids set forth in AAR33553 and the DNA of AAQ37823 inserted  
CC between nucleotides 1624 and 1625 of AAQ37821.

XX SQ Sequence 1091 AA;

Query Match 99.9%; Score 5437; DB 14; Length 1091;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1035; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLTQSLILIGPSEEPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
DB 1 MAAGCLLALTLTQSLILIGPSEEPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
QY 61 YERYQDLTYVPEPNARQLVEIARDIEKLSNRSKALVSLALEAEKVAAHQWREDFASN 120  
DB 61 YERYQDLTYVPEPNARQLVEIARDIEKLSNRSKALVSLALEAEKVAAHQWREDFASN 120  
QY 121 EVVYNAKDDLPEDKNDSEPGSRQIKPVIEDANFGQRQISYQHAHVHPTDIYEGSTIVL 180  
DB 121 EVVYNAKDDLPEDKNDSEPGSRQIKPVIEDANFGQRQISYQHAHVHPTDIYEGSTIVL 180  
QY 181 NELNWT SALDEVFKKNREEDPSLLWQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240  
DB 181 NELNWT SALDEVFKKNREEDPSLLWQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240

DB 181 NELNWT SALDEVFKKNREEDPSLLWQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240  
QY 241 RPWYIOGAASP KDM LILVDVSGVSG LTKLIRTSVSEMLET L SDDDFVNVASFNSNAQ 300  
DB 241 RPWYIOGAASP KDM LILVDVSGVSG LTKLIRTSVSEMLET L SDDDFVNVASFNSNAQ 300  
QY 301 VSCFQHLVQANVRNKVYLKDAVNNTAKGTDYKKGFSFAFEQLLNVNVRANCNKILML 360  
DB 301 VSCFQHLVQANVRNKVYLKDAVNNTAKGTDYKKGFSFAFEQLLNVNVRANCNKILML 360  
QY 361 FTDGGEERAQEIFNKYKNDKKVRVFRFSGVGHNYERGPQIOWMACENKGYIYEIPSGAIR 420  
DB 361 FTDGGEERAQEIFNKYKNDKKVRVFRFSGVGHNYERGPQIOWMACENKGYIYEIPSGAIR 420  
QY 421 INTOEYLDVIGRPMVLADGAKAKQVQWNTVYLDALGLVITGTLPVPNTITGQENKTNLK 480  
DB 421 INTOEYLDVIGRPMVLADGAKAKQVQWNTVYLDALGLVITGTLPVPNTITGQENKTNLK 480  
QY 481 NQLILGVMGVDVSLIEDIKRLTPRETLCPNGYIFAIDPNGVYLLHPNLQPNKSOEPTVL 540  
DB 481 NQLILGVMGVDVSLIEDIKRLTPRETLCPNGYIFAIDPNGVYLLHPNLQPNKSOEPTVL 540  
QY 541 DFLDAELENDIKVEIRNKMIDGSEKTFRTLVKSQDERYIDKGNRTYTTWTPVNGTDYSL 600  
DB 541 DFLDAELENDIKVEIRNKMIDGSEKTFRTLVKSQDERYIDKGNRTYTTWTPVNGTDYSL 600  
QY 601 ALVLPTYSFYIYKAKLEETITQARSKGKMKDSETLKPDNPFESGYTFIAPRDYCNDLKI 660  
DB 601 ALVLPTYSFYIYKAKLEETITQARSKGKMKDSETLKPDNPFESGYTFIAPRDYCNDLKI 660  
QY 661 SDNTEFLLNFEFIDRKTNNPCNADLINRVLLDAGFTNELVQNTWSKOKNIKGVKAR 720  
DB 661 SDNTEFLLNFEFIDRKTNNPCNADLINRVLLDAGFTNELVQNTWSKOKNIKGVKAR 720  
QY 721 FWVTDGGITRYYPKEAGENWOENPETYEDSFYKRSNDNDNVFTTAPYFNKSGPGAYESGI 780  
DB 721 FWVTDGGITRYYPKEAGENWOENPETYEDSFYKRSNDNDNVFTTAPYFNKSGPGAYESGI 780  
QY 781 MYSKAVEIYIOGKLLKPAVGIKIDVNSWNIENFTKTSIRDPCAGVCDCKRNSDVMDCVI 840  
DB 781 MYSKAVEIYIOGKLLKPAVGIKIDVNSWNIENFTKTSIRDPCAGVCDCKRNSDVMDCVI 840  
QY 841 LDDGGFLLMAHDDYTNOIGRFFGEIDPSLMRHLVNSVYAFNKSVDYQSVCEPGAAPKQ 900  
DB 841 LDDGGFLLMAHDDYTNOIGRFFGEIDPSLMRHLVNSVYAFNKSVDYQSVCEPGAAPKQ 900  
QY 901 GAGHRSAYVPSVADILQIGMWATAAASILQOFLLSLTFFPRLLEAVEMEDDDFTASLSKQ 960  
DB 901 GAGHRSAYVPSVADILQIGMWATAAASILQOFLLSLTFFPRLLEAVEMEDDDFTASLSKQ 960  
QY 961 SCITHTQTYFFDNDKSKFSVGLDCGNCRIHFHGEKLMNTNLIIFIMVESKGTCPDTRLLI 1020  
DB 961 SCITHTQTYFFDNDKSKFSVGLDCGNCRIHFHGEKLMNTNLIIFIMVESKGTCPDTRLLI 1020  
QY 1021 QAEQTS DGP NCDMVK 1036  
DB 1021 QAEQTS DGP NCDMVK 1036  
RESULT 12  
AAW63148  
ID AAW63148 standard; Protein; 1110 AA.  
XX AC AAW63148;  
XX DT 12-OCT-1998 (first entry)  
XX DE Human calcium channel alpha-2 subunit.  
XX KW Alpha-2 subunit; human; calcium channel; assay; detection;  
XX KW characterisation; Lambert Eaton Syndrome; LES; diagnosis.  
XX OS Homo sapiens.

XX US5792846-A.  
 XX 11-AUG-1998.  
 XX 31-MAY-1995; 95US-0455543.  
 XX 04-APR-1994; 94US-0223305.  
 XX 04-APR-1988; 88US-0176899.  
 XX 04-APR-1989; 89US-0603751.  
 XX 04-APR-1989; 89WO-US01408.  
 XX 20-FEB-1990; 90US-0482384.  
 XX 30-NOV-1990; 90US-0620250.  
 XX 15-AUG-1991; 91US-0745206.  
 XX 31-MAY-1995; 95US-0455543.  
 XX (SIBI-) SIBIA NEUROSCIENCES INC.  
 XX Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF,  
 XX Williams ME;  
 XX WPI; 1998-456192/39.  
 XX N-PSDB; AAV42694.  
 XX DNA encoding human calcium channel alpha 1B subunit protein -  
 XX useful for recombinant production of the channel for screening of  
 XX its modulators, and diagnosis of Lambert Eaton Syndrome  
 XX Disclosure; Columns 131-138; 166pp; English.  
 XX The present sequence represents the alpha-2 subunit of a human calcium  
 XX channel. Calcium channels are membrane-spanning, multi-subunit proteins  
 XX that allow controlled entry of calcium ions into cells. This leads  
 XX to depolarisation events required for muscle contraction. The recombinant  
 XX subunit, when expressed with nucleic acids encoding the complete calcium  
 XX channel, can be used in assays for the detection and characterisation of  
 XX compounds that modulate the channel. The DNA encoding the subunits can  
 XX be alternatively spliced when transcribed, giving more than one form of  
 XX the protein from the same transcript, each having slightly different  
 XX properties. In addition, the reactivity of the alpha 1 subunit with IgG  
 XX molecules from the serum of an individual with Lambert Eaton Syndrome  
 XX (LES) can be used as a diagnostic for the disease.  
 XX Sequence 1110 AA;  
 Query Match 99.6%; Score 5423.5; DB 19; Length 1110;  
 Best Local Similarity 98.2%; Pred. No. 0;  
 Matches 1036; Conservative 0; Mismatches 0; Indels 19; Gaps 1;  
 QY 1 MAAGCLLALTTLTFLQSLILGSPSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLYDI 60  
 DB 1 MAAGCLLALTTLTFLQSLILGSPSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLYDI 60  
 QY 61 YEKYQDLYTVEPNARQLVEIARIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120  
 DB 61 YEKYQDLYTVEPNARQLVEIARIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120  
 QY 121 EVVYNAKDDLPKNDSPGSRQIKPVIEDANFGROISYQHAHVHTPIIYEGSTIVL 180  
 DB 121 EVVYNAKDDLPKNDSPGSRQIKPVIEDANFGROISYQHAHVHTPIIYEGSTIVL 180  
 QY 181 NELNMTSALDEYFKKREDEPDLQVFGSATGLARYYPASPVVDNSRTPNKIDLYDVR 240  
 DB 181 NELNMTSALDEYFKKREDEPDLQVFGSATGLARYYPASPVVDNSRTPNKIDLYDVR 240  
 QY 241 RPWYIQAASPKDMLILVDVSGVSGGLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
 DB 241 RPWYIQAASPKDMLILVDVSGVSGGLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
 QY 301 VSCFQHLVQANVRNKKVLKDVANNITAKITDYKKGFSFAEQLLNLYNVRANCNKIIML 360  
 DB 301 VSCFQHLVQANVRNKKVLKDVANNITAKITDYKKGFSFAEQLLNLYNVRANCNKIIML 360

QY 361 FTDGGERAEIENKYNKDKKVRVFRFSVGOHNYERGPQIWMACENKGYEIPSGAIR 420  
 DB 361 FTDGGERAEIENKYNKDKKVRVFRFSVGOHNYERGPQIWMACENKGYEIPSGAIR 420  
 QY 421 INTQEYLDVLGRPMVLADGKAKQVQWTVNYLDALBELGLVITGTLVPVFNITQGFENKTNLK 480  
 DB 421 INTQEYLDVLGRPMVLADGKAKQVQWTVNYLDALBELGLVITGTLVPVFNITQGFENKTNLK 480  
 QY 481 NOLILGVMGVDVSLIEDIKRLTPREFTLCPNGYFAIDPNGYVLLHHPNLOPK----- 530  
 DB 481 NOLILGVMGVDVSLIEDIKRLTPREFTLCPNGYFAIDPNGYVLLHHPNLOPK----- 530  
 QY 531 -----NPKSQBPVTLDFLDAELENDIKVEIRNKMIDGESGKPTRTLVKSODERYI 581  
 DB 541 LKRRPNIONPKSQBPVTLDFLDAELENDIKVEIRNKMIDGESGKPTRTLVKSODERYI 600  
 QY 582 DKGNETYTWTPVNGTDYSIALVLPYSFYIAKALEETITQARSKKGMKDSSETLKPDNF 641  
 DB 601 DKGNETYTWTPVNGTDYSIALVLPYSFYIAKALEETITQARSKKGMKDSSETLKPDNF 660  
 QY 642 BESGYTFIAPRDYCNLDKISDNNTFELNFEFIDRKTTPNPNSCNADLINRVLLDAGFTN 701  
 DB 661 BESGYTFIAPRDYCNLDKISDNNTFELNFEFIDRKTTPNPNSCNADLINRVLLDAGFTN 720  
 QY 702 ELVQNYWQSKQNIKGKARFVVTGDTIRVYPKEAGENWQENPETYEDSFYKRSILDNDNY 761  
 DB 721 ELVQNYWQSKQNIKGKARFVVTGDTIRVYPKEAGENWQENPETYEDSFYKRSILDNDNY 780  
 QY 762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTTISRDP 821  
 DB 781 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTTISRDP 840  
 QY 822 CAGPVCDCKRNSDVMDCVILDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYA 881  
 DB 841 CAGPVCDCKRNSDVMDCVILDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYA 900  
 QY 882 FNKSYDQSVCEPAAFPQAGHRSAYVPSVADILQIGWATAAAWSILOOFLLSLTFPR 941  
 DB 901 FNKSYDQSVCEPAAFPQAGHRSAYVPSVADILQIGWATAAAWSILOOFLLSLTFPR 960  
 QY 942 LLEAVEMEDDDFTASLSKQSCITOTQYFFDNDKSGVLDGCGNCSRFHGEKLMNTNL 1001  
 DB 961 LLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDKSGVLDGCGNCSRFHGEKLMNTNL 1020  
 QY 1002 IFIMVESKGTCPDTRLLIQAEQTS DGPNPCDMVK 1036  
 DB 1021 IFIMVESKGTCPDTRLLIQAEQTS DGPNPCDMVK 1055  
 RESULT 13  
 AAR71013  
 ID AAR71013 standard; Protein; 1086 AA.  
 XX AAR71013;  
 XX AC AAR71013;  
 XX DT 01-DEC-1995 (first entry)  
 XX DE Human neuronal calcium channel subunit alpha 2c.  
 XX KW Calcium channel subunit; antagonist; agonist; diagnosis;  
 XX LW Lambert Eaton Syndrome.  
 XX OS Homo sapiens.  
 XX PN WO9504822-A.  
 XX PD 16-FEB-1995.  
 XX PF 11-AUG-1994; 94WO-US09230.  
 XX PR 11-AUG-1993; 93US-0105536.  
 XX PR 05-NOV-1993; 93US-0149097.

(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.

PA Ellis SB, Gillespie A, Harpold MM, McCue AF, Williams ME;

XX WPI: 1995-090900/12.

DR N-PSDB; AAQ84667.

XX DNA encoding human calcium channel sub-unit(s) - used for  
PT developing prods. for studying calcium channels, e.g. for  
PT obtaining agonists and antagonists

XX Disclosure; Page 237-242; 285pp; English.

XX Human neuronal alpha 2 coding sequence (AAQ84664) transcript is  
CC differentially processed in skeletal muscle, aorta, and CNS in  
CC the region corresp. to nt 1595-1942 of AAQ84664 in each of the  
CC tissues. Five alternatively spliced variant transcripts that differ  
CC in the presence or absence of one to three different portions of  
CC this region. There are three sequences involved (see AAQ84664 F1  
CC and AAQ84665 F1), sequence 1, sequence 2 and sequence 3. The five  
CC alpha 2 encoding transcripts from the different tissues include  
CC different combinations of the three sequences, except for one of  
CC the alpha 2 transcripts expressed in aorta which lacks all three  
CC sequences. The five alpha 2 forms identified are (1) a form that  
CC lacks sequence 3 called alpha 2a, expressed in skeletal muscle  
CC (2) one that lacks sequence 1 called alpha 2b, expressed in CNS  
CC (3) one that lacks sequences 1 and 2 called alpha 2c, expressed in  
CC aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,  
CC expressed in aorta and (5) one that lacks sequences 1 and 3  
CC called alpha 2e. The DNA and AA sequences of alpha 2a - alpha 2e  
CC are set forth in AAQ84666-Q84669 and AAR101012-R1015 respectively.

XX Sequence 1086 AA;

Query Match 99.3%; Score 5403.5; DB 16; Length 1086;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1031; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 MAAGCLLALTTLTQSLILGPSSEEPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
DB 1 MAAGCLLALTTLTQSLILGPSSEEPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
QY 61 YEKYQDLTYVEPNARQLVEIARDTEKLLSNRSKALVSLALEAEKVQAAHOREDFASN 120  
DB 61 YEKYQDLTYVEPNARQLVEIARDTEKLLSNRSKALVSLALEAEKVQAAHOREDFASN 120  
QY 121 EVVYNAKDDLDPEKNDSEPGSQRIPVFIEDANFGRQISYQHAHVHPTDIYEGSTIVL 180  
DB 121 EVVYNAKDDLDPEKNDSEPGSQRIPVFIEDANFGRQISYQHAHVHPTDIYEGSTIVL 180  
QY 181 NELNWTLSALDEVFKKNREEDPSLLWQVFGSATGLARYYPASPVWDNSRTPNKIDLYDVR 240  
DB 181 NELNWTLSALDEVFKKNREEDPSLLWQVFGSATGLARYYPASPVWDNSRTPNKIDLYDVR 240  
QY 241 RPWYIOGAASPKDMLILVDVSGSVGLTLKIRTSVSEMLETLSDDDFVNVAFSNQAQD 300  
DB 241 RPWYIOGAASPKDMLILVDVSGSVGLTLKIRTSVSEMLETLSDDDFVNVAFSNQAQD 300  
QY 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSFAFEGOLLNYSRANCNKIIML 360  
DB 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSFAFEGOLLNYSRANCNKIIML 360  
QY 361 FTDGERAQAIEFNKYNKKKVRFRFSVQGHNYERGPQIOWMACENKGYEIPSTIGATR 420  
DB 361 FTDGERAQAIEFNKYNKKKVRFRFSVQGHNYERGPQIOWMACENKGYEIPSTIGATR 420  
QY 421 INTQEYLDVLRPMWLAGDKAKOVQNTNLYDLALELGLVITGTLPVFNITGQFNKTNLK 480  
DB 421 INTQEYLDVLRPMWLAGDKAKOVQNTNLYDLALELGLVITGTLPVFNITGQFNKTNLK 480  
QY 481 NQLILGVMGVDSLEDEIKRLTPFTLPCNGYYFAIDPNGVYLLHPNLQPKNPKSQBPVTL 540  
DB 481 NQLILGVMGVDSLEDEIKRLTPFTLPCNGYYFAIDPNGVYLLHPNLQPKNPKSQBPVTL 540  
DB 481 NQLILGVMGVDSLEDEIKRLTPFTLPCNGYYFAIDPNGVYLLHPNLQPKNPKSQBPVTL 540

QY 541 DFLDAELENDIKVEIRNKMIDGESGEKFTRTLKVSQDERYIDKGNRTYTWTTPVNGTDSL 600  
DB 536 DFLDAELENDIKVEIRNKMIDGESGEKFTRTLKVSQDERYIDKGNRTYTWTTPVNGTDSL 595  
QY 601 ALVLPYTSFYIYKAKLEETITQARSKGKMKDSETLKPDNFEESGYTFIAPRDYCNOLKI 660  
DB 596 ALVLPYTSFYIYKAKLEETITQARSKGKMKDSETLKPDNFEESGYTFIAPRDYCNOLKI 655  
QY 661 SDNTEFLLNFEFTDRKTPNPNPCNADLINRVLLDAGFTNELVQNYWSKOKNKGKVKAR 720  
DB 656 SDNTEFLLNFEFTDRKTPNPNPCNADLINRVLLDAGFTNELVQNYWSKOKNKGKVKAR 715  
QY 721 FVWTDGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
DB 716 FVWTDGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 775  
QY 781 MYSKAVEIYIOGKLLKPAVGIKIDVNSWIENFTKTSIRDPCAGPVCDCRNSDVMDCVI 840  
DB 776 MYSKAVEIYIOGKLLKPAVGIKIDVNSWIENFTKTSIRDPCAGPVCDCRNSDVMDCVI 835  
QY 841 LDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNIISVYAFNKSIDYQSVCEPGAAPKQ 900  
DB 836 LDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNIISVYAFNKSIDYQSVCEPGAAPKQ 895  
QY 901 GAGHSAYVPSVADILQIGWATAAAWSILOQFLLSLTFFPRLLEAVEMEDDDFTASLSKQ 960  
DB 896 GAGHSAYVPSVADILQIGWATAAAWSILOQFLLSLTFFPRLLEAVEMEDDDFTASLSKQ 955  
QY 961 SCITEQTQYFFDNDKSKFSGLVDCGNCRIHFHGEKLMNTNLIIFIMVESKGTCPCDTRLII 1020  
DB 956 SCITEQTQYFFDNDKSKFSGLVDCGNCRIHFHGEKLMNTNLIIFIMVESKGTCPCDTRLII 1015  
QY 1021 QAEQTSDFGNPCDMVK 1036  
DB 1016 QAEQTSDFGNPCDMVK 1031  
RESULT 14  
AAW63153  
ID AAW63153 standard; Protein; 1086 AA.  
XX AAW63153;  
AC AAW63153;  
XX  
DT 12-OCT-1998 (first entry)  
XX Human calcium channel alpha-2c subunit.  
DE Alpha-2 subunit; human; calcium channel; assay; detection;  
KW characterisation; Lambert Eaton Syndrome; LES; diagnosis.  
XX Homo sapiens.  
XX  
XX US5792846-A.  
XX 11-AUG-1998.  
XX 31-MAY-1995; 95US-0455543.  
XX 04-APR-1994; 94US-0223305.  
XX 04-APR-1988; 88US-0176899.  
XX 04-APR-1989; 89US-0603751.  
XX 04-APR-1989; 89WO-US01408.  
XX 20-FEB-1990; 90US-0482384.  
XX 30-NOV-1990; 90US-0620250.  
XX 15-AUG-1991; 91US-0745206.  
XX 31-MAY-1995; 95US-0455543.  
XX (SIBI-) SIBIA NEUROSCIENCES INC.  
XX  
XX Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;  
PI Williams ME;  
XX

DR WPI: 1998-456192/39.  
 DR N-PSDB; AAV42702.  
 XX DNA encoding human calcium channel alpha 1B subunit protein -  
 PT useful for recombinant production of the channel for screening of  
 PT its modulators, and diagnosis of Lambert Eaton Syndrome  
 XX  
 PS Claim 3; Columns 293-300; 166pp; English.  
 XX  
 CC The present sequence represents the alpha-2c subunit of a human calcium  
 CC channel. Calcium channels are membrane-spanning, multi-subunit proteins  
 CC that allow controlled entry of calcium ions into cells. This leads  
 CC to depolarisation events required for muscle contraction. The recombinant  
 CC subunit, when expressed with nucleic acids encoding the complete calcium  
 CC channel, can be used in assays for the detection and characterisation of  
 CC compounds that modulate the channel. The DNA encoding the subunits can  
 CC be alternatively spliced when transcribed, giving more than one form of  
 CC the protein from the same transcript, each having slightly different  
 CC properties. In addition, the reactivity of the alpha 1 subunit with IgG  
 CC molecules from the serum of an individual with Lambert Eaton Syndrome  
 CC (LES) can be used as a diagnostic for the disease.  
 XX  
 SQ Sequence 1086 AA;

Query Match 99.3%; Score 5403.5; DB 19; Length 1086;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 1031; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 MAAGCLLALTTLTQSLLLGSPSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
 DB 1 MAAGCLLALTTLTQSLLLGSPSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
 QY 61 YEKYQDLYTVEPNARQVLEIARDEIKLLSNRSKALVSLALEAEKVQAAHQRDFASN 120  
 DB 61 YEKYQDLYTVEPNARQVLEIARDEIKLLSNRSKALVSLALEAEKVQAAHQRDFASN 120  
 QY 121 EVVYNAKDDLOPEKNDSEPGSQRIKPVFIEDANFGROIYSOHAHVHPDIYEGSTIVL 180  
 DB 121 EVVYNAKDDLOPEKNDSEPGSQRIKPVFIEDANFGROIYSOHAHVHPDIYEGSTIVL 180  
 QY 181 NELNWTSAIDVFKKREEDPSLLWQVFGSATGLARYYPASVPWVDSNRTPNKIDLYDVR 240  
 DB 181 NELNWTSAIDVFKKREEDPSLLWQVFGSATGLARYYPASVPWVDSNRTPNKIDLYDVR 240  
 QY 241 RPYIQGAASPKDMLLLVDVSGVSLTLKLRISVSEMLETLSDDDFVNVSFNSAQD 300  
 DB 241 RPYIQGAASPKDMLLLVDVSGVSLTLKLRISVSEMLETLSDDDFVNVSFNSAQD 300  
 QY 301 VSCFQHLVQANVRNKKVLDKAYNNITAKGIDYKKGFSAFEPQLLNVNVRANCNKIIML 360  
 DB 301 VSCFQHLVQANVRNKKVLDKAYNNITAKGIDYKKGFSAFEPQLLNVNVRANCNKIIML 360  
 QY 361 FTDGGEERAQEIYFNKYNDKKYVRFVSGQHYRGPQIWMACENKGYEYIPEISGAIR 420  
 DB 361 FTDGGEERAQEIYFNKYNDKKYVRFVSGQHYRGPQIWMACENKGYEYIPEISGAIR 420  
 QY 421 INTQYLDVLGRPMVLGADKAKOVQWTVNYLDALGLVITGLTPVFNITGOFENKTNLK 480  
 DB 421 INTQYLDVLGRPMVLGADKAKOVQWTVNYLDALGLVITGLTPVFNITGOFENKTNLK 480  
 QY 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHPNLQPNKPSQEPVTL 540  
 DB 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHPNLQPNKPSQEPVTL 540  
 QY 541 DFLDAELENDIKVEIRNKMIDSESEKFTRLVKSQDREYIDKGNRTYTWTPVNGTDYSL 600  
 DB 541 DFLDAELENDIKVEIRNKMIDSESEKFTRLVKSQDREYIDKGNRTYTWTPVNGTDYSL 600  
 QY 596 ALVLTYSFYIYKAKLEETITQARSKKGMKDSFLLKPDNFEESGYTFIAPDRCNDLKI 660  
 DB 596 ALVLTYSFYIYKAKLEETITQARSKKGMKDSFLLKPDNFEESGYTFIAPDRCNDLKI 660  
 QY 661 SDNTEFLNFEFTDRKTPNPNNSCNADLINRVLLDAGFTNELVQYWSKOKNIKGVKAR 720

DB 656 SDNTEFLNFEFTDRKTPNPNNSCNADLINRVLLDAGFTNELVQYWSKOKNIKGVKAR 715  
 QY 721 FVWTDGGITRIVYPKEAGENWQENPETYEDSFYKRSLDNDNVFTAPYFNKSGPGAYESGI 780  
 DB 716 FVWTDGGITRIVYPKEAGENWQENPETYEDSFYKRSLDNDNVFTAPYFNKSGPGAYESGI 775  
 QY 781 MVSKAVEYIIOGKLLKPAVWGKIDVNSWIEFTKTSIRDPCAGPVCDCRNSDVMDCVI 840  
 DB 776 MVSKAVEYIIOGKLLKPAVWGKIDVNSWIEFTKTSIRDPCAGPVCDCRNSDVMDCVI 835  
 QY 841 LDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNSVYAFNKSVDYQSVCEPGAAPKQ 900  
 DB 836 LDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNSVYAFNKSVDYQSVCEPGAAPKQ 895  
 QY 901 CAGHSRAYSVPVADILQIGWATAAASIIQOQLLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
 DB 896 CAGHSRAYSVPVADILQIGWATAAASIIQOQLLSLTFPRLLEAVEMEDDDFTASLSKQ 955  
 QY 961 SCITEQTYFFDNDKSFSGVLDGNGSRIFPHGEKLMNTNLIIFIMVBSKGTCTCDTRLII 1020  
 DB 956 SCITEQTYFFDNDKSFSGVLDGNGSRIFPHGEKLMNTNLIIFIMVBSKGTCTCDTRLII 1015  
 QY 1021 QAEQTSQDGNPCDMVK 1036  
 DB 1016 QAEQTSQDGNPCDMVK 1031

RESULT 15  
 AAB10587  
 ID AAB10587 standard; Protein; 1086 AA.  
 XX AAB10587;  
 AC AAB10587;  
 XX 22-DEC-2000 (first entry)  
 XX Human calcium channel alpha-2c subunit protein.  
 XX Human; calcium channel; calcium channel subunit; diagnosis;  
 KW Lambert Eaton Syndrome; calcium channel subunit alpha-2c.  
 XX Homo sapiens.  
 OS US6096514-A.  
 PN 01-AUG-2000.  
 PD 25-MAY-1995; 95US-0450562.  
 PF 04-APR-1988; 88US-0176899.  
 PR 02-FEB-1990; 90US-0482384.  
 PR 08-NOV-1990; 90US-0603751.  
 PR 30-NOV-1990; 90US-0620250.  
 PR 15-AUG-1991; 91US-0745206.  
 PR 10-APR-1992; 92US-0868354.  
 PR 13-JUL-1992; 92US-0914231.  
 PR 11-AUG-1993; 93US-0105536.  
 PR 03-NOV-1993; 93US-0149097.  
 PR 07-FEB-1994; 94US-0193078.  
 PR 04-APR-1994; 94US-0223305.  
 PR 11-AUG-1994; 94US-0290012.  
 PR 23-SEP-1994; 94US-0311363.  
 PR 28-SEP-1994; 94US-0314083.  
 PR 07-NOV-1994; 94US-0336257.  
 PR 13-MAR-1995; 95US-0404950.  
 XX (SIBI-) SIBIA NEUROSCIENCES INC.  
 XX Ellis SB, Williams MB, McCue AF, Harpold MM;  
 XX WPI: 2000-548230/50.  
 DR N-PSDB; AAV71725.  
 XX

PT Human calcium channel beta subunit polynucleotides, useful for  
PT producing recombinant eukaryotic cells and for diagnosing Lambert Eaton  
PT Syndrome  
XX  
XX Disclosure: Column 237-244; 153pp; English.  
XX  
XX This invention describes a novel isolated DNA molecule (I) comprising a  
CC sequence encoding a beta3-1 subunit of a human calcium channel.  
CC Nucleic acid probes comprising 14-30 contiguous nucleotides of  
CC beta\_3 subunit encoding DNA are useful for isolation and cloning of  
CC calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that  
CC express heterologous calcium channel are useful for identifying compounds  
CC that modulate calcium channel activity and in assays for identifying  
CC agonists and antagonists of calcium channel activity in humans. Human  
CC calcium channel subunit or eukaryotic cells expressing the channel are  
CC useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This  
CC sequence represents the human calcium channel alpha-2c subunit which is  
CC described in the method of the invention.  
XX  
XX  
SQ Sequence 1086 AA;

Query Match 99.3%; Score 5403.5; DB 21; Length 1086;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1031; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 MAAGCCLLAU... 60  
Db 1 MAAGCCLLAU... 60  
QY 61 YEKYQDLTY... 120  
Db 61 YEKYQDLTY... 120  
QY 121 EVVYNKAD... 180  
Db 121 EVVYNKAD... 180  
QY 181 NELNWTSA... 240  
Db 181 NELNWTSA... 240  
QY 241 RPWYIOGA... 300  
Db 241 RPWYIOGA... 300  
QY 301 VSCFQHLV... 360  
Db 301 VSCFQHLV... 360  
QY 361 FTDGGEER... 420  
Db 361 FTDGGEER... 420  
QY 421 INTQEVLD... 480  
Db 421 INTQEVLD... 480  
QY 481 NQLILGVM... 540  
Db 481 NQLILGVM... 540  
QY 541 DFLEDAEL... 600  
Db 541 DFLEDAEL... 600  
QY 596 ALVLPY... 655  
Db 596 ALVLPY... 655  
QY 661 SDNTEFL... 720  
Db 661 SDNTEFL... 720  
QY 715  
Db 715

QY 721 FVVTGGITRV... 780  
Db 716 FVVTGGITRV... 775  
QY 781 MYSKAVEI... 840  
Db 776 MYSKAVEI... 835  
QY 841 LDDGGFLL... 900  
Db 836 LDDGGFLL... 895  
QY 901 GAGHSAY... 960  
Db 896 GAGHSAY... 955  
QY 961 SCITBQ... 1020  
Db 956 SCITBQ... 1015  
QY 1021 QAEQTS... 1036  
Db 1016 QAEQTS... 1031

Search completed: February 10, 2003, 14:18:23  
Job time : 38.6207 secs





GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 10, 2003, 14:13:50 ; Search time 34.4969 Seconds  
(without alignments)  
4106.031 Million cell updates/sec

Title: US-10-090-827-15

Perfect score: 5599

Sequence: 1 MAAGCLLALTLFQSLIG.....PDVCFDNNVLEDTDCGGVS 1063

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_101002.\*

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23:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5599	100.0	1063	22 AAU01034	Human secreted sol
2	5599	100.0	1063	22 AAB62258	Porcine calcium ch
3	5599	100.0	1091	16 AAR71011	Human neuronal cal
4	5599	100.0	1091	19 AAW63145	Human calcium chan
5	5599	100.0	1091	21 AAB10576	Human calcium chan
6	5599	100.0	1091	22 AAU01035	Human secreted sol
7	5599	100.0	1091	22 AAB62259	Porcine calcium ch
8	5595	99.9	1091	19 AAR37879	Human calcium chan
9	5593	99.9	1091	14 AAR33553	Sequence of the al
10	5579.5	99.7	1110	19 AAW63148	Human calcium chan

11	5559.5	99.3	1086	16 AAR71013	Human neuronal cal
12	5559.5	99.3	1086	19 AAB63153	Human calcium chan
13	5559.5	99.3	1086	21 AAB10587	Human calcium chan
14	5542.5	99.0	1084	16 AAR71015	Human neuronal cal
15	5542.5	99.0	1084	19 AAW63155	Human calcium chan
16	5542.5	99.0	1084	21 AAB10589	Human calcium chan
17	5532	98.8	1063	22 AAU01030	Pig secreted solub
18	5532	98.8	1063	22 AAB62254	Porcine calcium ch
19	5532	98.8	1069	22 AAU01031	Pig secreted solub
20	5532	98.8	1069	22 AAB62255	Porcine calcium ch
21	5532	98.8	1091	22 AAU01027	Pig secreted solub
22	5532	98.8	1091	22 AAB62251	Porcine calcium ch
23	5523	98.6	1103	16 AAR71012	Human neuronal cal
24	5523	98.6	1103	19 AAB63151	Human calcium chan
25	5523	98.6	1103	21 AAB10586	Human calcium chan
26	5503	98.3	1079	19 AAW63154	Human calcium chan
27	5503	98.3	1079	21 AAB10588	Human calcium chan
28	5497	98.2	1079	16 AAR71014	Human neuronal cal
29	5443	97.2	1036	22 AAU01033	Human secreted sol
30	5443	97.2	1036	22 AAB62257	Porcine calcium ch
31	5385.5	96.2	1106	18 AAW37712	Rabbit skeletal ca
32	5385.5	96.2	1106	18 AAW18389	Rabbit skeletal ca
33	5385.5	96.2	1106	21 AAY77545	Rabbit skeletal ca
34	5380	96.1	1036	22 AAU01029	Pig secreted solub
35	5380	96.1	1036	22 AAB62253	Porcine calcium ch
36	5364.5	95.8	1106	16 AAR73056	Human secreted sol
37	5346	95.5	1018	22 AAU01032	Rabbit skeletal ca
38	5346	95.5	1018	22 AAB62256	Porcine calcium ch
39	5288	94.4	1018	22 AAU01028	Pig secreted solub
40	5288	94.4	1018	22 AAB62252	Porcine calcium ch
41	5237.5	93.9	1100	10 AAF95644	Rabbit skeletal mus
42	3004.5	53.7	1109	22 AAU01016	Human secreted sol
43	3004.5	53.7	1109	22 AAB62240	Human calcium chan
44	3004.5	53.7	1115	22 AAU01025	Human wild type al
45	3004.5	53.7	1115	22 AAB62249	Human calcium chan

#### ALIGNMENTS

RESULT 1

AAU01034  
ID AAU01034 standard; Protein: 1063 AA.

XX AAU01034;

AC AAU01034;

DT 04-JUL-2001 (first entry)

XX Human secreted soluble alpha2delta calcium channel subunit #14 protein.

DE Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;  
alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;  
gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;  
filter binding assay; wheat germ lectin flashplate assay.

XX Homo sapiens.

PN WO200119870-A2.

XX 22-MAR-2001.

XX 18-SEP-2000; 2000WO-EP09137.

XX 16-SEP-1999; 99US-0397550.

XX (WARN ) WARNER LAMBERT CO.

XX Brown JP, Bertelli F;

XX WPI; 2001-235262/24.

XX N-PSDB; AAS01425.

PT Calcium channel alpha2delta subunits, useful in e.g. SPA assays,

Flashplate assays, Nickel Flashplate assays, Filter binding assays or Wheat Germ Lectin Flashplate assays -  
 Claim 31; Page 137-140; 160pp; English.

The present sequence represents human secreted calcium channel alpha2delta subunit #14 which is soluble and retains the functional characteristics of the full length or wild type alpha2delta subunit (AAU01025) from which it is derived. The invention relates to truncated alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins which retain their affinity for radioactively labelled ligands. The alpha2delta subunit is 1 of the components of the heteromultimeric voltage-dependent calcium channel (VDCC) complexes present in neuronal and non-neuronal tissues including heart and skeletal muscle. Numerous soluble forms of the human calcium channel alpha2delta subunits (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the porcine calcium channel alpha2delta subunits (AAU01027-AAU01031) are described. The secreted soluble alpha2delta subunit may be used in assays e.g. scintillation proximity assay (SPA), flashplate, nickel flashplate, filter binding or wheat germ lectin flashplate assays to detect or measure the binding or interaction of a ligand (e.g. gabapentin, L-Norleucine, L-Allo-isoleucine, L-methionine, L-leucine, L-isoleucine, L-Valine, Spermine and/or L-Phenylalanine) of a calcium channel alpha2delta subunit.

SQ Sequence 1063 AA;

Query Match 100.0%; Score 5599; DB 22; Length 1063;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLFOSLLIGSSSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
 Db 1 MAAGCLLALTTLFOSLLIGSSSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
 QY 61 YEKYQDLYTVEPNARQLVEAARDIEKLLSNRSKALVSLALEAEKVQAAHOWREDFASN 120  
 Db 61 YEKYQDLYTVEPNARQLVEAARDIEKLLSNRSKALVSLALEAEKVQAAHOWREDFASN 120  
 QY 121 EVVYNAKDDLDPEKNDSEPSQRIKPVFIEDANFGROIYQHAHVHPTDIYEGSTIVL 180  
 Db 121 EVVYNAKDDLDPEKNDSEPSQRIKPVFIEDANFGROIYQHAHVHPTDIYEGSTIVL 180  
 QY 181 NELNWTSSALDEVFKKREEDPSLWQVPGSGATGLARYYPASPDWNSRTPNKIDLYDVR 240  
 Db 181 NELNWTSSALDEVFKKREEDPSLWQVPGSGATGLARYYPASPDWNSRTPNKIDLYDVR 240  
 QY 241 RPWYIQAASPKDMLILVDVSGVSGSLTKLIRTSVSEMLETLDSDDDFVNVASFNSNAQD 300  
 Db 241 RPWYIQAASPKDMLILVDVSGVSGSLTKLIRTSVSEMLETLDSDDDFVNVASFNSNAQD 300  
 QY 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGITDYKKGFSFAPEQLLNYNVSRANCNKTI 360  
 Db 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGITDYKKGFSFAPEQLLNYNVSRANCNKTI 360  
 QY 361 FTDGGEERAQETFNKYNKKVRFRESVGOHNYERGPQIOMACENKGYIETPSIGAIR 420  
 Db 361 FTDGGEERAQETFNKYNKKVRFRESVGOHNYERGPQIOMACENKGYIETPSIGAIR 420  
 QY 421 INTQEYLDVLGRPMVLADKAKQVQWNVYLDLDELGLVITGTLVPFNITGQFENKTNLK 480  
 Db 421 INTQEYLDVLGRPMVLADKAKQVQWNVYLDLDELGLVITGTLVPFNITGQFENKTNLK 480  
 QY 481 NQLILGVMGVDVSLDIKRLTPRTCLPNCNGYFAIDPNGYVLLHPNLOPKNPKSQEPVTL 540  
 Db 481 NQLILGVMGVDVSLDIKRLTPRTCLPNCNGYFAIDPNGYVLLHPNLOPKNPKSQEPVTL 540  
 QY 541 DFLDAELENLKVETRNKMDGESSEKTFRLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
 Db 541 DFLDAELENLKVETRNKMDGESSEKTFRLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
 QY 601 ALVLPYTSFYFIKAKLEETITQARSKKGMKDSKSETLKPDNFEESGYTFTIAPRDYCNDLKI 660  
 Db 601 ALVLPYTSFYFIKAKLEETITQARSKKGMKDSKSETLKPDNFEESGYTFTIAPRDYCNDLKI 660

Db 601 ALVLPYTSFYFIKAKLEETITQARSKKGMKDSKSETLKPDNFEESGYTFTIAPRDYCNDLKI 660  
 QY 661 SDNTEFLNFEFIDRKTPNPNPSCNADLINRVLLDAGETNELVQYWSKQKNKGVKAR 720  
 Db 661 SDNTEFLNFEFIDRKTPNPNPSCNADLINRVLLDAGETNELVQYWSKQKNKGVKAR 720  
 QY 721 FVYTDGGITRVYKPEAGENWQENPEYEDSFYKRSLDNDNYFTAPYFNKSGPGAYESGI 780  
 Db 721 FVYTDGGITRVYKPEAGENWQENPEYEDSFYKRSLDNDNYFTAPYFNKSGPGAYESGI 780  
 QY 781 MVSQKAVEIYIQGKLLPAPVAVGIIKIDVNSWTENFTKTSIRDPACAGPVCDCKRNSDVMDCVI 840  
 Db 781 MVSQKAVEIYIQGKLLPAPVAVGIIKIDVNSWTENFTKTSIRDPACAGPVCDCKRNSDVMDCVI 840  
 QY 841 LDGGLFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNIISVAFNKSVDYQSVCEPGAAPKQ 900  
 Db 841 LDGGLFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNIISVAFNKSVDYQSVCEPGAAPKQ 900  
 QY 901 GAGHRSAVPSVADIIQIGWATAAAWSIIQQFLLSLTPRLLLEAVEMEDDDFTASLSKQ 960  
 Db 901 GAGHRSAVPSVADIIQIGWATAAAWSIIQQFLLSLTPRLLLEAVEMEDDDFTASLSKQ 960  
 QY 961 SCITEQTQFFFDNDKSFSGVLDCGNCRIIFHCEKLMNTNLIIFIMVESKGTGCPDTRLLI 1020  
 Db 961 SCITEQTQFFFDNDKSFSGVLDCGNCRIIFHCEKLMNTNLIIFIMVESKGTGCPDTRLLI 1020  
 QY 1021 QABQTSQDPNCPDMVKQPRYKRGPDVCFDNNVLEDTDCGGVS 1063  
 Db 1021 QABQTSQDPNCPDMVKQPRYKRGPDVCFDNNVLEDTDCGGVS 1063  
 RESULT 2  
 AAB62258  
 ID AAB62258 standard; Protein; 1063 AA.  
 XX  
 AC AAB62258;  
 XX  
 DT 11-JUN-2001 (first entry)  
 XX  
 DE Porcine calcium channel alpha2delta subunit.  
 XX  
 KW Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;  
 KW nervous system disorder; pain; epilepsy; anxiety; pig.  
 XX  
 OS Sus scrofa.  
 XX  
 PN WO200120336-A2.  
 XX  
 PD 22-MAR-2001.  
 XX  
 PF 18-SEP-2000; 2000WO-EP09136.  
 XX  
 PR 16-SEP-1999; 99US-0397549.  
 XX  
 PA (WARN ) WARNER LAMBERT CO.  
 XX  
 PI Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;  
 XX WPI; 2001-257902/26.  
 DR N-PSDB; AAF57562.  
 XX  
 PT Competitive binding assay for screening ligands which bind a cerebral  
 PT cortical voltage-dependent calcium channel alpha2delta-1 subunit,  
 PT where the ligands identified are useful for treating disorders of the  
 PT nervous system, including pain -  
 XX  
 PS Claim 8; Page 135-139; 158pp; English.  
 XX  
 CC The invention relates to a new method for screening ligands which bind a  
 CC cerebral cortical voltage-dependent calcium channel alpha2delta subunit,  
 CC preferably alpha2delta-1 subunit. The method comprises contacting a  
 CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of  
 CC interest and a labelled compound which binds the subunit, followed by

CC measuring the level of binding of the labelled compound to alpha2delta-1  
 CC subunit. The method is useful for screening ligands, preferably  
 CC biologically active products that modulate a nervous system function,  
 CC which bind a cerebral cortical voltage-dependent calcium channel,  
 CC alpha2delta-1 subunit. The ligands identified by the method are useful  
 CC for treating disorders of the nervous system, including pain, epilepsy  
 CC and anxiety. The present sequence represents a porcine calcium channel  
 CC alpha2delta subunit.

XX Sequence 1063 AA;

Query Match 100.0%; Score 5599; DB 22; Length 1063;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLFQSLIGPSSEPPSPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
 DB 1 MAAGCLLALTTLFQSLIGPSSEPPSPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
 QY 61 YEKYODLYTVPEPNARQIVETARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120  
 DB 61 YEKYODLYTVPEPNARQIVETARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120  
 QY 121 EYVYNKADDDLPKNDSEPSQRIKPVIEDANFGROIISYQHAHVHIPTDIYEGSTIVL 180  
 DB 121 EYVYNKADDDLPKNDSEPSQRIKPVIEDANFGROIISYQHAHVHIPTDIYEGSTIVL 180  
 QY 181 NELNWTSSALDEVFKKNEEDPSLLQWFGSATGLARYYPASPPWVDNSRTPNKIDLYDVR 240  
 DB 181 NELNWTSSALDEVFKKNEEDPSLLQWFGSATGLARYYPASPPWVDNSRTPNKIDLYDVR 240  
 QY 241 RPWYIOGAASPKDMLILVDVSGVSLGLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
 DB 241 RPWYIOGAASPKDMLILVDVSGVSLGLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
 QY 301 VSCFQHLVQAVNRKVKLDVANNITAKGIDYKKGFSFAFEOLLNYSRANCNKIIML 360  
 DB 301 VSCFQHLVQAVNRKVKLDVANNITAKGIDYKKGFSFAFEOLLNYSRANCNKIIML 360  
 QY 361 FTDGGEBAQRIFNKYNKDKVRFVSQHNVERGPIOWMACENKGYIYEIPSGAIR 420  
 DB 361 FTDGGEBAQRIFNKYNKDKVRFVSQHNVERGPIOWMACENKGYIYEIPSGAIR 420  
 QY 421 INTOEYLDVLGRPMVLADGAKQVQWNTVLDLLEGLVITGTLVPFNITGQFENKTNLK 480  
 DB 421 INTOEYLDVLGRPMVLADGAKQVQWNTVLDLLEGLVITGTLVPFNITGQFENKTNLK 480  
 QY 481 NQLILGVMGVDVSLIEDIKRLTPRTLCPCNGYIFAIDPNGYVLLHPNLQPKNPKSQEPVTL 540  
 DB 481 NQLILGVMGVDVSLIEDIKRLTPRTLCPCNGYIFAIDPNGYVLLHPNLQPKNPKSQEPVTL 540  
 QY 541 DFLDAELENDIKVEIRKNMIDGESCEKTFRTLKVSQDERYIDKGNRTYTTPVNGTDYSL 600  
 DB 541 DFLDAELENDIKVEIRKNMIDGESCEKTFRTLKVSQDERYIDKGNRTYTTPVNGTDYSL 600  
 QY 601 ALVLPTYSFYIIKAKLEETITQARSKGKMKDSETLKPDPNFESGVTFTAPRDYCNLDLKI 660  
 DB 601 ALVLPTYSFYIIKAKLEETITQARSKGKMKDSETLKPDPNFESGVTFTAPRDYCNLDLKI 660  
 QY 661 SDNTEFLNFNEIDRKTNPNSCNADLINRVLLDAGFTNELVQVWSKQKNKGVKAR 720  
 DB 661 SDNTEFLNFNEIDRKTNPNSCNADLINRVLLDAGFTNELVQVWSKQKNKGVKAR 720  
 QY 721 FVYTDGGITRVYKPEAGENKQENPEYEDSFYKRSLDNDNYVTAPYFNKSGPGAYESGI 780  
 DB 721 FVYTDGGITRVYKPEAGENKQENPEYEDSFYKRSLDNDNYVTAPYFNKSGPGAYESGI 780  
 QY 781 MVSKAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRDPACGVPVCDCKRNSDVMDCVI 840  
 DB 781 MVSKAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRDPACGVPVCDCKRNSDVMDCVI 840  
 QY 841 LDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 900  
 DB 841 LDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 900

DB 841 LDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 900  
 QY 901 GAGHRSAYVPSVADILQIGWATAAAWSIIQQFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
 DB 901 GAGHRSAYVPSVADILQIGWATAAAWSIIQQFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
 QY 961 SCITEQTOYFFDNDKSKFSFGLDGCNGSRIFHGEKLMNTNLIFITMVESKGTCPCDTRLII 1020  
 DB 961 SCITEQTOYFFDNDKSKFSFGLDGCNGSRIFHGEKLMNTNLIFITMVESKGTCPCDTRLII 1020  
 QY 1021 QAEQTSQDGNPCDMVKQPRYKGPVDFCNVNNVLEDYDTCGGVS 1063  
 DB 1021 QAEQTSQDGNPCDMVKQPRYKGPVDFCNVNNVLEDYDTCGGVS 1063

# RESULT 3

AAR71011  
 ID AAR71011 standard; Protein; 1091 AA.  
 XX AAR71011;  
 XX 01-DEC-1995 (first entry)  
 DT Human neuronal calcium channel subunit alpha 2b.  
 XX Human neuronal calcium channel subunit alpha 2b.  
 DE Calcium channel subunit; antagonist; agonist; diagnosis;  
 XX Lambert Eaton Syndrome.  
 KW Homo sapiens.  
 XX OS  
 XX WO9504822-A.  
 XX 16-FEB-1995.  
 PD 11-AUG-1994; 94WO-US09230.  
 PF 11-AUG-1993; 93US-0105536.  
 PR 05-NOV-1993; 93US-0149097.  
 XX (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.  
 XX Ellis SB, Gillespie A, Harpold MM, McCue AF, Williams ME;  
 XX WPI; 1995-090900/12.  
 DR N-PSDB; AAQ84664.  
 XX DNA encoding human calcium channel sub-unit(s) - used for  
 PT developing prods. for studying calcium channels, e.g. for  
 .PT obtaining agonists and antagonists

Disclosure: Page 166-171; 285pp; English.

Human neuronal alpha 2 coding sequence (AAQ84664) transcript is  
 differentially processed in skeletal muscle, aorta, and CNS in  
 the region corresp. to nt 1595-1942 of AAQ84664 in each of the  
 tissues. Five alternatively spliced variant transcripts that differ  
 in the presence or absence of one or three different portions of  
 this region. There are three sequences involved (see AAQ84664 FT  
 and AAQ84665 FT), sequence 1, sequence 2 and sequence 3. The five  
 alpha 2 encoding transcripts from the different tissues include  
 different combinations of the three sequences, except for one of  
 the alpha 2 transcripts expressed in aorta which lacks all three  
 sequences. The five alpha 2 forms identified are (1) a form that  
 lacks sequence 3 called alpha 2a, expressed in skeletal muscle  
 (2) one that lacks sequence 1 called alpha 2b, expressed in CNS  
 (3) one that lacks sequences 1 and 2 called alpha 2c, expressed in  
 aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,  
 expressed in aorta and (5) one that lacks sequences 1 and 3  
 called alpha 2e.

Sequence 1091 AA;

Query Match 100.0%; Score 5599; DB 16; Length 1091;

Best Local Similarity 100.0%; Pred. No. 0;		Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	MAAGCLLALTTLTFLQSLTLLGSPSEPPPSAVTIKSWDKMQEDLVTLAKTAGVNLVDI	60
Db	1	MAAGCLLALTTLTFLQSLTLLGSPSEPPPSAVTIKSWDKMQEDLVTLAKTAGVNLVDI	60
QY	61	YKYYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN	120
Db	61	YKYYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN	120
QY	121	EVVYNAKDDLPKNDSPGSGRIKPVIEDANFGRQISYQAAVHIPTDIYEGSTIVL	180
Db	121	EVVYNAKDDLPKNDSPGSGRIKPVIEDANFGRQISYQAAVHIPTDIYEGSTIVL	180
QY	181	NELNWTLSALDEVFKKREDEPSSLWQVFGSATGLARYYPASPWVDSNRTPNPKIDLYDVR	240
Db	181	NELNWTLSALDEVFKKREDEPSSLWQVFGSATGLARYYPASPWVDSNRTPNPKIDLYDVR	240
QY	241	RPWYIQGAASPKDMLILVDVSGVSLTLKLRISVSEMLETSDDDFVNVASFNSNAQD	300
Db	241	RPWYIQGAASPKDMLILVDVSGVSLTLKLRISVSEMLETSDDDFVNVASFNSNAQD	300
QY	301	VSCFQHLVQANVKNKVLKADANNITAKGIDYKKGFSFAFQOLLNYSVRANCNKIIML	360
Db	301	VSCFQHLVQANVKNKVLKADANNITAKGIDYKKGFSFAFQOLLNYSVRANCNKIIML	360
QY	361	FTDGGERAQEIFNKYKDKKVRVFSYQHNRYERGPQIOWMACENKGYEIPISGAI	420
Db	361	FTDGGERAQEIFNKYKDKKVRVFSYQHNRYERGPQIOWMACENKGYEIPISGAI	420
QY	421	INTQYLDVLRPMVLGAKAKQVQNTNYLDALGLVITGTLPVFNITGOFENKTNLK	480
Db	421	INTQYLDVLRPMVLGAKAKQVQNTNYLDALGLVITGTLPVFNITGOFENKTNLK	480
QY	481	NQLILGMVGVDSLEDDIKRLTPFTLCPNGYFAIDPNCYVLLHPLNLPKPKSEPVTL	540
Db	481	NQLILGMVGVDSLEDDIKRLTPFTLCPNGYFAIDPNCYVLLHPLNLPKPKSEPVTL	540
QY	541	DFLDAELNDIKYIIRNMKIDGESGKFTTLVKSODERYIDKGNRTYTWTPVNGTDYSL	600
Db	541	DFLDAELNDIKYIIRNMKIDGESGKFTTLVKSODERYIDKGNRTYTWTPVNGTDYSL	600
QY	601	ALVLPYTSFYIIKALEETITQARSKKGMKQSETLKPDPNFESGYTFTAPROYCNDLKI	660
Db	601	ALVLPYTSFYIIKALEETITQARSKKGMKQSETLKPDPNFESGYTFTAPROYCNDLKI	660
QY	661	SDNTEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYWSKQNKIKGVKAR	720
Db	661	SDNTEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYWSKQNKIKGVKAR	720
QY	721	FVYTDGGITRVYKPEAGENQENPTYEDSFYKRSLDNDYNYFTAPYFNKSGPGAYESGI	780
Db	721	FVYTDGGITRVYKPEAGENQENPTYEDSFYKRSLDNDYNYFTAPYFNKSGPGAYESGI	780
QY	781	MVSKAVEIYIQGLLPVAVGIIKIDVNSWLENFTKTSIRDPACAGPVCDCKRNSDVMDCVI	840
Db	781	MVSKAVEIYIQGLLPVAVGIIKIDVNSWLENFTKTSIRDPACAGPVCDCKRNSDVMDCVI	840
QY	841	LDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNIYSVAFNKSVDYQSVCEPQAPKQ	900
Db	841	LDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNIYSVAFNKSVDYQSVCEPQAPKQ	900
QY	901	GAGHRSAYVPSVADIIQIGWATAAASIILOQFLLSLTPRLLAEVEMEDDFTASLSKQ	960
Db	901	GAGHRSAYVPSVADIIQIGWATAAASIILOQFLLSLTPRLLAEVEMEDDFTASLSKQ	960
QY	961	SCITEQTOYFFDNDKSKFSGLDCGNCRIHFHGEKLMNTNLFIMVESKGTGCPDTRLLI	1020
Db	961	SCITEQTOYFFDNDKSKFSGLDCGNCRIHFHGEKLMNTNLFIMVESKGTGCPDTRLLI	1020
QY	1021	QAEQTSDBPNPCDMVKQPRYKGPVCFDNNVLEDTYDCGGVS	1063
Db	1021	QAEQTSDBPNPCDMVKQPRYKGPVCFDNNVLEDTYDCGGVS	1063

Query Match 100.0%; Score 5599; DB 19; Length 1091;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLTFLQSLTLLGSPSEPPPSAVTIKSWDKMQEDLVTLAKTAGVNLVDI 60

Db 1 MAAGCLLALTTLTFLQSLTLLGSPSEPPPSAVTIKSWDKMQEDLVTLAKTAGVNLVDI 60

QY 61 YKYYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120

Db 61 YKYYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120

RESULT 4

AAW63145

ID AAW63145 standard; Protein; 1091 AA.

XX

AAW63145;

AC

XX

12-OCT-1998 (first entry)

DE

Human calcium channel alpha-2 subunit.

XX

Alpha-2 subunit; human; calcium channel; assay; detection;

KW characterisation; Lambert Eaton Syndrome; LES; diagnosis.

XX

Homo sapiens.

XX

US792846-A.

XX

11-AUG-1998.

XX

31-MAY-1995; 95US-0455543.

XX

04-APR-1994; 94US-0223305.

PR

04-APR-1989; 88US-0176899.

PR

04-APR-1989; 89US-0603751.

PR

04-APR-1989; 89WO-US01408.

PR

20-FEB-1990; 90US-0482384.

PR

30-NOV-1990; 90US-0620250.

PR

15-AUG-1991; 91US-0745206.

PR

31-MAY-1995; 95US-0455543.

XX

(SIBI-) SIBIA NEUROSCIENCES INC.

XX

Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;

PI Williams ME;

XX

WPI; 1998-456192/39.

DR

N-PSDB; AAV42689.

XX

DNA encoding human calcium channel alpha 1B subunit protein -

PT useful for recombinant production of the channel for screening of

its modulators, and diagnosis of Lambert Eaton Syndrome

XX

Claim 4; Columns 283-288; 166pp; English.

XX

The present sequence represents the alpha-2 subunit of a human calcium channel. Calcium channels are membrane-spanning, multi-subunit proteins that allow controlled entry of calcium ions into cells. This leads to depolarisation events required for muscle contraction. The recombinant subunit, when expressed with nucleic acids encoding the complete calcium channel, can be used in assays for the detection and characterisation of compounds that modulate the channel. The DNA encoding the subunits can be alternatively spliced when transcribed, giving more than one form of the protein from the same transcript, each having slightly different properties. In addition, the reactivity of the alpha 1 subunit with IgG molecules from the serum of an individual with Lambert Eaton Syndrome (LES) can be used as a diagnostic for the disease.

XX

Sequence 1091 AA;

SQ

QY 121 EVVYNAKDDLDPEKNDSEPGSRIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180  
Db 121 EVVYNAKDDLDPEKNDSEPGSRIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180  
QY 181 NELNWTISALDEVPKKNREDEPSLLNQVFGSATGLARYYPASPDVNSRTPNKIDLYDVR 240  
Db 181 NELNWTISALDEVPKKNREDEPSLLNQVFGSATGLARYYPASPDVNSRTPNKIDLYDVR 240  
QY 241 RPWYIQAASPRDMLILVDVSGVSLTKLIRTSVSEMLETLSDDDFVNVSFNSNAQD 300  
Db 241 RPWYIQAASPRDMLILVDVSGVSLTKLIRTSVSEMLETLSDDDFVNVSFNSNAQD 300  
QY 301 VSCFQHLVQANVRNKKVLDVAVNNTAGITDYKKGFSFAPEQLLNTNVSFRANCKIIML 360  
Db 301 VSCFQHLVQANVRNKKVLDVAVNNTAGITDYKKGFSFAPEQLLNTNVSFRANCKIIML 360  
QY 361 FTDGGEERAQELFNKYNDKVRFRFVSOGHNYERGPIONMACENKGYIYEPSTGAIR 420  
Db 361 FTDGGEERAQELFNKYNDKVRFRFVSOGHNYERGPIONMACENKGYIYEPSTGAIR 420  
QY 421 INTQYLDVGRPMVLAGDQKQVNTNVLDALELGLVITGLPVENITGQFENKTNLK 480  
Db 421 INTQYLDVGRPMVLAGDQKQVNTNVLDALELGLVITGLPVENITGQFENKTNLK 480  
QY 481 NOLILGVGVDSVLEDIKRLTPRETLCPPNGYYPFAIDPNGVYLLHPNLOPKNPKSQBPVTL 540  
Db 481 NOLILGVGVDSVLEDIKRLTPRETLCPPNGYYPFAIDPNGVYLLHPNLOPKNPKSQBPVTL 540  
QY 541 DFLDALENDIKVEIRNKMIDGSEKTFRTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
Db 541 DFLDALENDIKVEIRNKMIDGSEKTFRTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
QY 601 ALVLPYTSFYIKAKLETTIQAARKKMKDSETLKPDNFEESGYTFIAPRDYCNLDKI 660  
Db 601 ALVLPYTSFYIKAKLETTIQAARKKMKDSETLKPDNFEESGYTFIAPRDYCNLDKI 660  
QY 661 SDNTEFLNNEFTDRKTPNPNPCNADLINRVLLDAGFTNELVQNYWSKQNKIKGVAR 720  
Db 661 SDNTEFLNNEFTDRKTPNPNPCNADLINRVLLDAGFTNELVQNYWSKQNKIKGVAR 720  
QY 721 FVWTDGGITRVYKPEAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
Db 721 FVWTDGGITRVYKPEAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
QY 781 MVSKAVEIYIYOGKLLKPAVVGIIKIDVNSWIENTFTKTSIRDPACGPPVCDCKRNSDVNDY 840  
Db 781 MVSKAVEIYIYOGKLLKPAVVGIIKIDVNSWIENTFTKTSIRDPACGPPVCDCKRNSDVNDY 840  
QY 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRLVNIYVAFNKSVDYOSVCEPAAAPKQ 900  
Db 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRLVNIYVAFNKSVDYOSVCEPAAAPKQ 900  
QY 901 GAGHRSAYVPSVADIIQIGMWATAAASIILOQFLLSLTFPRLEAVEMEDDDFTASLSQ 960  
Db 901 GAGHRSAYVPSVADIIQIGMWATAAASIILOQFLLSLTFPRLEAVEMEDDDFTASLSQ 960  
QY 961 SCITEQTOYFEDNDKSFSGVLDCGNCRIFFHCEKLMNTNLIFIMVESKGTCPDTRLLI 1020  
Db 961 SCITEQTOYFEDNDKSFSGVLDCGNCRIFFHCEKLMNTNLIFIMVESKGTCPDTRLLI 1020  
QY 1021 QAEQTSQDPNCPDMVKQPRYRKGPDPVCFDNNVLEDYTDGCGYS 1063  
Db 1021 QAEQTSQDPNCPDMVKQPRYRKGPDPVCFDNNVLEDYTDGCGYS 1063

## RESULT 5

AAB10576

ID AAB10576 standard; Protein; 1091 AA.

XX AC

XX AC

XX AC

DT 22-DEC-2000 (first entry)

XX Human calcium channel alpha-2 subunit protein.

XX Human; calcium channel; calcium channel subunit; diagnosis;  
Lambert Eaton Syndrome; calcium channel subunit alpha-2.

XX Homo sapiens.

XX US6096514-A.

XX 01-AUG-2000.

XX 25-MAY-1995; 95US-0450562.

XX 04-APR-1988; 88US-0176899.

XX 02-FEB-1990; 90US-0482384.

XX 08-NOV-1990; 90US-0603751.

XX 30-NOV-1990; 90US-0620250.

XX 15-AUG-1991; 91US-0745206.

XX 10-APR-1992; 92US-0868354.

XX 13-JUL-1992; 92US-0914231.

XX 11-AUG-1993; 93US-0105536.

XX 05-NOV-1993; 93US-0149097.

XX 07-FEB-1994; 94US-0193078.

XX 04-APR-1994; 94US-0223305.

XX 11-AUG-1994; 94US-0290012.

XX 23-SEP-1994; 94US-0311363.

XX 28-SEP-1994; 94US-0314083.

XX 07-NOV-1994; 94US-0336257.

XX 13-MAR-1995; 95US-0404950.

XX (SIBI-) SIBIA NEUROSCIENCES INC.

XX Ellis SB, Williams ME, McCue AF, Harpold MM;

XX WPI; 2000-548230/50.

XX N-PSDB; AAA71707.

XX Human calcium channel beta subunit polynucleotides, useful for  
producing recombinant eukaryotic cells and for diagnosing Lambert Eaton  
Syndrome

XX Example IV; Column 135-144; 153pp; English.

XX This invention describes a novel isolated DNA molecule (I) comprising a  
sequence encoding a beta3-1 subunit of a human calcium channel.  
Nucleic acid probes comprising 14-30 contiguous nucleotides of  
beta3 subunit encoding DNA are useful for isolation and cloning of  
calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that  
express heterologous calcium channel are useful for identifying compounds  
that modulate calcium channel activity and in assays for identifying  
agonists and antagonists of calcium channel activity in humans. Human  
calcium channel subunit or eukaryotic cells expressing the channel are  
useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This  
sequence represents the human calcium channel alpha-2 subunit which is  
described in the method of the invention.

XX Sequence 1091 AA;

XX Query Match 100.0%; Score 5599; DB 21; Length 1091;

XX Best Local Similarity 100.0%; Pred. No. 0;

XX Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLIALTLTLFQSLILGPSSEPPPSAVTIKSWDKMOEDLVTLAKTAGVNLVDI 60

Db 1 MAAGCLIALTLTLFQSLILGPSSEPPPSAVTIKSWDKMOEDLVTLAKTAGVNLVDI 60

QY 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALYSALAEKVOAAHQWRDFASN 120

Db 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALYSALAEKVOAAHQWRDFASN 120

QY 121 EVVYNAKDDLDPEKNDSEPGSRIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180

Db 121 EVVYNAKDDLDPEKNDSEPGSRIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180

Db 121 EVVYNAKDDLDPEKNDSEPSQRIKPVIEDANFGRIQISYQAAVHIPTDIYEGSTIVL 180  
 QY 181 NELNWTSSALDEVFYKKNREEDPSLLWQVFGSATGLARYYPASPWDNSRTNPKIDLDYVRR 240  
 Db 181 NELNWTSSALDEVFYKKNREEDPSLLWQVFGSATGLARYYPASPWDNSRTNPKIDLDYVRR 240  
 QY 241 RPWYIOGAASPKDMLILVDVSGVSGLTGLKIRTSVSEMLETISDDDFVNVASFNSNAQD 300  
 Db 241 RPWYIOGAASPKDMLILVDVSGVSGLTGLKIRTSVSEMLETISDDDFVNVASFNSNAQD 300  
 QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNYNVSRANCNKIIML 360  
 Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNYNVSRANCNKIIML 360  
 QY 361 FTDGGEERAQEIFNKNYKDKKVRFRFSVGOHNYERGIOWMACENKGYIYEIPSGAIR 420  
 Db 361 FTDGGEERAQEIFNKNYKDKKVRFRFSVGOHNYERGIOWMACENKGYIYEIPSGAIR 420  
 QY 421 INTQYELDLVGRPMVLADGKAKQVQWNTVYLDLDELGLVITGLTPVFNITGQFENKTNLK 480  
 Db 421 INTQYELDLVGRPMVLADGKAKQVQWNTVYLDLDELGLVITGLTPVFNITGQFENKTNLK 480  
 QY 481 NQLILGVMGVDVSLDEDIKRLPRFTLCPNGYIFALDPNGYVLLHPNLOPKNPKSQEPVTL 540  
 Db 481 NQLILGVMGVDVSLDEDIKRLPRFTLCPNGYIFALDPNGYVLLHPNLOPKNPKSQEPVTL 540  
 QY 541 DFLDAELENKIVETRNKMGIDGSEKTRTLVKQSODERYIDKGNRTYTWTPVNGTDYSL 600  
 Db 541 DFLDAELENKIVETRNKMGIDGSEKTRTLVKQSODERYIDKGNRTYTWTPVNGTDYSL 600  
 QY 601 ALVLPYTFYIYKALEETITQARSKKGMKDSSETLPKDPNFEEGSGYTFIAPROYCNDLKI 660  
 Db 601 ALVLPYTFYIYKALEETITQARSKKGMKDSSETLPKDPNFEEGSGYTFIAPROYCNDLKI 660  
 QY 661 SDNTEFLNFEFIDRKTPNPNCSNADLINRVLLDAGFTNELVQNYWSKOKNKGKVKAR 720  
 Db 661 SDNTEFLNFEFIDRKTPNPNCSNADLINRVLLDAGFTNELVQNYWSKOKNKGKVKAR 720  
 QY 721 FVYTDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNVTFTAPYFNKSGPGAYESGI 780  
 Db 721 FVYTDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNVTFTAPYFNKSGPGAYESGI 780  
 QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIEFTKTSIRDPCAGVPCCKRNSDVMDCVI 840  
 Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIEFTKTSIRDPCAGVPCCKRNSDVMDCVI 840  
 QY 841 LDDGGFLLMANHDDYTNQIGRFTGEIDPSLMRHLVNIYVAFNKSVDYQSYCEPGAAPKQ 900  
 Db 841 LDDGGFLLMANHDDYTNQIGRFTGEIDPSLMRHLVNIYVAFNKSVDYQSYCEPGAAPKQ 900  
 QY 901 GAGHSAYVPSVADILQIGWATAAASWILQOFLSLTFPRLLLEAVEMEDDDFTASLSKQ 960  
 Db 901 GAGHSAYVPSVADILQIGWATAAASWILQOFLSLTFPRLLLEAVEMEDDDFTASLSKQ 960  
 QY 961 SCITEQTOYFFDNDKSFSGVLDCGNCRIHFGEKLMNTNLIIFIMVESKGCPCDTRLII 1020  
 Db 961 SCITEQTOYFFDNDKSFSGVLDCGNCRIHFGEKLMNTNLIIFIMVESKGCPCDTRLII 1020  
 QY 1021 QAEQTSQDGNPCDMWQKPYRKGPDVCFDNNVLEDYDCGGVVS 1063  
 Db 1021 QAEQTSQDGNPCDMWQKPYRKGPDVCFDNNVLEDYDCGGVVS 1063  
 RESULT 6  
 ID AAU01035  
 XX AAU01035 standard; Protein; 1091 AA.  
 AC AAU01035;  
 XX  
 DT 04-JUL-2001 (first entry)  
 XX Human secreted soluble alpha2delta calcium channel subunit #15 protein.  
 XX

KW Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;  
 KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;  
 KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;  
 XX filter binding assay; wheat germ lectin flashplate assay.  
 OS Homo sapiens.  
 PN WO200119870-A2.  
 XX  
 PD 22-MAR-2001.  
 XX  
 XX 18-SEP-2000; 2000WO-EP09137.  
 PF  
 XX 16-SEP-1999; 99US-03997550.  
 PR  
 PA (WARN ) WARNER LAMBERT CO.  
 XX  
 PI Brown JP, Bertelli F;  
 DR WPI; 2001-235262/24.  
 XX N-PSDB; AAS01426.  
 DR  
 XX Calcium channel alpha2delta subunits, useful in e.g. SPA assays,  
 PT Flashplate assays, Nickel Flashplate assays, Filter binding assays or  
 PT Wheat germ lectin Flashplate assays -  
 XX  
 PS Claim 30; Page 141-144; 160pp; English.  
 XX  
 CC The present sequence represents human secreted calcium channel  
 CC alpha2delta subunit #15 which is soluble and retains the functional  
 CC characteristics of the full length or wild type alpha2delta subunit  
 CC (AAU01025) from which it is derived. The invention relates to truncated  
 CC alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins  
 CC which retain their affinity for radioactively labelled gabapentin. The  
 CC alpha2delta subunit is 1 of the components of the heteromultimeric  
 CC voltage-dependent calcium channel (VDCC) complexes present in neuronal  
 CC and non-neuronal tissues including heart and skeletal muscle. Numerous  
 CC soluble forms of the human calcium channel alpha2delta subunits  
 CC (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the  
 CC porcine calcium channel alpha2delta subunits (AAU01027-AAU01031) are  
 CC described. The secreted soluble alpha2delta subunit may be used in assays  
 CC e.g. scintillation proximity assay (SPA), flashplate, nickel flashplate,  
 CC filter binding or wheat germ lectin flashplate assays to detect or  
 CC measure the binding or interaction of a ligand (e.g. gabapentin,  
 CC L-Norleucine, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Isoleucine,  
 CC L-Valine, Spermine and/or L-Phenylalanine) of a calcium channel  
 CC alpha2delta subunit.  
 XX  
 SQ Sequence 1091 AA;

Query Match 100.0%; Score 5599; DB 22; Length 1091;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCILLALTTLTFLQSLILGPSSEPFPSAVTIKSWDKMQEDLVTLAKTAGSVNQLVDI 60  
 Db 1 MAAGCILLALTTLTFLQSLILGPSSEPFPSAVTIKSWDKMQEDLVTLAKTAGSVNQLVDI 60  
 QY 61 YEKYQDLYTVEPNNAQVLEIARDIEKLLSNRSKALVSLAEKVKQAAHQRDEFASN 120  
 Db 61 YEKYQDLYTVEPNNAQVLEIARDIEKLLSNRSKALVSLAEKVKQAAHQRDEFASN 120  
 QY 121 EVVYNAKDDLDPEKNDSEPSQRIKPVIEDANFGRIQISYQAAVHIPTDIYEGSTIVL 180  
 Db 121 EVVYNAKDDLDPEKNDSEPSQRIKPVIEDANFGRIQISYQAAVHIPTDIYEGSTIVL 180  
 QY 181 NELNWTSSALDEVFYKKNREEDPSLLWQVFGSATGLARYYPASPWDNSRTNPKIDLDYVRR 240  
 Db 181 NELNWTSSALDEVFYKKNREEDPSLLWQVFGSATGLARYYPASPWDNSRTNPKIDLDYVRR 240  
 QY 241 RPWYIOGAASPKDMLILVDVSGVSGLTGLKIRTSVSEMLETISDDDFVNVASFNSNAQD 300  
 Db 241 RPWYIOGAASPKDMLILVDVSGVSGLTGLKIRTSVSEMLETISDDDFVNVASFNSNAQD 300

QY 301 VSCFOHLVQANVRNKKVILKDAVNNTAKGITDYKKGFSFAFEOQLLNNVSRANCKIIML 360  
Db 301 VSCFOHLVQANVRNKKVILKDAVNNTAKGITDYKKGFSFAFEOQLLNNVSRANCKIIML 360  
QY 361 FTDGGERAQEIEFNKYNKDKKVRFRFSVGOHNYERGPIOWMACENKGYEIPSGAIGR 420  
Db 361 FTDGGERAQEIEFNKYNKDKKVRFRFSVGOHNYERGPIOWMACENKGYEIPSGAIGR 420  
QY 421 INTQEYLDVLGRPMVLGADKAKOVQWNTNVLDALEGLVITGTLPVFNITGQFNKNLNLK 480  
Db 421 INTQEYLDVLGRPMVLGADKAKOVQWNTNVLDALEGLVITGTLPVFNITGQFNKNLNLK 480  
QY 481 NQILILGVMGVDVSLIEDIKRLTPRFTLCPNGYFAIDPNCYVLLHPNLQPKNKSQEPVTL 540  
Db 481 NQILILGVMGVDVSLIEDIKRLTPRFTLCPNGYFAIDPNCYVLLHPNLQPKNKSQEPVTL 540  
QY 541 DFLDAELNDIKVEIRNKMIDGESGKTFRTLKVSODERYIDKGNRTYTWTPVNGTDYSL 600  
Db 541 DFLDAELNDIKVEIRNKMIDGESGKTFRTLKVSODERYIDKGNRTYTWTPVNGTDYSL 600  
QY 601 ALVLPTYSFYIIKAKLEETITQARSKKGMKDSSETLKPONFEESGYTFIAPRDYCNLDKI 660  
Db 601 ALVLPTYSFYIIKAKLEETITQARSKKGMKDSSETLKPONFEESGYTFIAPRDYCNLDKI 660  
QY 661 SDNNTFELNFEIDRKTPNPNPSCNADLINRVLLDAGFTNVLQVWYKQKNIKGVKAR 720  
Db 661 SDNNTFELNFEIDRKTPNPNPSCNADLINRVLLDAGFTNVLQVWYKQKNIKGVKAR 720  
QY 721 FVYTDGGITRVYPKEAGENQENPEYEDSFYKRSIDNDNYVFTAPYFNKSGPGAYESGI 780  
Db 721 FVYTDGGITRVYPKEAGENQENPEYEDSFYKRSIDNDNYVFTAPYFNKSGPGAYESGI 780  
QY 781 MVS KAVEIYIQGLKLPVAVGKIDVNSWIENFTKTSIRDPCAGPVCDCKRNSDVMDCVI 840  
Db 781 MVS KAVEIYIQGLKLPVAVGKIDVNSWIENFTKTSIRDPCAGPVCDCKRNSDVMDCVI 840  
QY 841 LDGSGFLMANHDDYTNQIGRFFGEIDPSLMRHLNYSIYAFNKSVDYOSVCEPGAAPKQ 900  
Db 841 LDGSGFLMANHDDYTNQIGRFFGEIDPSLMRHLNYSIYAFNKSVDYOSVCEPGAAPKQ 900  
QY 901 GAGHSAYVPSVADIIQIGWATAAASIILOQFLLSLTFPRLLAEVEMEDDDFTASLSKQ 960  
Db 901 GAGHSAYVPSVADIIQIGWATAAASIILOQFLLSLTFPRLLAEVEMEDDDFTASLSKQ 960  
QY 961 SCITEQTQYFFDNDKSFSGVLDGNCNRSIFHGEKLMNTNLIFIMVESKGTCPDTRLLI 1020  
Db 961 SCITEQTQYFFDNDKSFSGVLDGNCNRSIFHGEKLMNTNLIFIMVESKGTCPDTRLLI 1020  
QY 1021 QAEQTS DGNPCDMVKQPRYKGPVCFDNNVLEDTDCGGYS 1063  
Db 1021 QAEQTS DGNPCDMVKQPRYKGPVCFDNNVLEDTDCGGYS 1063

## RESULT 7

AAB62259  
ID AAB62259 standard; Protein; 1091 AA.

XX AAB62259;

AC 11-JUN-2001 (first entry)

DT Porcine calcium channel alpha2delta subunit.

DE Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;  
KW nervous system disorder; pain; epilepsy; anxiety; pig.

XX Sus scrofa.

XX WO200120336-A2.

XX 22-MAR-2001.

XX

PF 18-SEP-2000; 200WO-EP09136.  
XX  
PR 16-SEP-1999; 99US-0397549.  
XX  
PA (WARN ) WARNER LAMBERT CO.  
XX  
PI Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;  
XX  
DR WPI; 2001-257902/26.  
DR N-PSDB; AAF57563.

Competitive binding assay for screening ligands which bind a cerebral  
cortical voltage-dependent calcium channel alpha2delta-1 subunit,  
where the ligands identified are useful for treating disorders of the  
nervous system, including pain -

PS Claim 7; Page 139-142; 150pp; English.

XX The invention relates to a new method for screening ligands which bind a  
cortical voltage-dependent calcium channel alpha2delta subunit,  
preferably alpha2delta-1 subunit. The method comprises contacting a  
secreted soluble recombinant alpha2delta-1 subunit with a ligand of  
interest and a labelled compound which binds the subunit, followed by  
measuring the level of binding of the labelled compound to alpha2delta-1  
subunit. The method is useful for screening ligands, preferably  
biologically active products that modulate a nervous system function,  
which bind a cerebral cortical voltage-dependent calcium channel  
alpha2delta-1 subunit. The ligands identified by the method are useful  
for treating disorders of the nervous system, including pain, epilepsy  
and anxiety. The present sequence represents a porcine calcium channel  
alpha2delta subunit.

XX Sequence 1091 AA;

Query Match 100.0%; Score 5599; DB 22; Length 1091;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLFQSLIGPSSEEPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

Db 1 MAAGCLLALTTLFQSLIGPSSEEPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

QY 61 YEKQDLYTVPNNARQIVEIARDDIEKLSNRKALVSLAEKVAQAHHQWREDFASN 120

Db 61 YEKQDLYTVPNNARQIVEIARDDIEKLSNRKALVSLAEKVAQAHHQWREDFASN 120

QY 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIYSQHAHVHTPTDIYEGSTIVL 180

Db 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIYSQHAHVHTPTDIYEGSTIVL 180

QY 181 NELNWTSAIDVEFKKNREEDPSLLWQVFGSATGLARYYPASPWDNSRTPNKIDLYDVR 240

Db 181 NELNWTSAIDVEFKKNREEDPSLLWQVFGSATGLARYYPASPWDNSRTPNKIDLYDVR 240

QY 241 RPWYIOGAASPKDMLILVDVSGVSGSLTKLIRTSVSEMLETSLDDDFVNVASFNQAQD 300

Db 241 RPWYIOGAASPKDMLILVDVSGVSGSLTKLIRTSVSEMLETSLDDDFVNVASFNQAQD 300

QY 301 VSCFOHLVQANVRNKKVILKDAVNNTAKGITDYKKGFSFAFEOQLLNNVSRANCKIIML 360

Db 301 VSCFOHLVQANVRNKKVILKDAVNNTAKGITDYKKGFSFAFEOQLLNNVSRANCKIIML 360

QY 361 FTDGGERAQEIEFNKYNKDKKVRFRFSVGOHNYERGPIOWMACENKGYEIPSGAIGR 420

Db 361 FTDGGERAQEIEFNKYNKDKKVRFRFSVGOHNYERGPIOWMACENKGYEIPSGAIGR 420

QY 421 INTQEYLDVLGRPMVLGADKAKOVQWNTNVLDALEGLVITGTLPVFNITGQFNKNLNLK 480

Db 421 INTQEYLDVLGRPMVLGADKAKOVQWNTNVLDALEGLVITGTLPVFNITGQFNKNLNLK 480

QY 481 NQILILGVMGVDVSLIEDIKRLTPRFTLCPNGYFAIDPNCYVLLHPNLQPKNKSQEPVTL 540

Db 481 NQILILGVMGVDVSLIEDIKRLTPRFTLCPNGYFAIDPNCYVLLHPNLQPKNKSQEPVTL 540

QY 541 DFLDAELENIDKVEIRNKMIDGESGKTRTLVKQSODERYIDKGNRTYTTWTPVNGTDYSL 600  
 DB 541 DFLDAELENIDKVEIRNKMIDGESGKTRTLVKQSODERYIDKGNRTYTTWTPVNGTDYSL 600  
 QY 601 ALVLPTYSFYIIKAKLEETITQARSKKGMKQSETLKPDPNFESGYTFAPRDYCNLDKI 660  
 DB 601 ALVLPTYSFYIIKAKLEETITQARSKKGMKQSETLKPDPNFESGYTFAPRDYCNLDKI 660  
 QY 661 SDNTEFLNNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYNSKQKNIKGVKAR 720  
 DB 661 SDNTEFLNNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYNSKQKNIKGVKAR 720  
 QY 721 FVYTDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDYVFTAPYFNKSPGAYESGI 780  
 DB 721 FVYTDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDYVFTAPYFNKSPGAYESGI 780  
 QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIEFTKTSIRDPKAGPVCCKRNSDVMDCVI 840  
 DB 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIEFTKTSIRDPKAGPVCCKRNSDVMDCVI 840  
 QY 841 LDGSGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNIISVYAFNKSVDYQSVCEPGAAPKQ 900  
 DB 841 LDGSGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNIISVYAFNKSVDYQSVCEPGAAPKQ 900  
 QY 901 GAGHSAYVPSVADILQIGWATAAASWTLQOFLLSLTPRLLLEAVEMEDDDFTASLSKQ 960  
 DB 901 GAGHSAYVPSVADILQIGWATAAASWTLQOFLLSLTPRLLLEAVEMEDDDFTASLSKQ 960  
 QY 961 SCITEQTQYFFNDKSKFSVGLDCGNCRIFFHGEKIMNTNLFIMVESKGTGCPDTRLLI 1020  
 DB 961 SCITEQTQYFFNDKSKFSVGLDCGNCRIFFHGEKIMNTNLFIMVESKGTGCPDTRLLI 1020  
 QY 1021 QABQTSDBGPNPCDMVKQPRYKGPVDFVNNVLEDYTDGCGVVS 1063  
 DB 1021 QABQTSDBGPNPCDMVKQPRYKGPVDFVNNVLEDYTDGCGVVS 1063

## RESULT 8

AAW37879  
 ID AAW37879 standard; Protein: 1091 AA.

XX AAW37879;  
 AC AAW37879;  
 DT 28-AUG-1998 (first entry)  
 XX Human calcium channel a2d subunit.  
 DE Calcium channel; human; central nervous system disorder;  
 KW Lambert-Eaton syndrome; diagnosis; therapy.

XX Homo sapiens.

XX WO9811131-A2.

XX 19-MAR-1998.

XX 11-SEP-1997; 97WO-US16146.

XX 16-SEP-1996; 96US-0713118.

XX (AMHP ) AMERICAN HOME PROD CORP.

XX Chen ARS, Franco R, Shuey DJ;

XX WPI; 1998-207325/18.

XX N-PSDB; AAW29060.

XX DNA encoding human neuronal calcium channel subunit(s) - useful for  
 diagnosis of and treatment of central nervous system disorders, e.g.  
 Lambert-Eaton syndrome

XX Disclosure; Fig 2; 89pp; English.

XX

CC This polypeptide comprises the a2d subunit of the human neuronal  
 CC calcium channel. cDNA clones (see AAW29059-61) encoding the a1b  
 CC subunit (see AAW37878), the a2d subunit and a b3 subunit (see AAW37880)  
 CC have been isolated. These have been inserted into expression  
 CC vectors and are stably expressed in transformed cell lines. The  
 CC transformed cells show omega-conotoxin GVIA binding activity,  
 CC and omega-conotoxin GVIA toxin sensitive potassium-stimulated  
 CC calcium uptake, indicating that the proteins expressed by the  
 CC clones are capable of forming a functioning calcium channel.  
 CC Nucleic acids encoding the 3 subunits, as well as vectors, host  
 CC cells and methods of isolating nucleic acids encoding related  
 CC calcium channels are disclosed. Fusion proteins incorporating the  
 CC subunit proteins, antibodies, and assays for identifying agents  
 CC that modulate calcium channel activity are also provided. Such  
 CC agents can be used to treat certain central nervous system  
 CC disorders by altering calcium channel activity. Methods of  
 CC diagnosing diseases associated with particular calcium channels,  
 CC such as Lambert-Eaton syndrome, are disclosed.

XX Sequence 1091 AA;

Query Match 99.9%; Score 5595; DB 19; Length 1091;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1062; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLTQSLIGPSSSEPPSAVTIKSWYDKMQEDLVTLAKTASGVNQLVDI 60

DB 1 MAAGCLLALTLTQSLIGPSSSEPPSAVTIKSWYDKMQEDLVTLAKTASGVNQLVDI 60

QY 61 YEKYQDLYTPEPNARQIVETIARDIEKLLSNRSKALVSLAEKVAQAAHQWREDFASN 120

DB 61 YEKYQDLYTPEPNARQIVETIARDIEKLLSNRSKALVSLAEKVAQAAHQWREDFASN 120

QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIQSYQAAVHIPTDIYEGSTIVL 180

DB 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIQSYQAAVHIPTDIYEGSTIVL 180

QY 181 NELNWT SALDEVFKKNEEDPSLLWQVFGSATGLARYYPASPWVDSRTPNKIDLDVRR 240

DB 181 NELNWT SALDEVFKKNEEDPSLLWQVFGSATGLARYYPASPWVDSRTPNKIDLDVRR 240

QY 241 RPWYIQGAASPKDMLILVDVSGVSGTLTKLIRTSVSEMLETSDDDFVNVASFNSAQD 300

DB 241 RPWYIQGAASPKDMLILVDVSGVSGTLTKLIRTSVSEMLETSDDDFVNVASFNSAQD 300

QY 301 VSCFQHLVQANVRNKKVLDVANNITAKGIDYKKGFSFAFEQLLNYSRANCKIIML 360

DB 301 VSCFQHLVQANVRNKKVLDVANNITAKGIDYKKGFSFAFEQLLNYSRANCKIIML 360

QY 361 FTGGEERAQEIFNKYNKDKKRVFRFVSQHNHYERGIOMACENKGYIYEIPISGAIR 420

DB 361 FTGGEERAQEIFNKYNKDKKRVFRFVSQHNHYERGIOMACENKGYIYEIPISGAIR 420

QY 421 INTOEYLDVLRPMVLAGDKAKOVQWTVNVDLAEGLGLVITGTLPVENITGQENKTNL 480

DB 421 INTOEYLDVLRPMVLAGDKAKOVQWTVNVDLAEGLGLVITGTLPVENITGQENKTNL 480

QY 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHPNLQPNKPSQEPVTL 540

DB 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHPNLQPNKPSQEPVTL 540

QY 541 DFLDAELENIDKVEIRNKMIDGESGKTRTLVKQSODERYIDKGNRTYTTWTPVNGTDYSL 600

DB 541 DFLDAELENIDKVEIRNKMIDGESGKTRTLVKQSODERYIDKGNRTYTTWTPVNGTDYSL 600

QY 601 ALVLPTYSFYIIKAKLEETITQARSKKGMKQSETLKPDPNFESGYTFAPRDYCNLDKI 660

DB 601 ALVLPTYSFYIIKAKLEETITQARSKKGMKQSETLKPDPNFESGYTFAPRDYCNLDKI 660

QY 661 SDNTEFLNNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYNSKQKNIKGVKAR 720

DB 661 SDNTEFLNNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYNSKQKNIKGVKAR 720



QY 721 FVYTDGGITRVYPKEAGENWQENPETYEDSFYKRSILDNDYVFTAPYFNKSGPAYESGI 780  
 |||||  
 Db 721 FVYTDGGITRVYPKEAGENWQENPETYEDSFYKRSILDNDYVFTAPYFNKSGPAYESGI 780  
 |||||  
 QY 781 MVSKEVEIYQGLLPAVVGKIDVNSWIEFTKTSIRDPGAGVCDCKRNSDVMDCVI 840  
 |||||  
 Db 781 MVSKEVEIYQGLLPAVVGKIDVNSWIEFTKTSIRDPGAGVCDCKRNSDVMDCVI 840  
 |||||  
 QY 841 LDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLNVSIVAFNKSVDYQSVCEPGAAPKQ 900  
 |||||  
 Db 841 LDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLNVSIVAFNKSVDYQSVCEPGAAPKQ 900  
 |||||  
 QY 901 GAGHRSAYVPSVADIIQIGWATAAWSILQOFLLSLTFPRLEAVEMEDDDFTASLSKQ 960  
 |||||  
 Db 901 GAGHRSAYVPSVADIIQIGWATAAWSILQOFLLSLTFPRLEAVEMEDDDFTASLSKQ 960  
 |||||  
 QY 961 SCITEQTYFFONDSSFSGLDCGNCRIFFHGEKLMNTNLIFIMVESKGTCPDTRLLI 1020  
 |||||  
 Db 961 SCITEQTYFFONDSSFSGLDCGNCRIFFHGEKLMNTNLIFIMVESKGTCPDTRLLI 1020  
 |||||  
 QY 1021 QAEQTSDDGPNCDMVKQPRYKRGPDVCFDNNVLEDYTDGCGVS 1063  
 |||||  
 Db 1021 QAEQTSDDGPNCDMVKQPRYKRGPDVCFDNNVLEDYTDGCGVS 1063  
 |||||

## RESULT 9

AAR33553  
 ID AAR33553 standard; Protein; 1091 AA.

AC AAR33553;

XX 30-JUN-1993 (first entry)

XX Sequence of the alpha 2 human calcium channel subunit.

XX Human calcium channel subunit; diagnosis; agonist; antagonist;  
 KW Lambert Eaton syndrome.

XX Homo sapiens.

XX W09304083-A.

XX 04-MAR-1993.

XX 14-AUG-1992; 92WO-US06903.

XX 15-AUG-1991; 91US-0745206.

XX 10-APR-1992; 92US-0868354.

XX (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.

XX Brenner R, Ellis SB, Feldman DH, Harpold MM, Mccue AF;  
 PI Williams ME;

XX WPI; 1993-093936/11.

XX N-PSDB; AAR37821.

XX DNA encoding specific human calcium channel sub-units - used for  
 PT identifying calcium channel agonists and antagonists and  
 PT diagnosing Lambert Eaton syndrome

XX Disclosure; Page 134-138; 150pp; English.

XX DNA encoding a human neuronal calcium channel alpha 2 subunit was  
 CC isolated from a human genomic DNA library probed under low and high  
 CC stringency conditions with a fragment of DNA encoding the rabbit  
 CC skeletal muscle calcium channel alpha 2 subunit. The fragment  
 CC included nucleotides having a sequence corresponding to the  
 CC nucleotide sequence between nucleotides 43 and 272 inclusive of  
 CC rabbit back skeletal muscle calcium channel alpha 2 subunit cDNA.  
 CC PCR analysis identified splice variants of the human calcium alpha  
 CC 2 subunit transcript. In particularly preferred embodiments, the

CC DNA encoding the alpha 2 subunit is produced by alternative  
 CC processing of a primary transcript that includes DNA encoding the  
 CC amino acids set forth in AAR33553 and the DNA of AAR37823 inserted  
 CC between nucleotides 1624 and 1625 of AAR37821.

XX Sequence 1091 AA;

Query Match 99.9%; Score 5593; DB 14; Length 1091;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1062; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLFQSLIGPSSSEPPPSAVTIKSWDKMOEDLVTLAKTASGVNQLVDI 60  
 |||||

Db 1 MAAGCLLALTTLFQSLIGPSSSEPPPSAVTIKSWDKMOEDLVTLAKTASGVNQLVDI 60  
 |||||

QY 61 YEKQDLYTVPPNARQLVEIARDEIEKLNSRKALVSLALEKVOAAHQRDEFASN 120  
 |||||

Db 61 YEKQDLYTVPPNARQLVEIARDEIEKLNSRKALVSLALEKVOAAHQRDEFASN 120  
 |||||

QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFTEDANFGQISYQHAHVHTPTDIYEGSTIVL 180  
 |||||

Db 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFTEDANFGQISYQHAHVHTPTDIYEGSTIVL 180  
 |||||

QY 181 NELNWTSAIDDEVFKKREEDPSLLQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVR 240  
 |||||

Db 181 NELNWTSAIDDEVFKKREEDPSLLQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVR 240  
 |||||

QY 241 RPWYIQGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSDDDDFVNVASFNSNAQD 300  
 |||||

Db 241 RPWYIQGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSDDDDFVNVASFNSNAQD 300  
 |||||

QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNVNVRANCNKIIML 360  
 |||||

Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNVNVRANCNKIIML 360  
 |||||

QY 361 FTDGGERAQBIFNKNKDKVRVFRFSVQGHNYERGPQIMMACENKGYIYEPSIGAIR 420  
 |||||

Db 361 FTDGGERAQBIFNKNKDKVRVFRFSVQGHNYERGPQIMMACENKGYIYEPSIGAIR 420  
 |||||

QY 421 INTOEYLDVLGRPMVLADGKAKOVQNTNVYLDALGLVITGTLPVENITGQFENKTNL 480  
 |||||

Db 421 INTOEYLDVLGRPMVLADGKAKOVQNTNVYLDALGLVITGTLPVENITGQFENKTNL 480  
 |||||

QY 481 NQLILGVMGVDVSLIEDIKRLTPRETLCPNGYFAIDPNGYVLLHPNLQPNKPSQEPVTL 540  
 |||||

Db 481 NQLILGVMGVDVSLIEDIKRLTPRETLCPNGYFAIDPNGYVLLHPNLQPNKPSQEPVTL 540  
 |||||

QY 541 DFLDAELENDIKVEIRNKMIDGESGEKTFRTLKVSQDERVIDKGNRTYTWTPVNGTDYSL 600  
 |||||

Db 541 DFLDAELENDIKVEIRNKMIDGESGEKTFRTLKVSQDERVIDKGNRTYTWTPVNGTDYSL 600  
 |||||

QY 601 ALVLPTYSFYIYKAKLEETITQARSKKGMKDSKSETLKPDPNFESGYTFIAPRDYCNLDKI 660  
 |||||

Db 601 ALVLPTYSFYIYKAKLEETITQARSKKGMKDSKSETLKPDPNFESGYTFIAPRDYCNLDKI 660  
 |||||

QY 661 SDNNTEFLNFEFIDRKTPNPNPSCNADLINRVLLDAGFTNELVQNVYSKQKNIKGVKAR 720  
 |||||

Db 661 SDNNTEFLNFEFIDRKTPNPNPSCNADLINRVLLDAGFTNELVQNVYSKQKNIKGVKAR 720  
 |||||

QY 721 FVYTDGGITRVYPKEAGENWQENPETYEDSFYKRSILDNDYVFTAPYFNKSGPAYESGI 780  
 |||||

Db 721 FVYTDGGITRVYPKEAGENWQENPETYEDSFYKRSILDNDYVFTAPYFNKSGPAYESGI 780  
 |||||

QY 781 MVSKEVEIYQGLLPAVVGKIDVNSWIEFTKTSIRDPGAGVCDCKRNSDVMDCVI 840  
 |||||

Db 781 MVSKEVEIYQGLLPAVVGKIDVNSWIEFTKTSIRDPGAGVCDCKRNSDVMDCVI 840  
 |||||

QY 841 LDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLNVSIVAFNKSVDYQSVCEPGAAPKQ 900  
 |||||

Db 841 LDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLNVSIVAFNKSVDYQSVCEPGAAPKQ 900  
 |||||

QY 901 GAGHRSAYVPSVADIIQIGWATAAWSILQOFLLSLTFPRLEAVEMEDDDFTASLSKQ 960  
 |||||

Db 901 GAGHSAYVPSVADILQIGWATARAWSILQQFLSLTPRLEAVEVEMDDDDFTASLSKQ 960  
 QY 961 SCITEQTFYFFDNDSKSFSGVLDGCGNCSRFPHGKELMNTNLFIMVESKGTGCPDTRLII 1020  
 Db 961 SCITEQTFYFFDNDSKSFSGVLDGCGNCSRFPHGKELMNTNLFIMVESKGTGCPDTRLII 1020  
 QY 1021 QABQTSDBGNPNCDMWKQPRYKGPDPVCFDNNVLEDTDCGGVS 1063  
 Db 1021 QABQTSDBGNPNCDMWKQPRYKGPDPVCFDNNVLEDTDCGGVS 1063

RESULT 10  
 AAW63148  
 ID AAW63148 standard; Protein: 1110 AA.  
 AC AC  
 XX AAW63148;  
 XX  
 DT 12-OCT-1998 (first entry)  
 XX  
 DE Human calcium channel alpha-2 subunit.  
 XX  
 KW Alpha-2 subunit; human; calcium channel; assay; detection;  
 KW characterisation; Lambert Eaton Syndrome; LES; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US5792846-A.  
 XX  
 PD 11-AUG-1998.  
 XX  
 PF 31-MAY-1995; 95US-0455543.  
 XX  
 PR 04-APR-1994; 94US-0223305.  
 PR 04-APR-1988; 88US-0176899.  
 PR 04-APR-1989; 89US-0603751.  
 PR 04-APR-1989; 89WO-TS01408.  
 PR 20-FEB-1990; 90US-0482384.  
 PR 30-NOV-1990; 90US-0620250.  
 PR 15-AUG-1991; 91US-0745206.  
 PR 31-MAY-1995; 95US-0455543.  
 XX  
 (SIBI-) SIBIA NEUROSCIENCES INC.  
 PA Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;  
 PI Williams ME;  
 XX  
 XX WPI; 1998-456192/39.  
 DR N-PSDB; AAW42694.  
 XX  
 PT DNA encoding human calcium channel alpha 1B subunit protein -  
 PT useful for recombinant production of the channel for screening of  
 PT its modulators, and diagnosis of Lambert Eaton Syndrome  
 XX  
 XX Disclosure; Columns 131-138; 166pp; English.  
 PS  
 CC The present sequence represents the alpha-2 subunit of a human calcium  
 CC channel. Calcium channels are membrane-spanning, multi-subunit proteins  
 CC that allow controlled entry of calcium ions into cells. This leads  
 CC to depolarisation events required for muscle contraction. The recombinant  
 CC subunit, when expressed with nucleic acids encoding the complete calcium  
 CC channel, can be used in assays for the detection and characterisation of  
 CC compounds that modulate the channel. The DNA encoding the subunits can  
 CC be alternatively spliced when transcribed, giving more than one form of  
 CC the protein from the same transcript, each having slightly different  
 CC properties. In addition, the reactivity of the alpha 1 subunit with IgG  
 CC molecules from the serum of an individual with Lambert Eaton Syndrome  
 CC (LES) can be used as a diagnostic for the disease.  
 XX  
 XX Sequence 1110 AA;  
 SQ

Query Match 99.7%; Score 5579.5; DB 19; Length 1110;  
 Best Local Similarity 98.2%; Pred. No. 0;  
 Matches 1063; Conservative 0; Mismatches 0; Indels 19; Gaps 1;

1 MAACLLALTLTLFQSLIGPSSPEPPSAVTIKSWDKMQEDLVTAKTASGVNQLVDI 60  
 1 MAACLLALTLTLFQSLIGPSSPEPPSAVTIKSWDKMQEDLVTAKTASGVNQLVDI 60  
 61 YEKYQDLTYTEPNARQLVEIARDEIKLLSNRSKALVSLAEAKVQAAHQHREFASN 120  
 61 YEKYQDLTYTEPNARQLVEIARDEIKLLSNRSKALVSLAEAKVQAAHQHREFASN 120  
 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFTEDANFGQISYQAAHVHIPTDIYEGSTIVL 180  
 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFTEDANFGQISYQAAHVHIPTDIYEGSTIVL 180  
 181 NELNWTSALEDEVFKKNEEDPSLLMQVFGSATGLARYYPASPWVDSRTPNKIDLYDVR 240  
 181 NELNWTSALEDEVFKKNEEDPSLLMQVFGSATGLARYYPASPWVDSRTPNKIDLYDVR 240  
 241 RPWYIOGAASPKDMLILVDYSGSVSGTLTKLIRTSVSEMLETISDDDFVNVASFNSNAQD 300  
 241 RPWYIOGAASPKDMLILVDYSGSVSGTLTKLIRTSVSEMLETISDDDFVNVASFNSNAQD 300  
 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEOQLLNYSRANCNKIIML 360  
 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEOQLLNYSRANCNKIIML 360  
 361 FTGGEERAQEIFNKYNKDKKRVRFESVGHNYERGIQMACENKGYEYIPIGAIR 420  
 361 FTGGEERAQEIFNKYNKDKKRVRFESVGHNYERGIQMACENKGYEYIPIGAIR 420  
 421 INTOEYLDVLRPMVLGADKAKOVNTNVDLDALEGLVITGLTPVFNITGQENKTNLK 480  
 421 INTOEYLDVLRPMVLGADKAKOVNTNVDLDALEGLVITGLTPVFNITGQENKTNLK 480  
 481 NQLILGVMGVDVSLIEDIKRLTPFTLCPNGYFAIDPNGYVLLHPNLQPK----- 530  
 481 NQLILGVMGVDVSLIEDIKRLTPFTLCPNGYFAIDPNGYVLLHPNLQPKPIGVGPTIN 540  
 531 -----NPKSQEPVTLDFDALENDIKVEIRNKMIDGESGEKTFRTLVKSQDERYI 581  
 541 LRKRPNIQNPKSQEPVTLDFDALENDIKVEIRNKMIDGESGEKTFRTLVKSQDERYI 600  
 582 DKGNTYTWTPVNGTDYSLALVLPYTFYIKAKLETTITQARSKGKMKDSLETLPDNF 641  
 601 DKGNTYTWTPVNGTDYSLALVLPYTFYIKAKLETTITQARSKGKMKDSLETLPDNF 660  
 642 EESGYTFIAPRDYCNLDKISDNNTFLLNFEFIDRKTNNPSCNADLINRVLLDAGFTN 701  
 661 EESGYTFIAPRDYCNLDKISDNNTFLLNFEFIDRKTNNPSCNADLINRVLLDAGFTN 720  
 702 ELVQNYHSKOKNIKGKARFVVDGGITRVYPKEAGENWOENPETEDSYKRSNDNY 761  
 721 ELVQNYHSKOKNIKGKARFVVDGGITRVYPKEAGENWOENPETEDSYKRSNDNY 780  
 762 VFTAPYENKSGPAGYESGIMVSKAVEIYIOGKLLKPAVVGIIKIDVNSWIENFTKTSIRDP 821  
 781 VFTAPYENKSGPAGYESGIMVSKAVEIYIOGKLLKPAVVGIIKIDVNSWIENFTKTSIRDP 840  
 822 CAGPVCCKRNSDMVCMCVILDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNISVYA 881  
 841 CAGPVCCKRNSDMVCMCVILDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNISVYA 900  
 882 FNKSYDYQSCEPAGAPKQAGHRSAYVPSVADILQIGWATAAANSILQOFLLSLTFPR 941  
 901 FNKSYDYQSCEPAGAPKQAGHRSAYVPSVADILQIGWATAAANSILQOFLLSLTFPR 960  
 942 LLEAVEMEDDDFTASLSKQSCITEQTOYFFDNDKSKFSFVLDGCGNCSRFPHGKELMNTNL 1001  
 961 LLEAVEMEDDDFTASLSKQSCITEQTOYFFDNDKSKFSFVLDGCGNCSRFPHGKELMNTNL 1020  
 1002 IFIMVESKGTGCPDTRLIIQAEQTSQGNPNCDMWKQPRYKGPDPVCFDNNVLEDTDCGG 1061  
 1021 IFIMVESKGTGCPDTRLIIQAEQTSQGNPNCDMWKQPRYKGPDPVCFDNNVLEDTDCGG 1080

QY 1062 VS 1063  
Db 1081 VS 1082

RESULT 11  
AAR71013  
ID AAR71013 standard; Protein; 1086 AA.  
XX  
AC AAR71013;  
XX  
XX  
DT 01-DEC-1995 (first entry)  
XX  
XX  
DE Human neuronal calcium channel subunit alpha 2c.  
XX  
KW Calcium channel subunit; antagonist; agonist; diagnosis;  
KW Lambert Eaton Syndrome.  
XX  
XX  
OS Homo sapiens.  
XX  
XX  
PN WO9504822-A.  
XX  
PD 16-FEB-1995.  
XX  
XX  
XX 11-AUG-1994; 94WO-US09230.  
XX  
PR 11-AUG-1993; 93US-0105536.  
PR 05-NOV-1993; 93US-0149097.  
XX  
XX  
PA (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.  
XX  
XX  
PI Ellis SB, Gillespie A, Harpold MM, McCue AF, Williams ME;  
XX  
XX  
DR WPI; 1995-090900/12.  
DR N-PSDB; AAQ84667.  
XX  
XX  
PT DNA encoding human calcium channel sub-unit(s) - used for  
PT developing prods. for studying calcium channels, e.g. for  
PT obtaining agonists and antagonists  
XX  
XX  
PS Disclosure; Page 237-242; 285pp; English.  
XX  
XX  
CC Human neuronal alpha 2 coding sequence (AAQ84664) transcript is  
CC differentially processed in skeletal muscle, aorta, and CNS in  
CC the region corresp. to nt 1595-1942 of AAQ84664 in each of the  
CC tissues. Five alternatively spliced variant transcripts that differ  
CC in the presence or absence of one to three different portions of  
CC this region. There are three sequences involved (see AAQ84664 FT  
CC and AAQ84665 FT), sequence 1, sequence 2 and sequence 3. The five  
CC alpha 2 encoding transcripts from the different tissues include  
CC different combinations of the three sequences, except for one of  
CC the alpha 2 transcripts expressed in aorta which lacks all three  
CC sequences. The five alpha 2 forms identified are (1) a form that  
CC lacks sequence 3 called alpha 2a, expressed in skeletal muscle  
CC (2) one that lacks sequence 1 called alpha 2b, expressed in CNS  
CC (3) one that lacks sequences 1 and 2 called alpha 2c, expressed in  
CC aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,  
CC expressed in aorta and (5) one that lacks sequences 1 and 3  
CC called alpha 2e. The DNA and AA sequences of alpha 2a - alpha 2e  
CC are set forth in AAQ84666-084669 and AAR71012-R71015 respectively.  
XX  
SQ Sequence 1086 AA;

Query Match 99.3%; Score 5559.5; DB 16; Length 1086;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1058; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 MAAGCLLALTLFQSLIGSPSEPPPSAVTIKSWDKMOEDLVTLAKTAGVNLQLVDI 60  
Db 1 MAAGCLLALTLFQSLIGSPSEPPPSAVTIKSWDKMOEDLVTLAKTAGVNLQLVDI 60  
QY 61 YEKYQDLYTVEPNNAQOLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDEFASN 120  
|||||

Db 61 YEKYQDLYTVEPNNAQOLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDEFASN 120  
QY 121 EVVYNAKDDLDPEKNDSEPGSQRIPKFIEDANFGQISYQHAHVHPTDIYEGSTIVL 180  
|||||  
Db 121 EVVYNAKDDLDPEKNDSEPGSQRIPKFIEDANFGQISYQHAHVHPTDIYEGSTIVL 180  
QY 181 NELNWTSADEVFVKKNREEDPSLLQVFGSATGLARYYPASPDVNSRTNPKNIDLYDVR 240  
|||||  
Db 181 NELNWTSADEVFVKKNREEDPSLLQVFGSATGLARYYPASPDVNSRTNPKNIDLYDVR 240  
QY 241 RPWTIOGAASPKDMLILVDVSGVSGLTLLKIRTSVSEMLETLLSDDDFVNVASFNSNAQ 300  
|||||  
Db 241 RPWTIOGAASPKDMLILVDVSGVSGLTLLKIRTSVSEMLETLLSDDDFVNVASFNSNAQ 300  
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNTNVRANCNKIIML 360  
|||||  
Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNTNVRANCNKIIML 360  
QY 361 FTDGGEERAQEIFNKYNKDKKVRVRFESVGOHNYERGPIONMACENKGYIYIPIPSIGAIR 420  
|||||  
Db 361 FTDGGEERAQEIFNKYNKDKKVRVRFESVGOHNYERGPIONMACENKGYIYIPIPSIGAIR 420  
QY 421 INTOEYLDVLRPMVLGRKAKQVQWNTNVDLDELGLVITGTLPVENITGQFENKTNLK 480  
|||||  
Db 421 INTOEYLDVLRPMVLGRKAKQVQWNTNVDLDELGLVITGTLPVENITGQFENKTNLK 480  
QY 481 NQLILGVMGVDVSLIEDIKLTPFTLCPNGYYPALDPNGYVLLHPNLOPKNSQBPVTL 540  
|||||  
Db 481 NQLILGVMGVDVSLIEDIKLTPFTLCPNGYYPALDPNGYVLLHPNLOPKNSQBPVTL 540  
QY 541 DFLDAELENDEIKVEIRNKMIDGESGEKTFRTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
|||||  
Db 541 DFLDAELENDEIKVEIRNKMIDGESGEKTFRTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
QY 601 ALVLPYTFYIIRAKLEETITQARSKKGMKDSSETLKPDPNFESGYTFIAPRYCNDLKI 660  
|||||  
Db 601 ALVLPYTFYIIRAKLEETITQARSKKGMKDSSETLKPDPNFESGYTFIAPRYCNDLKI 660  
QY 661 SDNTEFLNFEFIDRKTPNPNPSCNADLINRVLLDAGFTNELVQNSKQKNIKGVKAR 720  
|||||  
Db 661 SDNTEFLNFEFIDRKTPNPNPSCNADLINRVLLDAGFTNELVQNSKQKNIKGVKAR 720  
QY 721 FVYTDGGITRVYKPEAGENWOENPEYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
|||||  
Db 721 FVYTDGGITRVYKPEAGENWOENPEYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
QY 776 MVSKAVEIYIQGKLLPAVVGIIKIDVNSWIENFTKTSIRDPACAGPCDCRNSDVMDCVI 840  
|||||  
Db 776 MVSKAVEIYIQGKLLPAVVGIIKIDVNSWIENFTKTSIRDPACAGPCDCRNSDVMDCVI 840  
QY 841 LDDGGFLLMANHDDYTNOIGRFFGEIDPISLMRHLVNIISVYAFNKSVDYOSVCEPQAPKQ 900  
|||||  
Db 841 LDDGGFLLMANHDDYTNOIGRFFGEIDPISLMRHLVNIISVYAFNKSVDYOSVCEPQAPKQ 900  
QY 901 GAGHRSAYPSVADIIQIGWATAAASIIQOFLLSLTTPRLLEAVEMEDDDFTASLSQ 960  
|||||  
Db 901 GAGHRSAYPSVADIIQIGWATAAASIIQOFLLSLTTPRLLEAVEMEDDDFTASLSQ 960  
QY 961 SCITEQOTQVFFDNDKSKFSGLDCGNCSTRTFHGCKLMNTNLFIMVESKGTCTPCTRLLI 1020  
|||||  
Db 961 SCITEQOTQVFFDNDKSKFSGLDCGNCSTRTFHGCKLMNTNLFIMVESKGTCTPCTRLLI 1020  
QY 1021 QABQTSDBGPNPCDMVKQPRYRKGPDYCFDNNVLEDYDCGGVS 1063  
|||||  
Db 1021 QABQTSDBGPNPCDMVKQPRYRKGPDYCFDNNVLEDYDCGGVS 1063  
QY 1016 QABQTSDBGPNPCDMVKQPRYRKGPDYCFDNNVLEDYDCGGVS 1058  
|||||

RESULT 12  
AAR71013  
ID AAR71013 standard; Protein; 1086 AA.  
XX  
AC AAR71013;  
XX

DT 12-OCT-1998 (first entry)  
 XX Human calcium channel alpha-2c subunit.  
 DE  
 DE  
 XX Alpha-2 subunit; human; calcium channel; assay; detection;  
 KW characterisation; Lambert Eaton Syndrome; LES; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US5792846-A.  
 XX  
 PD 11-AUG-1998.  
 XX  
 PF 31-MAY-1995; 95US-0455543.  
 XX  
 PR 04-APR-1994; 94US-0223305.  
 PR 04-APR-1988; 88US-0176899.  
 PR 04-APR-1989; 89US-0603751.  
 PR 04-APR-1989; 89WO-US01408.  
 PR 20-FEB-1990; 90US-0482384.  
 PR 30-NOV-1990; 90US-0620250.  
 PR 15-AUG-1991; 91US-0745206.  
 PR 31-MAY-1995; 95US-0455543.  
 XX  
 PA (SIBI-) SIBIA NEUROSCIENCES INC.  
 XX  
 PI Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;  
 PI Williams ME;  
 XX  
 DR WPI: 1998-456192/39.  
 DR N-PSDB; AAV42702.  
 XX  
 XX DNA encoding human calcium channel alpha 1B subunit protein -  
 PT useful for recombinant production of the channel for screening of  
 PT its modulators, and diagnosis of Lambert Eaton Syndrome  
 XX  
 PS Claim 3; Columns 293-300; 166pp; English.  
 XX  
 CC The present sequence represents the alpha-2c subunit of a human calcium  
 CC channel. Calcium channels are membrane-spanning, multi-subunit proteins  
 CC that allow controlled entry of calcium ions into cells. This leads  
 CC to depolarisation events required for muscle contraction. The recombinant  
 CC subunit, when expressed with nucleic acids encoding the complete calcium  
 CC channel, can be used in assays for the detection and characterisation of  
 CC compounds that modulate the channel. The DNA encoding the subunits can  
 CC be alternatively spliced when transcribed, giving more than one form of  
 CC the protein from the same transcript, each having slightly different  
 CC properties. In addition, the reactivity of the alpha 1 subunit with IgG  
 CC molecules from the serum of an individual with Lambert Eaton Syndrome  
 CC (LES) can be used as a diagnostic for the disease.  
 XX  
 SQ Sequence 1086 AA;  
 Query Match 99.3%; Score 5559.5; DB 19; Length 1086;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 1058; Conservative 0; Mismatches 0; Indels 5; Gaps 1;  
 QY 1 MAAGCLLALTLFQSLGIPSEPPFSAVTKSWDKMQEDLVTLAKTAGVNLVDI 60  
 DB 1 MAAGCLLALTLFQSLGIPSEPPFSAVTKSWDKMQEDLVTLAKTAGVNLVDI 60  
 QY 61 YEKYQDLYTVEPNNAQQLVEIAARDEKLLSNRSKALVSLALEAKVQAAHQWREDFASN 120  
 DB 61 YEKYQDLYTVEPNNAQQLVEIAARDEKLLSNRSKALVSLALEAKVQAAHQWREDFASN 120  
 QY 121 EVVYNAKDDLPKNDSEPPGSRQKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180  
 DB 121 EVVYNAKDDLPKNDSEPPGSRQKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180  
 QY 181 NELNWTLSALDEVFKKNREDDPSLLQWVFGSATGLARYYPASFPWVDSNRTPNKIDLYDVR 240  
 DB 181 NELNWTLSALDEVFKKNREDDPSLLQWVFGSATGLARYYPASFPWVDSNRTPNKIDLYDVR 240  
 QY 241 RPWYIQGAASPDKMLLLVDVSGVSGLTLLKLRITSVSEMLETLSDDDFVNVASFNSAQD 300  
 DB 241 RPWYIQGAASPDKMLLLVDVSGVSGLTLLKLRITSVSEMLETLSDDDFVNVASFNSAQD 300  
 QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFQOLLNYSRANCNKIIML 360  
 DB 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFQOLLNYSRANCNKIIML 360  
 QY 361 FTDGGEERAQEIFNKYKDKVRVFRFSYGOHNYERGIQWACENKGYEIPISGAIR 420  
 DB 361 FTDGGEERAQEIFNKYKDKVRVFRFSYGOHNYERGIQWACENKGYEIPISGAIR 420  
 QY 421 INTQEYLDVLGRPMVLADKAKQVQWNTNYLDALGLGITGLPVFNITGOFENKTNLK 480  
 DB 421 INTQEYLDVLGRPMVLADKAKQVQWNTNYLDALGLGITGLPVFNITGOFENKTNLK 480  
 QY 481 NQILGVMGVDSLEDIKRLTPRFTLCPNGYFAIDPNGYVLLHPLNLPKPKSQBPVTL 540  
 DB 481 NQILGVMGVDSLEDIKRLTPRFTLCPNGYFAIDPNGYVLLHPLNLPKPKSQBPVTL 540  
 QY 541 DFLDAELENDIKVEIRNKMIDGESGEKTFRTLVKSODERYIDKGNRTYTWTPVNGTDYSL 600  
 DB 541 DFLDAELENDIKVEIRNKMIDGESGEKTFRTLVKSODERYIDKGNRTYTWTPVNGTDYSL 600  
 QY 595 DFLDAELENDIKVEIRNKMIDGESGEKTFRTLVKSODERYIDKGNRTYTWTPVNGTDYSL 595  
 DB 595 DFLDAELENDIKVEIRNKMIDGESGEKTFRTLVKSODERYIDKGNRTYTWTPVNGTDYSL 595  
 QY 601 ALVLPYTFYIIKAKLEETITQARSKKGMKQSEITLKPONFEESGYTFIAPRDYCNLDKI 660  
 DB 601 ALVLPYTFYIIKAKLEETITQARSKKGMKQSEITLKPONFEESGYTFIAPRDYCNLDKI 660  
 QY 655 SDNTEFLNFEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQVWSKQKNKGVKAR 715  
 DB 655 SDNTEFLNFEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQVWSKQKNKGVKAR 715  
 QY 721 FVTDGGITRVPKEAGENQENPETEYDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
 DB 721 FVTDGGITRVPKEAGENQENPETEYDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
 QY 775 FVTDGGITRVPKEAGENQENPETEYDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 775  
 DB 775 FVTDGGITRVPKEAGENQENPETEYDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 775  
 QY 781 MVSQAVEIYIQGLKLPVAVGIIKIDVNSWIENTFTKSIRDPACAGPVCDCKRNSDVMDCVI 840  
 DB 781 MVSQAVEIYIQGLKLPVAVGIIKIDVNSWIENTFTKSIRDPACAGPVCDCKRNSDVMDCVI 840  
 QY 835 MVSQAVEIYIQGLKLPVAVGIIKIDVNSWIENTFTKSIRDPACAGPVCDCKRNSDVMDCVI 835  
 DB 835 MVSQAVEIYIQGLKLPVAVGIIKIDVNSWIENTFTKSIRDPACAGPVCDCKRNSDVMDCVI 835  
 QY 841 LDGGLFLMANHDDYTNQIGRFFGEIDPSLMRHLVNSVYAFNKSVDYOSVCEPGAAPKQ 900  
 DB 841 LDGGLFLMANHDDYTNQIGRFFGEIDPSLMRHLVNSVYAFNKSVDYOSVCEPGAAPKQ 900  
 QY 895 LDGGLFLMANHDDYTNQIGRFFGEIDPSLMRHLVNSVYAFNKSVDYOSVCEPGAAPKQ 895  
 DB 895 LDGGLFLMANHDDYTNQIGRFFGEIDPSLMRHLVNSVYAFNKSVDYOSVCEPGAAPKQ 895  
 QY 901 GAGHRSAYVPSVADIIQIGHWATAAASIIQQFLSLTTPRLLLEAVEMEDDDFTASLSKQ 960  
 DB 901 GAGHRSAYVPSVADIIQIGHWATAAASIIQQFLSLTTPRLLLEAVEMEDDDFTASLSKQ 960  
 QY 955 SCITEQTYQFFDNDKSFSGVLDCGNCSTRIFHGKELMNTNLIIFIMVESKGTCTCDTRLII 1020  
 DB 955 SCITEQTYQFFDNDKSFSGVLDCGNCSTRIFHGKELMNTNLIIFIMVESKGTCTCDTRLII 1020  
 QY 1021 QAQETSDGPNPCDMVKQPRYRKGPVCFDNNVLEDYTDGCVS 1063  
 DB 1021 QAQETSDGPNPCDMVKQPRYRKGPVCFDNNVLEDYTDGCVS 1063  
 QY 1016 QAQETSDGPNPCDMVKQPRYRKGPVCFDNNVLEDYTDGCVS 1058  
 DB 1016 QAQETSDGPNPCDMVKQPRYRKGPVCFDNNVLEDYTDGCVS 1058  
 RESULT 13  
 AAB10587  
 ID AAB10587 standard; Protein; 1086 AA.  
 XX  
 AC AAB10587;  
 XX  
 DT 22-DEC-2000 (first entry)  
 XX  
 DE Human calcium channel alpha-2c subunit protein.  
 XX  
 KW Human; calcium channel; calcium channel subunit; diagnosis;  
 KW Lambert Eaton Syndrome; calcium channel subunit alpha-2c.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6096514-A.

XX 01-AUG-2000.  
 XX 25-MAY-1995; 95US-0450562.  
 XX 02-APR-1988; 88US-0176899.  
 PR 02-FEB-1990; 90US-0482384.  
 PR 08-NOV-1990; 90US-0603751.  
 PR 30-NOV-1990; 90US-0620250.  
 PR 15-AUG-1991; 91US-0745206.  
 PR 10-APR-1992; 92US-0868354.  
 PR 13-JUL-1992; 92US-0914231.  
 PR 11-AUG-1993; 93US-0105536.  
 PR 05-NOV-1993; 93US-0149097.  
 PR 07-FEB-1994; 94US-0193078.  
 PR 04-APR-1994; 94US-0223305.  
 PR 11-AUG-1994; 94US-0290012.  
 PR 23-SEP-1994; 94US-0311363.  
 PR 28-SEP-1994; 94US-0314083.  
 PR 07-NOV-1994; 94US-0336257.  
 PR 13-MAR-1995; 95US-0404950.  
 XX (SIBI-) SIBIA NEUROSCIENCES INC.  
 PA Ellis SB, Williams ME, McCue AF, Harpold MM;  
 PI  
 XX WPI; 2000-548230/50.  
 DR N-PSDB; AAA711725.  
 XX Human calcium channel beta subunit polynucleotides, useful for  
 PT producing recombinant eukaryotic cells and for diagnosing Lambert Eaton  
 PT Syndrome -  
 XX Disclosure; Column 237-244; 153pp; English.  
 XX This invention describes a novel isolated DNA molecule (1) comprising a  
 CC sequence encoding a beta3-1 subunit of a human calcium channel.  
 CC Nucleic acid probes comprising 14-30 contiguous nucleotides of  
 CC beta.3 subunit encoding DNA are useful for isolation and cloning of  
 CC calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that  
 CC express heterologous calcium channel are useful for identifying compounds  
 CC that modulate calcium channel activity and in assays for identifying  
 CC agonists and antagonists of calcium channel activity in humans. Human  
 CC calcium channel subunit or eukaryotic cells expressing the channel are  
 CC useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This  
 CC sequence represents the human calcium channel alpha-2c subunit which is  
 CC described in the method of the invention.  
 XX  
 XX Sequence 1086 AA;  
 SQ  
 Query Match 99.3%; Score 5559.5; DB 21; Length 1086;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 1058; Conservative 0; Mismatches 0; Indels 5; Gaps 1;  
 QY 1 MAAGCLLALTLTFLQSLIGPSEEPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
 DB 1 MAAGCLLALTLTFLQSLIGPSEEPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
 QY 61 YEKYQDLYTVEPNARQLVEIAARDTEKLLSNRSKALVSLALEAEKVAQAAHQRDEFASN 120  
 DB 61 YEKYQDLYTVEPNARQLVEIAARDTEKLLSNRSKALVSLALEAEKVAQAAHQRDEFASN 120  
 QY 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISYQAAVHIPTDIYEGSTIVL 180  
 DB 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISYQAAVHIPTDIYEGSTIVL 180  
 QY 181 NELNWTLSALDEVKPKNREEDPSLLWQVFGSATGLARYYPASPWNDSRTPNPKIDLYDVR 240  
 DB 181 NELNWTLSALDEVKPKNREEDPSLLWQVFGSATGLARYYPASPWNDSRTPNPKIDLYDVR 240  
 QY 241 RPWYIOGAASPKDMLILVDVSGVSLGLTKLIRTSVSEMLETILSDDDFVNVASFNSNAQD 300  
 DB 241 RPWYIOGAASPKDMLILVDVSGVSLGLTKLIRTSVSEMLETILSDDDFVNVASFNSNAQD 300

QY 301 VSCFOHLVQANVRNKKVLLKDAVNNTAKGITDYKKGSFAFEQLLNYNVSRANCKIIML 360  
 DB 301 VSCFOHLVQANVRNKKVLLKDAVNNTAKGITDYKKGSFAFEQLLNYNVSRANCKIIML 360  
 QY 361 FTDGGEERAQELFNKYNKDKKVRFRFESVGOHNERGPIQWACENKGYEYFISGAIR 420  
 DB 361 FTDGGEERAQELFNKYNKDKKVRFRFESVGOHNERGPIQWACENKGYEYFISGAIR 420  
 QY 421 INTQYLDVLRGPMVLGADKAKQVQWNTVYLDALGLGVIITGLPVFNITQGFENKKNL 480  
 DB 421 INTQYLDVLRGPMVLGADKAKQVQWNTVYLDALGLGVIITGLPVFNITQGFENKKNL 480  
 QY 481 NQLILGVMGVDSVLEDIKRLTPRETLCPCNGYFAIDPNGYVLLHPNLPKPKSQEPVTL 540  
 DB 481 NQLILGVMGVDSVLEDIKRLTPRETLCPCNGYFAIDPNGYVLLHPNLPKPKSQEPVTL 540  
 QY 541 DFLDAELENDIKVEIRNKMIDGESGEKTRFLVKSQDERYIDKGNRYTWTVPVNGTDSL 600  
 DB 541 DFLDAELENDIKVEIRNKMIDGESGEKTRFLVKSQDERYIDKGNRYTWTVPVNGTDSL 600  
 QY 595 DFLDAELENDIKVEIRNKMIDGESGEKTRFLVKSQDERYIDKGNRYTWTVPVNGTDSL 595  
 DB 595 DFLDAELENDIKVEIRNKMIDGESGEKTRFLVKSQDERYIDKGNRYTWTVPVNGTDSL 595  
 QY 601 ALVPTYSFYIKAKLEETITQARSKGKMDSETLKPDPNFEESGYTFIAPRDYCNDLKI 660  
 DB 601 ALVPTYSFYIKAKLEETITQARSKGKMDSETLKPDPNFEESGYTFIAPRDYCNDLKI 660  
 QY 655 ALVPTYSFYIKAKLEETITQARSKGKMDSETLKPDPNFEESGYTFIAPRDYCNDLKI 655  
 DB 655 ALVPTYSFYIKAKLEETITQARSKGKMDSETLKPDPNFEESGYTFIAPRDYCNDLKI 655  
 QY 720 SDNTEFLNFEFIDRKTPNPNPCNADLINRVLLDAGFTNELYQVYWSKOKNIKGVKAR 720  
 DB 720 SDNTEFLNFEFIDRKTPNPNPCNADLINRVLLDAGFTNELYQVYWSKOKNIKGVKAR 720  
 QY 775 FVVTDDGGITRYVPKEAGENWOENPETYEDSFYKRSNDNDVFTAPYFNKSGPGAYESGI 775  
 DB 775 FVVTDDGGITRYVPKEAGENWOENPETYEDSFYKRSNDNDVFTAPYFNKSGPGAYESGI 775  
 QY 840 MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPCAGVCDCKRNSDVMDCVI 840  
 DB 840 MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPCAGVCDCKRNSDVMDCVI 840  
 QY 835 LDDGGFLLMANHDDVTNIGRFFGEIDPSLMRHLVNIISVYAFNKSVDYQSCFCAAPKQ 900  
 DB 835 LDDGGFLLMANHDDVTNIGRFFGEIDPSLMRHLVNIISVYAFNKSVDYQSCFCAAPKQ 900  
 QY 901 GAGHSAYVPSVADILQIGWATAAAWSILOQFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
 DB 901 GAGHSAYVPSVADILQIGWATAAAWSILOQFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
 QY 955 GAGHSAYVPSVADILQIGWATAAAWSILOQFLLSLTFPRLLEAVEMEDDDFTASLSKQ 955  
 DB 955 GAGHSAYVPSVADILQIGWATAAAWSILOQFLLSLTFPRLLEAVEMEDDDFTASLSKQ 955  
 QY 1020 SCITEQTOYFFDNDKSKFSGLDCGNCRSIFHGEKLMNTLIFIMVESKGTCPDTRLLI 1020  
 DB 1020 SCITEQTOYFFDNDKSKFSGLDCGNCRSIFHGEKLMNTLIFIMVESKGTCPDTRLLI 1020  
 QY 1015 QAEQTSDDGNPCDMVKOPRYRKGPDVCFDNNVLEDYTDGCGVS 1063  
 DB 1015 QAEQTSDDGNPCDMVKOPRYRKGPDVCFDNNVLEDYTDGCGVS 1063  
 QY 1016 QAEQTSDDGNPCDMVKOPRYRKGPDVCFDNNVLEDYTDGCGVS 1058  
 DB 1016 QAEQTSDDGNPCDMVKOPRYRKGPDVCFDNNVLEDYTDGCGVS 1058  
 RESULT 14  
 AAR71015  
 ID AAR71015 standard; Protein; 1084 AA.  
 XX AC AAR71015;  
 XX AC AAR71015;  
 DT 01-DEC-1995 (first entry)  
 XX Human neuronal calcium channel subunit alpha 2e.  
 DE DE  
 XX Calcium channel subunit; antagonist; agonist; diagnosis;  
 KW Lambert Eaton Syndrome.  
 OS Homo sapiens.  
 XX WO9504822-A.  
 PN 16-FEB-1995.  
 XX PD

PF 11-AUG-1994; 94WO-US09230.  
 PR 11-AUG-1993; 93US-0105536.  
 PR 05-NOV-1993; 93US-0149097.  
 XX (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.  
 PA Ellis SB, Gillespie A, Harpold MM, McCue AF, Williams ME;  
 PI WPI; 1995-090900/12.  
 XX N-PSDB; AAQ84669.  
 DR DNA encoding human calcium channel sub-unit(s) - used for  
 XX developing prods. for studying calcium channels, e.g. for  
 PT obtaining agonists and antagonists  
 PT Disclosure; Page 248-253; 285pp; English.  
 PS Human neuronal alpha 2 coding sequence (AAQ84664) transcript is  
 XX differentially processed in skeletal muscle, aorta, and CNS in  
 CC the region corresp. to nt 1595-1942 of AAQ84664 in each of the  
 CC tissues. Five alternatively spliced variant transcripts that differ  
 CC in the presence or absence of one to three different portions of  
 CC this region. There are three sequences involved (see AAQ84664.FT  
 CC and AAQ84665.FT), sequence 1, sequence 2 and sequence 3. The five  
 CC alpha 2 encoding transcripts from the different tissues include  
 CC different combinations of the three sequences, except for one of  
 CC the alpha 2 transcripts expressed in aorta which lacks all three  
 CC sequences. The five alpha 2 forms identified are (1) a form that  
 CC lacks sequence 3 called alpha 2a, expressed in skeletal muscle  
 CC (2) one that lacks sequence 1 called alpha 2b, expressed in CNS  
 CC (3) one that lacks sequences 1 and 2 called alpha 2c, expressed in  
 CC aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,  
 CC expressed in aorta and (5) one that lacks sequences 1 and 3  
 CC called alpha 2e. The DNA and AA sequences of alpha 2a - alpha 2e  
 CC are set forth in AAQ84666-Q84669 and AAR71012-R71015 respectively.  
 XX Sequence 1084 AA;  
 SQ

Query Match 99.08; Score 5542.5; DB 16; Length 1084;  
 Best Local Similarity 99.28; Pred. No. 0;  
 Matches 1055; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 1 MAAGCLLALTTLTFLSLLIGPSSPEPPSAVTIKSWVDKMOEDLVTLAKTAGVNLQVLDI 60  
 DB 1 MAAGCLLALTTLTFLSLLIGPSSPEPPSAVTIKSWVDKMOEDLVTLAKTAGVNLQVLDI 60  
 QY 61 YEKYODLYTVEPNNAQLVEIARDEIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120  
 DB 61 YEKYODLYTVEPNNAQLVEIARDEIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120  
 QY 121 EVVYNAKDDLDPEKNDSEPSQRIKPVFIEDANFGROIYQHAHVHIPTDIYEGSTIVL 180  
 DB 121 EVVYNAKDDLDPEKNDSEPSQRIKPVFIEDANFGROIYQHAHVHIPTDIYEGSTIVL 180  
 QY 181 NELNWTSLALDEVEKKNREDEPSLQVPGSGATGLARYPASPWDNSRTNPKIDLYDVR 240  
 DB 181 NELNWTSLALDEVEKKNREDEPSLQVPGSGATGLARYPASPWDNSRTNPKIDLYDVR 240  
 QY 241 RPWYIQAASPKMDLILVDVSGVSGSLTKLIRTSVSEMLETLSDDDFVNVSFNSNAQD 300  
 DB 241 RPWYIQAASPKMDLILVDVSGVSGSLTKLIRTSVSEMLETLSDDDFVNVSFNSNAQD 300  
 QY 301 VSCFOHLVQANVRNKKVYLKDVANNITAKGTDYKKGFSFAPEQLLNYNVSRANCKIIML 360  
 DB 301 VSCFOHLVQANVRNKKVYLKDVANNITAKGTDYKKGFSFAPEQLLNYNVSRANCKIIML 360  
 QY 361 FTDGGEERAQEIFNKNYKDKVRFVRSVGOHNYERGP IOWMACENKGYEYIPSGAIR 420  
 DB 361 FTDGGEERAQEIFNKNYKDKVRFVRSVGOHNYERGP IOWMACENKGYEYIPSGAIR 420  
 QY 421 INTOEYLDVLRPMVLADGKAKOVQWNTNVYLDALDELGLVITGTLVPFNTITGQFENKTNLK 480  
 DB 421 INTOEYLDVLRPMVLADGKAKOVQWNTNVYLDALDELGLVITGTLVPFNTITGQFENKTNLK 480

Db 421 INTOEYLDVLRPMVLADGKAKOVQWNTNVYLDALDELGLVITGTLVPFNTITGQFENKTNLK 480  
 QY 481 NQILGVMGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHPNLQPKNKSQBPVTL 540  
 Db 481 NQILGVMGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHPNLQPKNKSQBPVTL 540  
 QY 541 DFDAELENIDIKVEIRNKMIDGESGKTFRTLVKSODERYIDKGNRTYTWTVPVNGTDYSL 600  
 Db 541 DFDAELENIDIKVEIRNKMIDGESGKTFRTLVKSODERYIDKGNRTYTWTVPVNGTDYSL 600  
 QY 601 ALVPTYSFYYIKAKLEETITOARSKKMKDSETIKLPDNFESGYTFIAPRDYCNLDLKI 660  
 Db 601 ALVPTYSFYYIKAKLEETITOARSKKMKDSETIKLPDNFESGYTFIAPRDYCNLDLKI 660  
 QY 661 SDNNTFLLNFNEFIDRKTPNPNPSCNADLINRVLLDAGFTNELVQNYWSKQNIKGVKAR 720  
 Db 661 SDNNTFLLNFNEFIDRKTPNPNPSCNADLINRVLLDAGFTNELVQNYWSKQNIKGVKAR 720  
 QY 721 FVVTGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
 Db 721 FVVTGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
 QY 781 MVSQAVEIYIQGLKLPVAVVIGIKIDVNSWNTENFTKTSIRPCAGPVCDCKRNSDVMDCVI 840  
 Db 781 MVSQAVEIYIQGLKLPVAVVIGIKIDVNSWNTENFTKTSIRPCAGPVCDCKRNSDVMDCVI 840  
 QY 841 LDGGLFLLMANHDDYTNIQIRPFGEIDPISLRHLVNIISVYAFNKSVDYQSVCEPGAAPKQ 900  
 Db 841 LDGGLFLLMANHDDYTNIQIRPFGEIDPISLRHLVNIISVYAFNKSVDYQSVCEPGAAPKQ 900  
 QY 901 GAGHRSAVPSVADIIQIGWATAAASWILQFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960  
 Db 901 GAGHRSAVPSVADIIQIGWATAAASWILQFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960  
 QY 961 SCITEQTOYFFDNDSKFSFGLVDCGNCRIHFHCEKLMNTNLIFIMVESKGTCTCDTRLII 1020  
 Db 961 SCITEQTOYFFDNDSKFSFGLVDCGNCRIHFHCEKLMNTNLIFIMVESKGTCTCDTRLII 1020  
 QY 1021 QABQTSQGNPCDMVKOPRYKRGPDVCFDNNVLEDTDCGGVS 1063  
 Db 1021 QABQTSQGNPCDMVKOPRYKRGPDVCFDNNVLEDTDCGGVS 1063  
 QY 1063 QABQTSQGNPCDMVKOPRYKRGPDVCFDNNVLEDTDCGGVS 1063  
 Db 1063 QABQTSQGNPCDMVKOPRYKRGPDVCFDNNVLEDTDCGGVS 1063

RESULT 15  
 ID AAW63155 standard; Protein; 1084 AA.  
 XX AAW63155;  
 XX AC  
 XX XX  
 DT 12-OCT-1998 (first entry)  
 XX  
 DE Human calcium channel alpha-2e subunit.  
 XX  
 KW Alpha-2 subunit; human; calcium channel; assay; detection;  
 KW characterisation; Lambert Eaton Syndrome; LES; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US5792846-A.  
 XX  
 PD 11-AUG-1998.  
 XX  
 PF 31-MAY-1995; 95US-0455543.  
 XX  
 PR 04-APR-1994; 94US-0223305.  
 PR 04-APR-1988; 88US-0176899.  
 PR 04-APR-1989; 89US-0603751.  
 PR 04-APR-1985; 89WO-US01408.  
 PR 20-FEB-1990; 90US-0482384.  
 PR 30-NOV-1990; 90US-0620250.  
 PR 15-AUG-1991; 91US-0745206.  
 PR 31-MAY-1995; 95US-0455543.  
 XX

PA (SIBI-) SIBIA NEUROSCIENCES INC.  
 PI Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;  
 PI Williams ME;  
 XX WPI; 1998-456192/39.  
 DR N-PSDB; AAV42704.  
 XX  
 PT DNA encoding human calcium channel alpha 1B subunit protein -  
 PT useful for recombinant production of the channel for screening of  
 PT its modulators, and diagnosis of Lambert Eaton Syndrome  
 XX  
 PS Claim 3; Columns 305-310; 166pp; English.  
 XX  
 CC The present sequence represents the alpha-2e subunit of a human calcium  
 CC channel. Calcium channels are membrane-spanning, multi-subunit proteins  
 CC that allow controlled entry of calcium ions into cells. This leads  
 CC to depolarisation events required for muscle contraction. The recombinant  
 CC subunit, when expressed with nucleic acids encoding the complete calcium  
 CC channel, can be used in assays for the detection and characterisation of  
 CC compounds that modulate the channel. The DNA encoding the subunits can  
 CC be alternatively spliced when transcribed, giving more than one form of  
 CC the protein from the same transcript, each having slightly different  
 CC properties. In addition, the reactivity of the alpha 1 subunit with IgG  
 CC molecules from the serum of an individual with Lambert Eaton Syndrome  
 CC (LES) can be used as a diagnostic for the disease.  
 XX  
 SQ Sequence 1084 AA;

Query Match 99.0%; Score 5542.5; DB 19; Length 1084;  
 Best Local Similarity 99.2%; Pred. No. 0;  
 Matches 1055; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 1 MAAGCLLALTTLFOSLLIGSPSEPPPSAVTIKSWDKMOEDLVTLAKTAGSVNQLVDI 60  
 DB 1 MAAGCLLALTTLFOSLLIGSPSEPPPSAVTIKSWDKMOEDLVTLAKTAGSVNQLVDI 60  
 QY 61 YEKYQDLYTVEPNNARQLVEIAARDIEKLLNSRKALVSLALEAEKQVAAHQWREDFASN 120  
 DB 61 YEKYQDLYTVEPNNARQLVEIAARDIEKLLNSRKALVSLALEAEKQVAAHQWREDFASN 120  
 QY 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIYQHOAAVHIPTDIYEGSTIVL 180  
 DB 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIYQHOAAVHIPTDIYEGSTIVL 180  
 QY 181 NELNNTSALDEVFVKKNREDEPSLLMQVFGSATGLARYYPASPVVDNSRTPNKIDLYDVR 240  
 DB 181 NELNNTSALDEVFVKKNREDEPSLLMQVFGSATGLARYYPASPVVDNSRTPNKIDLYDVR 240  
 QY 241 RPWYIOGAASPKDMLILVDVSGSVSGLTLKLRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
 DB 241 RPWYIOGAASPKDMLILVDVSGSVSGLTLKLRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
 QY 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAEQLLNLYNVRANCNKIIML 360  
 DB 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAEQLLNLYNVRANCNKIIML 360  
 QY 361 FTDGGEERAQELFNKYNDKKVRFRFSVGOHNYERGPQIOWMACENKGYEYIIPSIGAIR 420  
 DB 361 FTDGGEERAQELFNKYNDKKVRFRFSVGOHNYERGPQIOWMACENKGYEYIIPSIGAIR 420  
 QY 421 INTQEYLDVLRPMVLGDKAKQVQWNTNLYLDALELGLVITGTLPVFNITGFQENKTNLK 480  
 DB 421 INTQEYLDVLRPMVLGDKAKQVQWNTNLYLDALELGLVITGTLPVFNITGFQENKTNLK 480  
 QY 481 NQLILGVMGVDVSLIEDIKRLTPRFLPCNGYFFAIDPNGYVLLHPNLPKPKSOEPVTL 540  
 DB 481 NQLILGVMGVDVSLIEDIKRLTPRFLPCNGYFFAIDPNGYVLLHPNLPKPKSOEPVTL 540  
 QY 541 DFLDAELENDIKVEIRNKMIDGESGEKTRTLVKSDERYIDKGNRTYTWTVPNGTDYSL 600  
 DB 541 DFLDAELENDIKVEIRNKMIDGESGEKTRTLVKSDERYIDKGNRTYTWTVPNGTDYSL 600

QY 601 ALVLPYTFYIIKAKLEETITQARSKKGMKOSSETLKPONFEESGYTFIAPRDYCNDLKI 660  
 DB 601 ALVLPYTFYIIKAKLEETITQARY-----SETLKPONFEESGYTFIAPRDYCNDLKI 653  
 QY 661 SDNTEFLNFEFIDRKTPNPNPSCNADLINRVLLDAGFTNELVQNYWSKQKNIKGVKAR 720  
 DB 654 SDNTEFLNFEFIDRKTPNPNPSCNADLINRVLLDAGFTNELVQNYWSKQKNIKGVKAR 713  
 QY 721 FVYTDGGITRVYPKEAGENQWENPETEYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
 DB 714 FVYTDGGITRVYPKEAGENQWENPETEYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 773  
 QY 781 MYSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTSIRDPACAGPVCDCCKRNSDVMDCVI 840  
 DB 774 MYSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTSIRDPACAGPVCDCCKRNSDVMDCVI 833  
 QY 841 LDGGLMANHDDYTNQIGRFGEIDPSLMRHLNIVSYAFNKSVDYQSVCEPGAAPKQ 900  
 DB 834 LDGGLMANHDDYTNQIGRFGEIDPSLMRHLNIVSYAFNKSVDYQSVCEPGAAPKQ 893  
 QY 901 GAGHRSAYVPSVADIIQIGWATAAASIIQOFLLSITFPRLLEAVEMEDDDFTASLSKQ 960  
 DB 894 GAGHRSAYVPSVADIIQIGWATAAASIIQOFLLSITFPRLLEAVEMEDDDFTASLSKQ 953  
 QY 961 SCITEQTQYFFDNDKSFSGVLDGNCNCRIFHGKELMNTNLIIFIMVESKGTGCPDTRLLI 1020  
 DB 954 SCITEQTQYFFDNDKSFSGVLDGNCNCRIFHGKELMNTNLIIFIMVESKGTGCPDTRLLI 1013  
 QY 1021 QAEQTSQPNPCDMVKOPRYRKGPDYCFDNNVLEDTDCGGVS 1063  
 DB 1014 QAEQTSQPNPCDMVKOPRYRKGPDYCFDNNVLEDTDCGGVS 1056

Search completed: February 10, 2003, 14:18:27

Job time : 38.4969 secs





GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 10, 2003, 14:13:55 ; Search time 41.7178 Seconds  
(without alignments)  
5279.867 Million cell updates/sec

Title: US-10-090-827-9  
Perfect score: 5650  
Sequence: 1 MAAGCLLALTLFQSLIG.....NNALEDYDTCGVSHHHHHH 1069

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL.21.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archheap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	5602	99.2	1091	6	O77773
2	5528.5	97.8	1110	4	Q9UIU0
3	5477	96.9	1091	11	Q9ERS3
4	5405	95.7	1103	11	O08532
5	5381	95.2	1079	11	O8VHS9
6	3786	67.0	745	4	Q9UDQ3
7	3066	54.3	1150	4	Q9NY47
8	3038.5	53.8	1143	4	Q9NY48
9	3038.5	53.8	1156	11	Q9EQG2
10	3025.5	53.5	1145	4	Q9Y268
11	3013	53.3	1084	11	Q920H6
12	3004.5	53.2	1076	4	Q9UEW0
13	2829	50.1	975	4	Q9NSA6
14	1145.5	20.3	1091	11	Q9Z1L5
15	1074.5	19.0	997	4	Q9NY16
16	1034	18.3	1218	5	Q8T9C3

17	953	16.9	2190	5	Q9NK64
18	938	16.6	2172	5	Q9VJW0
19	906.5	16.0	1191	5	Q9VJN7
20	905	16.0	1255	5	Q9NK83
21	875	15.5	170	4	Q9UDL7
22	861	15.2	1022	5	Q9V6T7
23	759.5	13.4	519	4	Q9NY18
24	661	11.7	317	11	Q920H5
25	587	10.4	1148	5	Q17517
26	561.5	9.9	842	5	Q9SR75
27	516.5	9.1	104	4	Q9UD81
28	515	9.1	100	6	Q9GLH1
29	496.5	8.8	121	4	Q9UD82
30	479	8.5	98	4	Q9UDU5
31	470.5	8.3	223	11	Q9R142
32	467	8.3	97	4	Q9UD80
33	404	7.2	77	4	Q95026
34	335	5.9	1185	4	Q9HCJ9
35	233.5	4.1	978	6	Q95KE0
36	221	3.9	1449	5	Q9V917
37	201.5	3.6	886	11	Q91WG9
38	190.5	3.4	1450	16	Q9CE07
39	177.5	3.1	494	5	Q9U7P4
40	170.5	3.0	1819	16	Q97K40
41	167	3.0	796	17	Q9HJRO
42	167	3.0	800	17	Q97AH3
43	165	2.9	459	16	O25905
44	164.5	2.9	789	2	Q45793
45	164	2.9	614	16	Q8XN21

#### ALIGNMENTS

#### RESULT 1

O77773	ID	O77773	PRELIMINARY;	PRT;	1091 AA.
AC	O77773;				
DT	01-NOV-1998	(TReMBLrel. 08, Created)			
DT	01-NOV-1998	(TReMBLrel. 08, Last sequence update)			
DT	01-MAR-2002	(TReMBLrel. 20, Last annotation update)			
DE	Voltage-dependent calcium channel alpha-2 delta subunit precursor.				
OS	Sus scrofa (Pig).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OX	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.				
NCBI_TaxID=9823;					
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=BRAIN CORTEX;				
RX	MEDLINE=98411353; PubMed=9738015;				
RA	Brown J.P., Gee N.S.;				
RT	"Cloning and deletion mutagenesis of the alpha2 delta calcium channel subunit from porcine cerebral cortex. Expression of a soluble form of the protein that retains [3H]gabapentin binding activity.";				
RL	J. Biol. Chem. 273:25458-25465(1998).				
DR	EMBL; AF077665; AAC36289.1;				
DR	InterPro; IPR004010; Cache.				
DR	Pfam; PF02743; Cache; 1.				
DR	SMART; SM00327; vwa; 1.				
DR	PROSITE; PS00234; VWFA; 1.				
KW	Signal.				
FT	SIGNAL	1	24	POTENTIAL.	
FT	CHAIN	25	1091	VOLTAGE-DEPENDENT CALCIUM CHANNEL ALPHA-2 DELTA SUBUNIT.	
FT					
SO	SEQUENCE	1091 AA;	123150 MW;	293DDC7EBE9EE60E CRC64;	

Query Match 99.2%; Score 5602; DB 6; Length 1091;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAAGCLLALTLFQSLIGPSQEPPTSAVTIKSWYDKMQEDLVTLAKTASGVNQLVDI 60



```
QY 61 YKYQDLYTVEPNNAQVLAARDIEKLLSNRSKALVRLALEAEKVQAAHQWREDFASN 120
Db 61 YKYQDLYTVEPNNAQVLAARDIEKLLSNRSKALVRLALEAEKVQAAHQWREDFASN 120
QY 121 EVVYNAKDLDPEKNDSEPGSQRIPVFIDANFGROIYSQHAHVHPTDIYEGSTIVL 180
Db 121 EVVYNAKDLDPEKNDSEPGSQRIPVFIDANFGROIYSQHAHVHPTDIYEGSTIVL 180
QY 181 NELNWTSALEDEVFKKREDEPDLQVFGSATGLARYYPASPVWDSNRPKNKIDLYDVR 240
Db 181 NELNWTSALEDEVFKKREDEPDLQVFGSATGLARYYPASPVWDSNRPKNKIDLYDVR 240
QY 241 RPWYIOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSLDDDFVNVASFNSAQD 300
Db 241 RPWYIOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSLDDDFVNVASFNSAQD 300
QY 301 VSCFQHLVQANVRNKKVLAARDIEKLLSNRSKALVRLALEAEKVQAAHQWREDFASN 360
Db 301 VSCFQHLVQANVRNKKVLAARDIEKLLSNRSKALVRLALEAEKVQAAHQWREDFASN 360
QY 361 FTDGGEERAQEIFAKYKNDKVKRVFTFSVGHNYDRGPIQWACENKGYIYEIPISGAIR 420
Db 361 FTDGGEERAQEIFAKYKNDKVKRVFTFSVGHNYDRGPIQWACENKGYIYEIPISGAIR 420
QY 421 INTQEYLDVLRPMVLAGKAKQVQWNTVYLDALGLVITGTLPVFNITGQENKTNLK 480
Db 421 INTQEYLDVLRPMVLAGKAKQVQWNTVYLDALGLVITGTLPVFNITGQENKTNLK 480
QY 481 NQILGVMGVDVSLIEDIKRLTPRTFLCPNGYFAIDPNCYVLLHPNLQPK 540
Db 481 NQILGVMGVDVSLIEDIKRLTPRTFLCPNGYFAIDPNCYVLLHPNLQPK 540
QY 541 NQILGVMGVDVSLIEDIKRLTPRTFLCPNGYFAIDPNCYVLLHPNLQPK 600
Db 541 NQILGVMGVDVSLIEDIKRLTPRTFLCPNGYFAIDPNCYVLLHPNLQPK 600
QY 531 -----NPKSQBPVTLDFDLAELENDIKVEIRNKMIDGESGKTRFLVKQSDERYI 581
Db 531 -----NPKSQBPVTLDFDLAELENDIKVEIRNKMIDGESGKTRFLVKQSDERYI 581
QY 581 LKRRPNIONPKSQBPVTLDFDLAELENDIKVEIRNKMIDGESGKTRFLVKQSDERYI 600
Db 581 LKRRPNIONPKSQBPVTLDFDLAELENDIKVEIRNKMIDGESGKTRFLVKQSDERYI 600
QY 601 DKGNTYTWTPVNGTDYSLALVPTYSFYTKAKIETITQARSKKGMKDSKSETLKP 641
Db 601 DKGNTYTWTPVNGTDYSLALVPTYSFYTKAKIETITQARSKKGMKDSKSETLKP 641
QY 642 EESGYTFTAPRDYCNLDKISDNNTFELNFEFIDRKTTPNPNPCNTDLINVLDDAGFTN 701
Db 642 EESGYTFTAPRDYCNLDKISDNNTFELNFEFIDRKTTPNPNPCNTDLINVLDDAGFTN 701
QY 702 ELVQYWSKQKNIKGVKARFVVTGDTTRVYPKEAGENWQENPETYEDSFYKRSLDNDY 761
Db 702 ELVQYWSKQKNIKGVKARFVVTGDTTRVYPKEAGENWQENPETYEDSFYKRSLDNDY 761
QY 762 VFTAPYFNKSGPGAYESGIMYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTSTRDP 821
Db 762 VFTAPYFNKSGPGAYESGIMYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTSTRDP 821
QY 822 CAGPVCDCKRNSDVMDCVILDDGGFLLMANHDDYTNOIGRFFGIDPDSLMRHLNIVSYA 881
Db 822 CAGPVCDCKRNSDVMDCVILDDGGFLLMANHDDYTNOIGRFFGIDPDSLMRHLNIVSYA 881
QY 882 FNSYDYSQVCEPAGAPKQAGHRSAYVPSTADILHIGWATAAASILQOFLSLTFPR 941
Db 882 FNSYDYSQVCEPAGAPKQAGHRSAYVPSTADILHIGWATAAASILQOFLSLTFPR 941
QY 901 FNSYDYSQVCEPAGAPKQAGHRSAYVPSTADILHIGWATAAASILQOFLSLTFPR 960
Db 901 FNSYDYSQVCEPAGAPKQAGHRSAYVPSTADILHIGWATAAASILQOFLSLTFPR 960
QY 942 LLEAVEMEDDDFTASLSKQSCITQOTQYFFDNDKSPSGVLDGNCNRSRIFHEKLMNTN 1001
Db 942 LLEAVEMEDDDFTASLSKQSCITQOTQYFFDNDKSPSGVLDGNCNRSRIFHEKLMNTN 1001
QY 1002 IFIMVESKGTCPDTRLLIQAEQTSQDGPDCDMVKQPRYKRGPDVCFDNNALDYTCGG 1061
Db 1002 IFIMVESKGTCPDTRLLIQAEQTSQDGPDCDMVKQPRYKRGPDVCFDNNALDYTCGG 1061
QY 1062 VS 1063
Db 1062 VS 1063
QY 1081 VS 1082
Db 1081 VS 1082
```

```
RESULT 3
Q9ERS3
ID Q9ERS3 PRELIMINARY; PRT; 1091 AA.
AC Q9ERS3;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Voltage-gated calcium channel alpha2/delta-1 subunit.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=SUPERIOR CERVICAL GANGLIA;
RA Lin. Y., Lipscombe D.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF286488; AAG28164.1;
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 1.
DR Pfam; PF00092; vwa; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS0234; VWEA; 1.
FT VARIANT 209 212 GSAT -> AADR.
FT VARIANT 338 338 S -> T.
FT VARIANT 599 600 SL -> RY.
FT VARIANT 869 869 S -> R.
SQ SEQUENCE 1091 AA; 123467 MW; C15088971628E19 CRC64;
```

```
Query Match 96.9%; Score 5477; DB 11; Length 1091;
Best Local Similarity 97.0%; Pred. No. 0;
Matches 1031; Conservative 21; Mismatches 11; Indels 0; Gaps 0;
QY 1 MAAGCLLALTLTFLQSLIGPSSOEPPSAVTIKSWYDKMQEDLVTLAKTASGNQLVDI 60
Db 1 MAAGCLLALTLTFLQSLIGPSSOEPPSAVTIKSWYDKMQEDLVTLAKTASGNQLVDI 60
QY 61 YKYQDLYTVEPNNAQVLAARDIEKLLSNRSKALVRLALEAEKVQAAHQWREDFASN 120
Db 61 YKYQDLYTVEPNNAQVLAARDIEKLLSNRSKALVRLALEAEKVQAAHQWREDFASN 120
QY 121 EVVYNAKDLDPEKNDSEPGSQRIPVFIDANFGROIYSQHAHVHPTDIYEGSTIVL 180
Db 121 EVVYNAKDLDPEKNDSEPGSQRIPVFIDANFGROIYSQHAHVHPTDIYEGSTIVL 180
QY 181 NELNWTSALEDEVFKKREDEPDLQVFGSATGLARYYPASPVWDSNRPKNKIDLYDVR 240
Db 181 NELNWTSALEDEVFKKREDEPDLQVFGSATGLARYYPASPVWDSNRPKNKIDLYDVR 240
QY 241 RPWYIOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSLDDDFVNVASFNSAQD 300
Db 241 RPWYIOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSLDDDFVNVASFNSAQD 300
QY 301 VSCFQHLVQANVRNKKVLAARDIEKLLSNRSKALVRLALEAEKVQAAHQWREDFASN 360
Db 301 VSCFQHLVQANVRNKKVLAARDIEKLLSNRSKALVRLALEAEKVQAAHQWREDFASN 360
QY 361 FTDGGEERAQEIFAKYKNDKVKRVFTFSVGHNYDRGPIQWACENKGYIYEIPISGAIR 420
Db 361 FTDGGEERAQEIFAKYKNDKVKRVFTFSVGHNYDRGPIQWACENKGYIYEIPISGAIR 420
QY 421 INTQEYLDVLRPMVLAGKAKQVQWNTVYLDALGLVITGTLPVFNITGQENKTNLK 480
Db 421 INTQEYLDVLRPMVLAGKAKQVQWNTVYLDALGLVITGTLPVFNITGQENKTNLK 480
QY 481 NQILGVMGVDVSLIEDIKRLTPRTFLCPNGYFAIDPNCYVLLHPNLQPK 540
Db 481 NQILGVMGVDVSLIEDIKRLTPRTFLCPNGYFAIDPNCYVLLHPNLQPK 540
QY 541 NQILGVMGVDVSLIEDIKRLTPRTFLCPNGYFAIDPNCYVLLHPNLQPK 600
Db 541 NQILGVMGVDVSLIEDIKRLTPRTFLCPNGYFAIDPNCYVLLHPNLQPK 600
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Db 541 DFLDALENDIKVEIRNMKIDGESKEFTFRLVKSQDERYIDKGNRTYTTWTVNGTDSL 600  
 Qy 601 ALVLPYTFYIKAKIETITIOARSKKMDSETLKPDPNEESGYTFIAPRDCNDLKI 660  
 Db 601 ALVLPYTFYIKAKIETITIOARSKKMDSETLKPDPNEESGYTFIAPRDCNDLKP 660  
 Qy 661 SDNTEFLNFEIDRTPNPNPCNTDLINRVLLDAGFTNELVQYWSKOKNKGVKAR 720  
 Db 661 SDNTEFLNFEIDRTPNPNPCNTDLINRVLLDAGFTNELVQYWSKOKNKGVKAR 720  
 Qy 721 FVWTDGGITRYPKREGENWQENPETEDSFYKRSNDNDNVFTAPFNKSGPGAYESGI 780  
 Db 721 FVWTDGGITRYPKREGENWQENPETEDSFYKRSNDNDNVFTAPFNKSGPGAYESGI 780  
 Qy 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPCAGPVCDCRNSDVMDCVI 840  
 Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPCAGPVCDCRNSDVMDCVI 840  
 Qy 841 LDGGLFLMANHDDYTNQIGRFFGEIDPSLMHLVNIISVAFNKSVDYQSVCEPAAAPKQ 900  
 Db 841 LDGGLFLMANHDDYTNQIGRFFGEIDPSLMHLVNIISVAFNKSVDYQSVCEPAAAPKQ 900  
 Qy 901 GAGHSVAVPSTADILHTGWATAAASILQOFLSLTFPRLLAEVEMEDDFTASLSKQ 960  
 Db 901 GAGHSVAVPSTADILHTGWATAAASILQOFLSLTFPRLLAEVEMEDDFTASLSKQ 960  
 Qy 961 SCITETQYFFDNDKSFSGVLDGNCNRSRIFHVEKLMNTNLFIMVSKGTCPCDTRLII 1020  
 Db 961 SCITETQYFFDNDKSFSGVLDGNCNRSRIFHVEKLMNTNLFIMVSKGTCPCDTRLII 1020  
 Qy 1021 QAEQTSQDGPDCDMVQKPRYKRGPDVCDNNALEDYTDGCGVS 1063  
 Db 1021 QAEQTSQDGPDCDMVQKPRYKRGPDVCDNNALEDYTDGCGVS 1063

RESULT 4  
 O08532 PRELIMINARY; PRT: 1103 AA.  
 ID O08532; O08533; O08534; O08535; O08536;  
 DT 01-JUN-1998 (Tremblrel. 06, Created)  
 DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)  
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
 DE Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta  
 DE subunits precursor.  
 GN CACNA2D1 OR CACNA2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=971113514; PubMed=8955374;  
 RA Angelotti T., Hofmann F.;  
 RL FEBS Lett. 397:331-337(1996).  
 CC -!- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN  
 CC EXCITATION-CONTRACTION COUPLING.  
 CC -!- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:  
 CC ALPHA-1, ALPHA-2, BETA AND GAMMA.  
 CC -!- SUBUNIT: ALPHA-2 AND DELTA FORM HETERODIMERS THAT ARE DISULFIDE-  
 CC LINKED.  
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -!- ALTERNATIVE PRODUCTS: FIVE FORMS OF THE PROTEIN, ISOFORMS 2A-2E,  
 CC ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THE  
 CC SEQUENCE SHOWN HERE IS THAT OF ISOFORM 2A.  
 CC -!- TISSUE SPECIFICITY: ISOFORM 2A IS EXPRESSED IN SKELETAL MUSCLE AND  
 CC AORTA. 2B IS EXPRESSED IN BRAIN, 2C IS EXPRESSED IN HEART, 2D IS  
 CC EXPRESSED IN HEART AND SMOOTH MUSCLE, AND 2E IS EXPRESSED IN  
 CC SMOOTH MUSCLE. ALL FIVE ISOFORMS ARE EXPRESSED IN THE  
 CC CARDIOVASCULAR SYSTEM.  
 CC -!- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM  
 CC A PRECURSOR FORM.  
 CC -!- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.

DR EMBL; U73484; AAB50139.1; -.  
 DR EMBL; U73485; AAB50140.1; -.  
 DR EMBL; U73483; AAB50138.1; -.  
 DR EMBL; U73486; AAB50141.1; -.  
 DR EMBL; U73487; AAB50142.1; -.  
 DR MGI; 88295; Caca2d1.  
 DR InterPro; IPR004010; Cache.  
 DR Pfam; PF02743; Cache; 1.  
 DR Pfam; PF00092; vwa; 1.  
 DR SMART; SM00327; VWA; 1.  
 DR PROSITE; PS00234; VWEA; 1.  
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;  
 KW Calcium channel; Glycoprotein; Phosphorylation; Signal;  
 KW Alternative splicing.  
 FT SIGNAL 1 24  
 FT CHAIN 25 957  
 FT CHAIN 958 1103  
 FT TRANSMEM 446 469  
 FT TRANSMEM 918 942  
 FT TRANSMEM 1079 1098  
 FT MOD\_RES 501 501  
 FT MOD\_RES 845 845  
 FT CARBOHYD 92 92  
 FT CARBOHYD 136 136  
 FT CARBOHYD 184 184  
 FT CARBOHYD 324 324  
 FT CARBOHYD 348 348  
 FT CARBOHYD 475 475  
 FT CARBOHYD 604 604  
 FT CARBOHYD 613 613  
 FT CARBOHYD 675 675  
 FT CARBOHYD 781 781  
 FT CARBOHYD 824 824  
 FT CARBOHYD 888 888  
 FT CARBOHYD 895 895  
 FT CARBOHYD 985 985  
 FT CARBOHYD 998 998  
 FT VARSPPLIC 531 531  
 FT VARSPPLIC 554 554  
 FT VARSPPLIC 644 644  
 FT SEQUENCE 1103 AA; 124629 MW; 103773B4735120D4 CRC64;

Query Match 95.7%; Score 5405; DB 11; Length 1103;  
 Best Local Similarity 94.5%; Pred. No. 0;  
 Matches 1023; Conservative 23; Mismatches 10; Indels 26; Gaps 2;

Qy 1 MAAGCCLLALTLTLFQSLIGPSSQEPFPPSAVTIKSWDKMOEDLVTLAKTASGVNOLVDI 60  
 Db 1 MAAGCCLLALTLTLFQSLIGPSSQEPFPPSAVTIKSWDKMOEDLVTLAKTASGVNOLVDI 60

Qy 61 YEKYQDLYTVEPNARQLVEIAARDIEKLSNRSKALVRLALAEKVAQAAHWRDFASN 120  
 Db 61 YEKYQDLYTVEPNARQLVEIAARDIEKLSNRSKALVRLALAEKVAQAAHWRDFASN 120

Qy 121 EVVYNAKDDLDEKNDSEPGSORIKPVFDDANFRQISYQAAVHIPTDIYEGSTIVL 180  
 Db 121 EVVYNAKDDLDEKNDSEPGSORIKPVFDDANFRQISYQAAVHIPTDIYEGSTIVL 180

Qy 181 NELNWTLSALDEVKKNREDEPSSLWVFGSATGLARYYPASPWVDSRTPNKIDLDVRR 240  
 Db 181 NELNWTLSALDEVKKNREDEPSSLWVFGSATGLARYYPASPWVDSRTPNKIDLDVRR 240

Qy 241 RPWYIQGAASPKDMLILVDVSGVSGVGLTKLIRTSVSEMLETISDDDFVNVASFNSNAQ 300  
 Db 241 RPWYIQGAASPKDMLILVDVSGVSGVGLTKLIRTSVSEMLETISDDDFVNVASFNSNAQ 300

Qy 301 VSCFQHLVQANVRNKKVYLKDAVNNTAKGTDYKKGFSFAFEGQLLNVTNSRANCKIIML 360  
 Db 301 VSCFQHLVQANVRNKKVYLKDAVNNTAKGTDYKKGFSFAFEGQLLNVTNSRANCKIIML 360

Qy 361 FTDGGEERAQEIFAKYKNKKVRVTFPSVQGHNYDRGPQIOWMACENKNGYYEIPSGAIR 420

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Db 361 FTGGEERAQEIFAKYNKDKKRVFTSVGQHNVDKGPQIOMMACENKGYEIPSGAIR 420
QY 421 INTQEYLDVLRPMVLGADKAKQVQWTVNYDLAELGLVITGTLPVFNITQGNENKTNLK 480
Db 421 INTQEYLDVLRPMVLGADKAKQVQWTVNYDLAELGLVITGTLPVFNITQGNENKTNLK 480
QY 481 NQLILGVMGVDSLEDIKRLTPRFTLCPNGYFAIDPNGYVLLHLPNLPK-----530
Db 481 NQLILGVMGVDSLEDIKRLTPRFTLCPNGYFAIDPNGYVLLHLPNLPKPGVIGPTIN 540
QY 531 -----NPKSOEPTVLDLDAELENDIKVEIRKNKMDGSEKFTFRLVKSQDERYI 581
Db 541 LKRRPNVQPKSOEPTVLDLDAELENDIKVEIRKNKMDGSEKFTFRLVKSQDERYI 600
QY 582 DGNRTYVTPVNGTDSLALVLPYTFYIYKAKIETITQARSKGKMKDSETLKPDNF 641
Db 601 DGNRTYVTPVNGTDSLALVLPYTFYIYKAKIETITQARSKGKMKDSETLKPDNF 653
QY 642 EESGYTFIAPRDYCNLIKISDNTEFLLNPFIDRKTPNNPSCNTDLINRVLLDAGFTN 701
Db 654 EESGYTFIAPRDYCNLIKISDNTEFLLNPFIDRKTPNNPSCNTDLINRVLLDAGFTN 713
QY 702 ELQNTYWSKOKNKGKARVVTGGITRVYPKEAGENWOENPETYEDSFYKRSLDNDNY 761
Db 714 ELQNTYWSKOKNKGKARVVTGGITRVYPKEAGENWOENPETYEDSFYKRSLDNDNY 773
QY 762 VFTAPYFNKSGPGAYESGIMVSKAVIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRD 821
Db 774 VFTAPYFNKSGPGAYESGIMVSKAVIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRD 833
QY 822 CAGPVCCKRNSDMVDCVILDDGGFLLMANHDDYTQIGRFFGEIDPMSMRHLVNISVYA 881
Db 834 CAGPVCCKRNSDMVDCVILDDGGFLLMANHDDYTQIGRFFGEIDPMSMRHLVNISVYA 893
QY 882 FNKSYDYQSVCPEGAAPKOGAGHRSAYVPSIADILHIGWATAAASIIQQFLISLTFPR 941
Db 894 FNKSYDYQSVCPEGAAPKOGAGHRSAYVPSIADILHIGWATAAASIIQQFLISLTFPR 953
QY 942 LLEAVEMEDDFTASLSKQSCITEQTYFFDNDKSFSGVLDGCGNSRIFHVEKLMNTNL 1001
Db 954 LLEAVEMEDDFTASLSKQSCITEQTYFFDNDKSFSGVLDGCGNSRIFHVEKLMNTNL 1013
QY 1002 IFTWVSKGTCPCDTRLLMQAETSDGPDPCDMVKOPRYKGPDPVCFDNNVLEDYDCGG 1061
Db 1014 IFTWVSKGTCPCDTRLLMQAETSDGPDPCDMVKOPRYKGPDPVCFDNNVLEDYDCGG 1073
QY 1062 VS 1063
Db 1074 VS 1075

RESULT 5
Q8VHS9 PRELIMINARY; PRT; 1079 AA.
AC Q8VHS9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE L-type calcium channel alpha2/delta subunit.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=HEART;
RX MEDLINE=21601730; PubMed=11604404;
RA Yamada Y., Nagashima M., Tsutsura M., Kobayashi T., Seki S.,
RA Makita N., Horio Y., Touse N.;
RT "Cloning of a functional splice variant of L-type calcium channel
RT beta2 subunit from rat heart."
RL J. Biol. Chem. 276:47163-47170(2001).
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DR EMBL; AF400662; AAL47093.1; -
DR InterPro; IPR004010; Cache.
DR Pfam; PF02743; Cache; 1.
DR Pfam; PF00092; vwa; 1.
DR SMART; SM00327; vwa; 1.
DR PROSITE; PS0234; VWFA; 1.
SQ SEQUENCE 1079 AA; 122172 MW; DC4A3641195B546C CRC64;

Query Match 95.2%; Score 5381; DB 11; Length 1079;
Best Local Similarity 95.8%; Pred. No. 0;
Matches 1018; Conservative 21; Mismatches 12; Indels 12; Gaps 2;

QY 1 MAAGCLLALTTLFOSLLIGSSQBPFPSPVITKSWDKMQEDLVTLAKTAGVGNQLVDI 60
Db 1 MAAGCLLALTTLFOSLLIGSSQBPFPSPVITKSWDKMQEDLVTLAKTAGVGNQLVDI 60
QY 61 YEKYQDLTVPEPNARQLVEITAARDIEKLLSNRSKALVRLALEAEKVQAAHQRDFASN 120
Db 61 YEKYQDLTVPEPNARQLVEITAARDIEKLLSNRSKALVRLALEAEKVQAAHQRDFASN 120
QY 121 EYVYNAKDDLDPEKNDSPEGSORIKPVFIDANFGROIYSQHAHVHPTDIYEGSTIVL 180
Db 121 EYVYNAKDDLDPEKNDSPEGSORIKPVFIDANFGROIYSQHAHVHPTDIYEGSTIVL 180
QY 181 NELNWTSAIDVEYFKKNREEDPSLLMQVFGSATGLARYYPASVPWVDSNRTPNKIDLYDVR 240
Db 181 NELNWTSAIDVEYFKKNREEDPSLLMQVFGSATGLARYYPASVPWVDSNRTPNKIDLYDVR 240
QY 241 RPWYLOGAASPKDMLILVDVSGSVSGLTKLIRTSVSEMLETLSDDDPVNVASFNSNAQD 300
Db 241 RPWYLOGAASPKDMLILVDVSGSVSGLTKLIRTSVSEMLETLSDDDPVNVASFNSNAQD 300
QY 301 VSCFQHLVQANVRNKKVLKDVANNITAKGITYDKGFSFAPEOLLNLYNSRANCKIIML 360
Db 301 VSCFQHLVQANVRNKKVLKDVANNITAKGITYDKGFSFAPEOLLNLYNSRANCKIIML 360
QY 361 FTDGGEERAQEIFAKYNKDKKRVFTSVGQHNVDKGPQIOMMACENKGYEIPSGAIR 420
Db 361 FTDGGEERAQEIFAKYNKDKKRVFTSVGQHNVDKGPQIOMMACENKGYEIPSGAIR 420
QY 421 INTQYLDVLRPMVLGADKAKQVQWTVNYDLAELGLVITGTLPVFNITQGNENKTNLK 480
Db 421 INTQYLDVLRPMVLGADKAKQVQWTVNYDLAELGLVITGTLPVFNITQGNENKTNLK 480
QY 481 NQLILGVMGVDSLEDIKRLTPRFTLCPNGYFAIDPNGYVLLHLPNLPK-----EPVTL 540
Db 481 NQLILGVMGVDSLEDIKRLTPRFTLCPNGYFAIDPNGYVLLHLPNLPK-----EPVTL 540
QY 541 DFLDAELENDIKVEIRKNKMDGSEKFTFRLVKSQDERYIDKGNRTYVTPVNGTDSL 600
Db 541 DFLDAELENDIKVEIRKNKMDGSEKFTFRLVKSQDERYIDKGNRTYVTPVNGTDSL 600
QY 601 ALVLPYTFYIYKAKIETITQARSKGKMKDSETLKPDNFEESGYTFIAPRDYCNLDIK 660
Db 601 ALVLPYTFYIYKAKIETITQARSKGKMKDSETLKPDNFEESGYTFIAPRDYCNLDIK 660
QY 661 SDNTEFLLNPFIDRKTPNNPSCNTDLINRVLLDAGFTNELVONYSKOKNKGKVAR 720
Db 661 SDNTEFLLNPFIDRKTPNNPSCNTDLINRVLLDAGFTNELVONYSKOKNKGKVAR 720
QY 721 FVVTGGITRVYPKEAGENWOENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
Db 721 FVVTGGITRVYPKEAGENWOENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
QY 781 MVSKAVELYIQGKLLKPAVVGKIDVNSWIENFTKTSIRDPCAGVCDCKRNSDMVDCVI 840
Db 781 MVSKAVELYIQGKLLKPAVVGKIDVNSWIENFTKTSIRDPCAGVCDCKRNSDMVDCVI 840
QY 841 LDDGGFLLMANHDDYTQIGRFFGEIDPMSMRHLVNISVYAFNKSQDYQSVCPEGAAPK 900
Db 841 LDDGGFLLMANHDDYTQIGRFFGEIDPMSMRHLVNISVYAFNKSQDYQSVCPEGAAPK 900
QY 829 LDDGGFLLMANHDDYTQIGRFFGEIDPMSMRHLVNISVYAFNKSQDYQSVCPEGAAPK 888
Db 829 LDDGGFLLMANHDDYTQIGRFFGEIDPMSMRHLVNISVYAFNKSQDYQSVCPEGAAPK 888
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QY 901 GAGHSAYVPSIADILHIGWATAAAWSILQQFLSLTFPRLLLEAVEMEDDDFTASLSKQ 960
DB 889 GAGHSAYVPSITDIILQIGWATAAAWSILQQFLSLTFPRLLLEAVEMEDDDFTASLSKQ 948
QY 961 SCITEQTQFFNDKSKFSVGLDCGNCSTRIFHVEKLMNTLNFIMVESKGTGCPDTRLLI 1020
DB 949 SCITEQTQFFNDKSKFSVGLDCGNCSTRIFHVEKLMNTLNFIMVESKGTGCPDTRLLM 1008
QY 1021 QAEQTSDDGPDMDKQPRYKRGPDVCFDNNALDYTDGCGVS 1063
DB 1009 QAEQTSDDGPDMDKQPRYKRGPDVCFDNNVLEDYTDGCGVS 1051

RESULT 6
Q9UDQ3 PRELIMINARY; PRT; 745 AA.
AC Q9UDQ3;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE WUGSC:H_DJ0560014.1 protein (Fragment).
GN WUGSC:H_DJ0560014.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9063792; PubMed=9847074;
RA Sulston J.E., Waterston R.;
RT "Toward a complete human genome sequence.";
RL Genome Res. 8:1097-1108(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX Waterston R.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC006145; AAD20938.1; -.
DR InterPro: IPR004010; Cache.
DR InterPro: IPR002035; VWFA.
DR Pfam: PF02743; Cache; 1.
DR PROSITE: PS0234; VWFA; 1.
FT NON_TER 1
SQ SEQUENCE 745 AA; 84396 MW; BC07B53484B71EA4 CRC64;

Query Match 67.0%; Score 3786; DB 4; Length 745;
Best Local Similarity 98.7%; Pred. No. 1.8e-223;
Matches 708; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 347 YNVSRRANCKNIIMLFTDGEERAQEIFAKYKNDKVRVFTFSVGQHNVDGRPIQNMACHEN 406
DB 1 YNVSRRANCKNIIMLFTDGEERAQEIFAKYKNDKVRVFTFSVGQHNVDGRPIQNMACHEN 60
QY 407 KGYEIPSGAIRINTQBYLDVLRPMVLGDKAKQVQWNTNVLDALEGLVITGTLVP 466
DB 61 KGYEIPSGAIRINTQBYLDVLRPMVLGDKAKQVQWNTNVLDALEGLVITGTLVP 120
QY 467 FNITGQENKTNLKNQILGVNGVDVSLIEDIKRLTPRTCLPNGYFFAIDPNGYVLLHPN 526
DB 121 FNITGQENKTNLKNQILGVNGVDVSLIEDIKRLTPRTCLPNGYFFAIDPNGYVLLHPN 180
QY 527 LQPKNPKSQEPTVTLDFDLAELENDIKVEIRKNMIDGESKFTFRLVKSQDERYIDKGNR 586
DB 181 LQPKNPKSQEPTVTLDFDLAELENDIKVEIRKNMIDGESKFTFRLVKSQDERYIDKGNR 240
QY 587 TYTWTVPNGTDYSLALVLPYTFYFYIKAKIEFTITQARSKKMKDSETLKPDPNFESGY 646
DB 241 TYTWTVPNGTDYSLALVLPYTFYFYIKAKIEFTITQARSKKMKDSETLKPDPNFESGY 300

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QY 647 TFIAPROYCNDLKISDNTNTEFLNFEFIDRKTPNPNPCNTDLINRVLLDAGFTNELVQN 706
DB 301 TFIAPROYCNDLKISDNTNTEFLNFEFIDRKTPNPNPCNTDLINRVLLDAGFTNELVQN 360
QY 707 YWSQKKNIGVKARFVYTDGSTRVYKPEAGENQWENPETEDSFYKRSLDNDNYVFTAP 766
DB 361 YWSQKKNIGVKARFVYTDGSTRVYKPEAGENQWENPETEDSFYKRSLDNDNYVFTAP 420
QY 767 YFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVVGIKIDVNSWIENFTKTSIRDPGAGPV 826
DB 421 YFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVVGIKIDVNSWIENFTKTSIRDPGAGPV 480
QY 827 CDCKRNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRLHVNISVAFNKS 886
DB 481 CDCKRNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRLHVNISVAFNKS 540
QY 887 DYQSVCEPGAAPKOGAGHSAYVPSIADILHIGWATAAAWSILQQFLSLTFPRLLLEAV 946
DB 541 DYQSVCEPGAAPKOGAGHSAYVPSIADILHIGWATAAAWSILQQFLSLTFPRLLLEAV 600
QY 947 EMEDDDFTASLSKQSCITEQTQYFFDNDKSKFSVGLDCGNCSTRIFHVEKLMNTLNFIMV 1006
DB 601 EMEDDDFTASLSKQSCITEQTQYFFDNDKSKFSVGLDCGNCSTRIFHVEKLMNTLNFIMV 660
QY 1007 ESKGTCTCDTRLLIQAEQTSDDGPDMDKQPRYKRGPDVCFDNNALDYTDGCGVS 1063
DB 661 ESKGTCTCDTRLLIQAEQTSDDGPDMDKQPRYKRGPDVCFDNNVLEDYTDGCGVS 717

RESULT 7
Q9NY47 PRELIMINARY; PRT; 1150 AA.
AC Q9NY47;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Calcium channel, alpha 2/delta subunit 2.
GN CACNA2D2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Tissue=THYROID;
RA Klugbauer N.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX Tissue=THYROID;
RA Hobom M., Dai S., Marais E., Lacinova L.;
RT "Neuronal distribution and functional characterization of the calcium channel alpha2delta-2 subunit.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ251368; CAB86193.1; -.
DR InterPro: IPR004010; Cache.
DR InterPro: IPR002035; VWFA.
DR Pfam: PF02743; Cache; 1.
DR SMART: SM00327; VWFA; 1.
DR PROSITE: PS0234; VWFA; 1.
SQ SEQUENCE 1150 AA; 129876 MW; 37B75F687AFE573C CRC64;

Query Match 54.3%; Score 3066; DB 4; Length 1150;
Best Local Similarity 54.8%; Pred. No. 4.5e-179;
Matches 591; Conservative 175; Mismatches 178; Indels 34; Gaps 14;

QY 7 LALTTLTFLQSLILGPPSQEPFPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDIYKYQD 66
DB 44 LALTTLTFLQSLILGPPSQEPFPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDIYKYQD 103
QY 67 LYTVPEPNNAQOLVIAARDIEKLSNRKALVRLALEAEKVAQAAHWRQEDFASNEVYVN 126
DB 104 LFEVQENEPQKLYEKVAGDIESLLDRKQALKRLADAENFQKAHRWQDNKEEDIVYD 163

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EMBL; X70393; CAA49843.1; .  
DR MGD; MGI:96620; Itih3.  
DR InterPro; IPR002035; VWF\_A.  
DR Pfam; PF00092; vwa; 1.  
DR SMART; SM00327; vwa; 1.  
DR PROSITE; PS0234; VWF; 1.  
KW Serine protease inhibitor; Repeat; Signal; Multigene family;  
KW Glycoprotein.  
FT SIGNAL 1 18  
FT PROPEP 19 30  
FT CHAIN 31 646  
FT  
FT PROPEP 647 886  
FT DOMAIN 279 439  
FT CARBOHYD 88 88  
FT CARBOHYD 577 577  
FT BINDING 646 646  
SQ SEQUENCE 886 AA; 98977 MW; 15955308C7F5030A CRC64;

Query Match 3.6%; Score 194.5; DB 1; Length 886;  
Best Local Similarity 19.9%; Pred. No. 0.00049;  
Matches 185; Conservative 138; Mismatches 347; Indels 261; Gaps 44;

QY 27 FPSAVTIKSWDKQEDLVLTAKTASGVNQLVDIYKQDLYTVEPNNAQRLVEIAARDI 86  
DB YGPNVKEVEYAKQYKAVSOGKTAG---LVKASGRKLEKFTVSVNVAAGSKVTFELTY 153  
QY 87 EKLNSRKSALVSALEAEKQAAHQWREDFASNEVYNAKDDLDPEKNDSEPGSQRTK 146  
DB BELL-KRNGKGYEMLYKQPKQLVRHFEID-----AHIFEP-----Q 189  
QY 147 PVFTEDANFGRIQSYQAAVHIPTDIYEGSTVILNEINMTSALDEVEFKKNREDEPSSLWQ 206  
DB GLSMIDAE-----ASFINDL-LGSALTKEF----- 214  
QY 207 VEGSATGLARYYPASPVDNSRT-PNKID-----LYDVRRP-----WYI-- 245  
DB 215 -----SGKKGHVSEKPSLDQORSCPTCTDSLLNGDFTIVDVNRESGNVQIVNGTFVHF 269  
QY 246 ---QG-AASPDMILFDVSGVSGSLTKLIRTSVSEMLETSDDDFVNVSFNSNAQDV 301  
DB 270 FAPQGLPVVPRNIVFVIDVSGMSGRKIQTPREALLKILDVKEDDYLNFILEST---DV 326  
QY 302 SCFO-HLVOANVRNKKVLKDAVNNTAKGIDYKKGFSFAFEQLLNLYNVRAN-----C 354  
DB 327 TTKDHLVQATPANLKEAKTFVKNIHQDSMTNINDGLLKGIEML---NKAREDTHTVPERS 383  
QY 355 NKILMFTDG---CEERAQEIFNKYNK--DKKVRVFRFSVGOHNYERGPLOWMACENKG 408  
DB 384 TSIITMLDGDANTGESPEKIQENVRNAGKPLYNLGLF-NLNYNLETALENHG 442  
QY 409 YVEIPSIGAIRNTQEXYLDVLRPMVLGDKAKQVQWNTYLDALLEG--VITGLPLV 466  
DB 443 LARRIYEDSDANLQGGFVEEVANPLL-----TNVEVEYEPENAILDITRNSYPH 491  
QY 467 FNTGQFENKTNLKNQILGVMGVDVSLIEDIKLTPRTLCPNGYYPADPNGVLLHPN 526  
DB 492 F-----YDG-----SEIVAGRLVDRNDN-----FKADVKGHALN-- 523  
QY 527 LQPKNPKSOPVTLDFDLDALENDIKVEIRKNMIDGESGEK--TFRTLVKSQDERYIDKG 584  
DB 524 ----DLTFTEEDVMEEDALK-----EQGYIFGDIYERLWAYLTLEQLLEKRNKAG 572  
QY 585 NRTYTTVPNGTDYSIA--LVLPYTSFYIKAKLEETIQARSKGKMKDSEI-----LK 637  
DB 573 DEKENIT-ABALDLSLKHFVTLPLTSMVYVTKPKEDNEDQSTIADNAGERAFATETMTSMFLT 631

QY 638 PDNFEEGVTFTIAPRDYCNLDLKISDNNTFLLNFEIDRKTNNPSCNADLINRVLLDA 697  
DB 632 TQSSQSSQSYVYV-----DGDPHFIQI-----PGKNDISICFNIDKPK 668  
QY 698 GTNELVONYWSKQKNIKGVKARFVYTDGGITRVYYPKXGENWQENPETVEDSFYKRSLD 757  
DB 669 GTVLRLLIQD-----PVT--GIT-VTQIIGD-----KIS-- 694  
QY 758 NDNVYFTAPYFNKSGPGAVESGIMVSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTS 817  
DB 695 NASSRTGKTYFKGLGITNAWMDFRVEVTEKILG-----TGAELSTFSWLDVTVTQ 747  
QY 818 IRDPACAGPVCDCKRNSDVNDCVILDDG--GFLLMAN-----HDDYTNQIGREFGEIDP 868  
DB 748 -----TGLSVTINRKNMV--VSFGDGSIFVILHQVKKHPVHODFLG-----FYVVD 795  
QY 869 SLMRHLVNISSVAFNKSXYDQSV-CEPGAAP 898  
DB 796 HRMSAOTHGLLQGFQFPDFKVGIRPGSDP 826  
RESULT 7  
ITIH3\_HUMAN STANDARD; PRT; 885 AA.  
ID ITIH3\_HUMAN Q06033; Q99085;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Inter-alpha-trypsin inhibitor heavy chain H3 precursor (ITI heavy chain H3) (Serum-derived hyaluronan-associated protein) (SHAP).  
DE ITIH3.  
GN Homo sapiens (Human).  
OS Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OC NCBI\_TaxID=9606;  
RX [1]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Liver;  
RC MEDLINE=93215656; PubMed=7681778;  
RA Bourguignon J., Diarra-Mehrpour M., Thiberville L., Bost F., Sesboue R., Martin J.P.;  
RA "Human pre-alpha-trypsin inhibitor-precursor heavy chain. cDNA and deduced amino-acid sequence."  
RL Eur. J. Biochem. 212:771-776(1993).  
RP [2]  
RN SEQUENCE OF 341-885 FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=89137072; PubMed=2465147;  
RA Diarra-Mehrpour M., Bourguignon J., Sesboue R., Mattei M.-G., Passage E., Salier J.P., Martin J.P.;  
RA "Human plasma inter-alpha-trypsin inhibitor is encoded by four genes on three chromosomes."  
RL Eur. J. Biochem. 179:147-154(1989).  
RP [3]  
RN SEQUENCE OF 30-49; 463-477 AND 497-515.  
RX MEDLINE=89380192; PubMed=2476436;  
RA Enghild J.J., Thøgersen I.B., Pizzo S.V., Salvesen G.;  
RA "Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-alpha-trypsin inhibitor, from human plasma."  
RL J. Biol. Chem. 264:15975-15981(1989).  
RP [4]  
RN SEQUENCE OF 631-647, AND CROSS-LINKAGE SITE TO BIKUNIN.  
RX MEDLINE=91093267; PubMed=1898736;  
RA Enghild J.J., Salvesen G., Hefta S.A., Thøgersen I.B., Rutherford S., Pizzo S.V.;  
RA "Chondroitin 4-sulfate covalently cross-links the chains of the human blood protein pre-alpha-inhibitor."  
RL J. Biol. Chem. 266:747-751(1991).  
CC -!- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES.



Qy 331 TDYKGFSAFEQLNYN-----VSRANCNKIIMLFTDGEERAQEIFPKYKNKKRVVF 385  
Db 331 AEYBKALPLAFSVLLIDINNGGONNRGCENVIMLITDGAPNAYKKIFDMYNADKKRVF 390  
Qy 386 RFSYGQHNYERGPQIOMKACENKGYYEIPSGAIRINTQEYL----DVLRPMVLGDKA 441  
Db 391 TFLVGDEAIDFNREVEMACNRCGYMHVANWADVDEKIHIIYIRMSRVVGRHYKESGGUS 450  
Qy 442 KQOVNTWYLDALBLGL--VITGTLPVNITGGOFENKTN----- 478  
Db 451 ---WMTCGVYRERYLPRPEIFAEPVPVITNOSFAVMNMASRRKRIRLOKSEARSRFVTTV 507  
Qy 479 ----LKNOILILGYMGVDVSLEIKRLTPRETLCPCNGYYFAIDPBGVYLHPNLQPKNP--- 532  
Db 508 SYPVIVNETFMGAVERNIPUTEVAQKSHPANIGSKSYFFMLDQNGFVMTHPQLRPIDPET 567  
Qy 533 --KSQEPVTLDFLD-----AELENDIKVEIRNKMD 561  
Db 568 KYHKQNTNNMDDLLELVGQNQRVRSOKSQAVSDLYCESGANVAECVDLDRKAVRMIID 627  
Qy 562 GESGEKTRFLVKQSBERY----IDK---GNRTYTPTVNGTDYSIALVLPTSPFYIKA 614  
Db 628 CDNSD-----VOOLDVLTATELLDRVPQTNTTYAACINHANFVLGLAVAKGDDYRVVK 681  
Qy 615 KLEETITOARSKKGMK 631  
Db 682 K-----QKYDFGRVK 692

RESULT 6

ITH3\_MOUSE STANDARD; PRT: 886 AA.

ID ITH3\_MOUSE STANDARD; PRT: 886 AA.  
OC O61704;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DE 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Inter-alpha-trypsin inhibitor heavy chain H3 precursor (ITI heavy chain H3).  
GN ITIH3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
ON NCBI\_TaxID=10090;  
RX [1]  
RC SEQUENCE FROM N.A.  
RP STRAIN=C57BL/6N; TISSUE=Liver;  
RX MEDLINE=95194326; PubMed=7534067;  
RA Chan P., Risler J.-L., Raguenes G., Salier J.-P.;  
RT "The three heavy-chain precursors for the inter-alpha-inhibitor family in mouse: new members of the multicopper oxidase protein group with differential transcription in liver and brain.";  
RL Biochem. J. 306:505-512(1995).  
CC -! FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY SIMILARITY).  
CC -! SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN. BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2 AND BIKUNIN. INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.  
CC -! TISSUE SPECIFICITY: EXPRESSED IN BOTH LIVER AND BRAIN.  
CC -! PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY SIMILARITY).  
CC -! SIMILARITY: BELONGS TO THE ITIH FAMILY.  
CC -! SIMILARITY: CONTAINS 1 VWFA DOMAIN.

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CC -1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:  
 CC ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS  
 CC HETERODIMERS THAT ARE DISULFIDE-LINKED.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE  
 CC SPLICING.  
 CC -1- TISSUE SPECIFICITY: SKELETAL MUSCLE.  
 CC -1- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM  
 CC A PRECURSOR FORM.  
 CC -1- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.  
 CC -1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.  
 CC  
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 CC the European Bioinformatics Institute. There are no restrictions on its  
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 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; M21948; AAA81562.1; .  
 CC PIR; S10579; CHRA2.  
 CC InterPro: IPR004010; Cache.  
 CC InterPro: IPR002035; VWFA\_A.  
 CC Pfam; PF00092; vwa; 1.  
 CC Pfam; PF02743; Cache; 1.  
 CC SMART; SM00327; VWFA; 1.  
 CC PROSITE; PS0234; VWFA; 1.  
 CC Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;  
 CC Calcium channel; Glycoprotein; Phosphorylation; Signal;  
 CC Alternative splicing.  
 CC SIGNAL 26  
 CC CHAIN 27 960  
 CC FT CHAIN 1 1106  
 CC FT TRANSMEM 448 471  
 CC FT TRANSMEM 921 945  
 CC FT TRANSMEM 1082 1101  
 CC FT DOMAIN 255 432  
 CC FT CARBOHYD 94 94  
 CC FT CARBOHYD 138 138  
 CC FT CARBOHYD 186 186  
 CC FT CARBOHYD 326 326  
 CC FT CARBOHYD 350 350  
 CC FT CARBOHYD 477 477  
 CC FT CARBOHYD 606 606  
 CC FT CARBOHYD 615 615  
 CC FT CARBOHYD 678 678  
 CC FT CARBOHYD 784 784  
 CC FT CARBOHYD 827 827  
 CC FT CARBOHYD 891 891  
 CC FT CARBOHYD 898 898  
 CC FT CARBOHYD 988 988  
 CC FT CARBOHYD 1001 1001  
 CC FT MOD\_RES 503 503  
 CC FT MOD\_RES 848 848  
 CC SQ SEQUENCE 1106 AA; 125042 MW; 800DE7F3C877B618 CRC64;  
 CC  
 CC Query Match 96.0%; Score 5132.5; DB 1; Length 1106;  
 CC Best Local Similarity 94.7%; Pred. No. 1.2e-298;  
 CC Matches 985; Conservative 14; Mismatches 12; Indels 29; Gaps 4;  
 CC  
 CC 1 MAAGCILLALTLTLOS--LLIGSSSEPPSPFSAVTTKSWVDKMQEDLVTLAKTASGVNQLV 58  
 CC Db 1 MAAGRPLAWTLTULQAWLILIGSSSEPPSPFSAVTTKSWVDKMQEDLVTLAKTASGVHQLV 60  
 CC  
 CC 59 DIYEKYQDLTYVBNARQLVEIARDIEKLLSNRSKALVSLALEAEKVAQAAHQWREDA 118  
 CC Db 61 DIYEKYQDLTYVBNARQLVEIARDIEKLLSNRSKALVRLALEAEKVAQAAHQWREDA 120  
 CC  
 CC 119 SNEWYTNKADLDLPKNDSEPGSQRIKPVFTIEDANFGRIQISYQAAVHIPTDIYEGSTI 178  
 CC Db 121 SNEWYTNKADLDLPKNDSEPGSQRIKPVFTIEDANFRQVSYQAAVHIPTDIYEGSTI 180

QY 179 VLNELNWTSAIDVEPKKNEEDPSLLMQVFGSATGLARYYPASPWVDNSRTPNKIDLYDV 238  
 Db 181 VLNELNWTSAIDVEPKKNEEDPSLLMQVFGSATGLARYYPASPWVDNSRTPNKIDLYDV 240  
 QY 239 RRRPMWYIGGAASPKDMLILVDVSGVSGLTLLKLRITSVSEMLETLDSDDFVNVASFNSNA 298  
 Db 241 RRRPMWYIGGAASPKDMLILVDVSGVSGLTLLKLRITSVSEMLETLDSDDFVNVASFNSNA 300  
 QY 299 ODVSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFQQLLNNVSRANCNKII 358  
 Db 301 ODVSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFQQLLNNVSRANCNKII 360  
 QY 359 MLFTDGGERAQEIFNKYNDKKVRFRFVSQGNHYRGPIONMACENKGYEIPISGA 418  
 Db 361 MLFTDGGERAQEIFNKYNDKKVRFRFVSQGNHYRGPIONMACENKGYEIPISGA 420  
 QY 419 IRINTQYLDVLGPRMVLADKAKQVQWNTNYLDALGLVITGTLVPVFNITQGFENKTN 478  
 Db 421 IRINTQYLDVLGPRMVLADKAKQVQWNTNYLDALGLVITGTLVPVFNITQGFENKTN 480  
 QY 479 LKNOLLILGVMGVDVSLIEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHPNLQPK----- 530  
 Db 481 LKNOLLILGVMGVDVSLIEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHPNLQPKIGVGIP 540  
 QY 531 -----NPKSQEPVTLDFDLAELENDIKVEIRNKMIDGESGEKTFRTLVKSQDER 579  
 Db 541 INLRKRPNVONPKSQEPVTLDFDLAELENDIKVEIRNKMIDGESGEKTFRTLVKSQDER 600  
 QY 580 YIDKGNRTYTWTPVNGTDY--SLALVLPYTSFYFIKAELETTQAKSKKMKMDSSTLKP 638  
 Db 601 YIDKGNRTYTWTPVNGTDYSSIALVLPYTSFYFIKAELETTQAKSKKMKMDSSTLKP 653  
 QY 639 DNFEESSYTFIADPYCNDLKISDNNTFELNNEEDIRKTPNPNPCNADLINRVLLDAG 698  
 Db 654 DNFEESSYTFIADPYCNDLKISDNNTFELNNEEDIRKTPNPNPCNADLINRVLLDAG 713  
 QY 699 FTNELVONTWSKOKNIGVKARFVVDGGITRVYPKEAGENQENPETVEDSFYKRSLDN 758  
 Db 714 FTNELVONTWSKOKNIGVKARFVVDGGITRVYPKEAGENQENPETVEDSFYKRSLDN 773  
 QY 759 DNVFTAPYFNKSGGAYESGIMVSKAVIYTGKLLKPAVVGIIKIDVNSWIENFTKTSI 818  
 Db 774 DNVFTAPYFNKSGGAYESGIMVSKAVIYTGKLLKPAVVGIIKIDVNSWIENFTKTSI 833  
 QY 819 RDPGAGPVCDCKRNSDVMDCVILDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI 878  
 Db 834 RDPGAGPVCDCKRNSDVMDCVILDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI 893  
 QY 879 VYAFNKSVDYQSVCEPAGAPKOGAGHRSAYVPSVADILQIGWATAAAWSILQQFLLSIT 938  
 Db 894 VYAFNKSVDYQSVCEPAGAPKOGAGHRSAYVPSVADILQIGWATAAAWSILQQFLLSIT 953  
 QY 939 FPRLLAEVEMEDDDTASLSKOSCIETQTFEDNDSKFSFGLDCGNCGRIFHGEKLMN 998  
 Db 954 FPRLLAEVEMEDDDTASLSKOSCIETQTFEDNDSKFSFGLDCGNCGRIFHGEKLMN 1013  
 QY 999 TNLIFIMVESKGTCPCDTRL 1018  
 Db 1014 TNLIFIMVESKGTCPCDTRL 1033

RESULT 4

YLJ9\_CAEEL

ID YLJ9\_CAEEL

AC P34372;

DT 01-FEB-1994 (Rel. 28, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Hypothetical protein C50C3.9 in chromosome III precursor.

GN C50C3.9.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis.

DR SMART: SM00327; VWA; 1.  
DR PROSITE: P550234; VWA; 1.  
KW Calicium channel; Transmembrane; Ion transport; Voltage-gated channel;  
KW Calicium channel; Glycoprotein; Phosphorylation; Signal;  
KW Alternative splicing.  
FT SIGNAL 1 24  
FT CHAIN 25 944  
FT CHAIN 945 1091  
FT CHAIN 945 1091  
FT TRANSMEM 445 468  
FT TRANSMEM 906 930  
FT TRANSMEM 1067 1086  
FT DOMAIN 252 429  
FT CARBOHYD 92 92  
FT CARBOHYD 136 136  
FT CARBOHYD 184 184  
FT CARBOHYD 323 323  
FT CARBOHYD 347 347  
FT CARBOHYD 474 474  
FT CARBOHYD 584 584  
FT CARBOHYD 593 593  
FT CARBOHYD 663 663  
FT CARBOHYD 769 769  
FT CARBOHYD 812 812  
FT CARBOHYD 876 876  
FT CARBOHYD 883 883  
FT CARBOHYD 973 973  
FT CARBOHYD 986 986  
FT MOD\_RES 500 500  
FT MOD\_RES 833 833  
SQ SEQUENCE 1091 AA; 123822 MW; 7054907D9D343B34 CRC64;

Query Match 96.2%; Score 5145; DB 1; Length 1091;  
Best local Similarity 95.8%; Pred. No. 2e-299;  
Matches 976; Conservative 22; Mismatches 19; Indels 2; Gaps 2;  
QY 1 MAACCLLALTLTFLQSLIGPSSPEPPSAVTIKSWYDKMOEDLVTLAKTASGVNOLVDI 60  
DB 1 MAACCLLALTLTFLQSLIGPSSPEPPSAVTIKSWYDKMOEDLVTLAKTASGVNOLADI 60  
QY 61 YEKQDLYTEVPNNAROLVETARDIEKLLSNRSKALVSLALEAEKVOAAHOMREFASN 120  
DB 61 YEKQDLYTEVPNNAROLVETARDIEKLLSNRSKALVSLALEAEKVOAAHOMREFASN 120  
QY 121 EVVYNAKDDLDPKNDSEPGSQRIKVFIEDANFGRIQISYQAAHVIPTDIYEGSTIVL 180  
DB 121 EVVYNAKDDLDPKNDSEPGSQRIKVFIEDANFGRIQISYQAAHVIPTDIYEGSTIVL 180  
QY 181 NELNWTALDEVFKNREEDPSLLQVFGSATGLARYYPASPPWDSNRTPNKIDLYDVR 240  
DB 181 NELNWTALDEVFKNREEDPSLLQVFGSATGLARYYPASPPWDSNRTPNKIDLYDVR 240  
QY 241 RPWYIOGAASPKDMLILVDVSGVSGLTGLKIRTSVSEMLETSDDDFVNVAFNSNAQD 300  
DB 241 RPWYIOGAASPKDMLILVDVSGVSGLTGLKIRTSVSEMLETSDDDFVNVAFNSNAQD 300  
QY 301 VSCFQHLVQANVRNKKVLKDAVNNTAKGITDYKKGSFAFEQLLNVSRANCKITML 360  
DB 301 VSCFQHLVQANVRNKKVLKDAVNNTAKGITDYKKGSFAFEQLLNVSRANCKITML 360  
QY 361 FTDGGEERAQEIFKNYKDKKVRFRSVGOHNYERGPIONMACENKGYEIPISGAIR 420  
DB 361 FTDGGEERAQEIFKNYKDKKVRFRSVGOHNYERGPIONMACENKGYEIPISGAIR 420  
QY 421 INTQBYDLVGRPMVLADGKAKQVQWNTVYLDALGLVITGTLPVFNITQGFENKTLN 480  
DB 421 INTQBYDLVGRPMVLADGKAKQVQWNTVYLDALGLVITGTLPVFNITQGFENKTLN 480  
QY 481 NOLILGVMGVDVSLIEDIKRLPRTFLCPNGYFFAIDPNQVYLLHPNLPKPKSQEPVTL 540  
DB 481 NOLILGVMGVDVSLIEDIKRLPRTFLCPNGYFFAIDPNQVYLLHPNLPKPKSQEPVTL 540  
QY 540 NOLILGVMGVDVSLIEDIKRLPRTFLCPNGYFFAIDPNQVYLLHPNLPKPKSQEPVTL 540  
DB 540 NOLILGVMGVDVSLIEDIKRLPRTFLCPNGYFFAIDPNQVYLLHPNLPKPKSQEPVTL 540

QY 541 DFLDAELNDIKVIRNKMIDGESGKTFRTLKVSQDERYIDKGNRTYTTWTPVNGTDYS- 599  
DB 540 DFLDAELNDIKVIRNKMIDGESGKTFRTLKVSQDERYIDKGNRTYTTWTPVNGTDYR 599  
QY 600 LALVLPYSFYIKAKLEETITQARSKKGMKDSKTLKPNFESGYTFIAPRYCNDL 659  
DB 600 LALVLPYSFYIKAKLEETITQARSKKGMKDSKTLKPNFESGYTFIAPRYCNDL 659  
QY 660 ISDNTEFLNFNFIIDRKTNNPNSCNADLINRLLDAGFTNVLQVNSKQKNIKVKA 719  
DB 660 PSNDTEFLNFNFIIDRKTNNPNSCNADLINRLLDAGFTNVLQVNSKQKNIKVKA 719  
QY 720 RFVVTGGITRIVYKPEAGENQENPETEYEDSFYKRSLDNDNYVETAPYFNKSGGAYESG 779  
DB 720 RFVVTGGITRIVYKPEAGENQENPETEYEDSFYKRSLDNDNYVETAPYFNKSGGAYESG 779  
QY 780 IMVSKAVIYIQGKLLKPAVVGIKIDVNSWIENTFKTSIRPCAGPVCDCKRNSDVMDCV 839  
DB 780 IMVSKAVIYIQGKLLKPAVVGIKIDVNSWIENTFKTSIRPCAGPVCDCKRNSDVMDCV 839  
QY 840 ILDDGGFLLMANHDDYTNOIGRFFGEIDPDSLMRHLVNSLVAFNKSVDYQSVCEGPAAPK 899  
DB 840 ILDDGGFLLMANHDDYTNOIGRFFGEIDPDSLMRHLVNSLVAFNKSVDYQSVCEGPAAPK 899  
QY 900 QGAGHRSAYVPSVADILQIGWATAAASIILOQFLLSLTEPRLLLEAVEMEDDDFTASLSK 959  
DB 900 QGAGHRSAYVPSVADILQIGWATAAASIILOQFLLSLTEPRLLLEAVEMEDDDFTASLSK 959  
QY 960 QSCITEQTYQFFDNDKSKFSVGLDCGNCGRIFHGEKLMNTNLIFIMVESKTCPCDTRL 1018  
DB 960 QSCITEQTYQFFDNDKSKFSVGLDCGNCGRIFHGEKLMNTNLIFIMVESKTCPCDTRL 1018  
RESULT 3  
CIC2 RABIT STANDARD; PRT: 1106 AA.  
AC P13806;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta  
DE subunits precursor.  
DE CACNA2D1 OR CACNA2A OR CCHL2A.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88336904; PubMed=2458626;  
RA Ellis S.B., Williams M.E., Ways N.R., Brenner R., Sharp A.H.,  
RA Leung A.F., Campbell K.P., McKenna E., Koch W.J., Hui A.,  
RA Schwartz A., Harpold M.M.;  
RT "Sequence and expression of mRNAs encoding the alpha 1 and alpha 2  
RT subunits of a DHP-sensitive calcium channel.";  
RL Science 241:1661-1664(1988).  
RN [2]  
RP SEQUENCE OF 961-973.  
RX MEDLINE=91131638; PubMed=1847144;  
RA Jay S.D., Sharp A.H., Kahl S.D., Vedvick T.S., Harpold M.M.,  
RA Campbell K.P.;  
RT "Structural characterization of the dihydropyridine-sensitive calcium  
RT channel alpha 2-subunit and the associated delta peptides.";  
RL J. Biol. Chem. 266:3287-3293(1991).  
RN [3]  
RP SEQUENCE OF 961-975; 992-1000 AND 1033-1050.  
RX MEDLINE=90368635; PubMed=2168391;  
RA de Jongh K.S., Warner C., Catterall W.A.;  
RT "Subunits of purified calcium channels. Alpha 2 and delta are encoded  
RT by the same gene.";  
RL J. Biol. Chem. 265:14738-14741(1990).  
CC -1- FUNCTION: 265:14738-14741(1990).  
CC EXCITATION-CONTRACTION COUPLING.

FT CHAIN 945 1091 (BY SIMILARITY).  
 FT L-TYPE CALCIUM CHANNEL DELTA SUBUNIT (BY  
 FT SIMILARITY).  
 FT TRANSMEM 446 469 POTENTIAL.  
 FT TRANSMEM 906 930 POTENTIAL.  
 FT TRANSMEM 1067 1086 POTENTIAL.  
 FT DOMAIN 253 430 WFA.  
 FT CARBOHYD 92 92 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 184 184 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 324 324 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 348 348 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 475 475 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 585 585 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 594 594 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 663 663 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 769 769 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 812 812 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 876 876 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 883 883 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 973 973 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 986 986 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT MOD\_RES 501 501 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).  
 FT MOD\_RES 833 833 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).  
 SQ SEQUENCE 1091 AA; 123183 MW; 2E4E13EE29A47837 CRC64;

Query Match 100.0%; Score 5346; DB 1; Length 1091;

Best Local Similarity 100.0%; Pred. No. 2e-311;

Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLATLTQLQSLIGSSSEPPPSAVTIKSWDKMOEDLVITAKTASGVNQLVDI 60  
 DB 1 MAAGCLLATLTQLQSLIGSSSEPPPSAVTIKSWDKMOEDLVITAKTASGVNQLVDI 60  
 QY 61 YEKYQDLYTVPNNARQLVEIAARDIEKLLNSRKALVSLALEAEKQVQAHHORREDFASN 120  
 DB 61 YEKYQDLYTVPNNARQLVEIAARDIEKLLNSRKALVSLALEAEKQVQAHHORREDFASN 120  
 QY 121 EYVYNAKDDLDPEKNSEPGSQRIPKFIEDANFGRQISYQHAHVHIPTDIYEGSTIVL 180  
 DB 121 EYVYNAKDDLDPEKNSEPGSQRIPKFIEDANFGRQISYQHAHVHIPTDIYEGSTIVL 180  
 QY 181 NELNWTSALEDFVKKNEEDPSLLQWFGSATGLARYYPASPPVDNERTNKKIDLYDVR 240  
 DB 181 NELNWTSALEDFVKKNEEDPSLLQWFGSATGLARYYPASPPVDNERTNKKIDLYDVR 240  
 QY 241 RPWTIOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSDDDDFVNVASFNSNAQD 300  
 DB 241 RPWTIOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSDDDDFVNVASFNSNAQD 300  
 QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSAFEQLLNYNVSRANCNKIIML 360  
 DB 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSAFEQLLNYNVSRANCNKIIML 360  
 QY 361 FTDGGEERAQEIFNKNKDKVRFRESVGOHNYERGPQIOWMACENKGYIYEIPSGAIR 420  
 DB 361 FTDGGEERAQEIFNKNKDKVRFRESVGOHNYERGPQIOWMACENKGYIYEIPSGAIR 420  
 QY 421 INTQYLDVLGRPMVLADGAKAKOVQWNVYLDALGLVITGTLPVNTIGQFENKTNLK 480  
 DB 421 INTQYLDVLGRPMVLADGAKAKOVQWNVYLDALGLVITGTLPVNTIGQFENKTNLK 480  
 QY 481 NQLILGVNGVDVSLIEDIKRTPRTLCNPGYFAIDPNGVLLHPNLPKNPKSQEPVTL 540  
 DB 481 NQLILGVNGVDVSLIEDIKRTPRTLCNPGYFAIDPNGVLLHPNLPKNPKSQEPVTL 540  
 QY 541 DFLDAELNDLKVEIRNKMIDGESSEKFTFLYKSDQERIVDKGNRTYTWTPVNGTDYSL 600  
 DB 541 DFLDAELNDLKVEIRNKMIDGESSEKFTFLYKSDQERIVDKGNRTYTWTPVNGTDYSL 600  
 QY 601 ALVLPYTSFYIKAKLEETITQARSKKGMKDSETLKPDNFEESGYFTFIAPDYCNLDKI 660  
 DB 601 ALVLPYTSFYIKAKLEETITQARSKKGMKDSETLKPDNFEESGYFTFIAPDYCNLDKI 660

QY 661 SDNTEPELLNFNEFIDRKTTPNPNNSCNADLINRVLLDAGFTNELVQVWSKQNIKGVKAR 720  
 DB 661 SDNTEPELLNFNEFIDRKTTPNPNNSCNADLINRVLLDAGFTNELVQVWSKQNIKGVKAR 720  
 QY 721 FVVTGGSITRVYPKEAGENMOENPEYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
 DB 721 FVVTGGSITRVYPKEAGENMOENPEYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
 QY 781 MVSKAIVEIYTOGKLLKPAVVGKIDVNSWIENFTKTSIRDPCAGPYCDDCKRNSDVMDCVI 840  
 DB 781 MVSKAIVEIYTOGKLLKPAVVGKIDVNSWIENFTKTSIRDPCAGPYCDDCKRNSDVMDCVI 840  
 QY 841 LDGGFLMANHDDYTNQIGRFFGEIDPDSIMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 900  
 DB 841 LDGGFLMANHDDYTNQIGRFFGEIDPDSIMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 900  
 QY 901 GAGHRSAYVPSVADILQIGWATAAAWSILQOFLLSITFPRLLEAVEMEDDDFTASLSQ 960  
 DB 901 GAGHRSAYVPSVADILQIGWATAAAWSILQOFLLSITFPRLLEAVEMEDDDFTASLSQ 960  
 QY 961 SCITEQTQTFDFNDSDKSFSGVLDGCGNSRIFHGEKLMNTNLIFIMVESKGTCPDTRL 1018  
 DB 961 SCITEQTQTFDFNDSDKSFSGVLDGCGNSRIFHGEKLMNTNLIFIMVESKGTCPDTRL 1018  
 RESULT 2  
 CIC2\_RAT  
 ID CIC2\_RAT STANDARD; PRT; 1091 AA.  
 AC P54290;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta  
 DE subunits precursor.  
 GN CACNA2D1 OR CACNA12A OR CCHL2A.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92228762; PubMed=1314383;  
 RA Kim H.L.; Kim H.; Lee P.; King R.G.; Chin H.;  
 RT "Rat brain expresses an alternatively spliced form of the  
 RT dihydropyridine-sensitive L-type calcium channel alpha 2 subunit.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:3251-3255(1992).  
 CC -!- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN  
 CC EXCITATION-CONTRACTION COUPLING.  
 CC -!- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:  
 CC ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS  
 CC HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE  
 CC SPLICING.  
 CC -!- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM  
 CC A PRECURSOR FORM (BY SIMILARITY).  
 CC -!- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.  
 CC -!- SIMILARITY: CONTAINS 1 WFA DOMAIN.

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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; M86621; AAA41088.1;  
 DR InterPro: IPR004010; Cache.  
 DR InterPro: IPR002035; WFA.  
 DR Pfam: PF00092; WFA; 1.  
 DR Pfam: PF02743; Cache; 1.

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 10, 2003, 14:13:50 ; Search time 9.33945 Seconds  
(without alignments)  
4520.920 Million cell updates/sec

Title: US-10-090-827-13

Perfect score: 5346

Sequence: 1 MAAGCLLALTLFQSLIG.....TNLFIMVESKGTCPDTRL 1018

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5346	100.0	1091	1	CIC2_HUMAN
2	5145	96.2	1091	1	CIC2_RAT
3	5132.5	96.0	1106	1	CIC2_RABIT
4	739.5	13.8	1205	1	YLJ9_CAEEL
5	607	11.4	734	1	UN36_CAEEL
6	194.5	3.6	886	1	ITH3_MOUSE
7	182	3.4	885	1	ITH3_HUMAN
8	180.5	3.4	887	1	ITH3_RAT
9	164.5	3.1	886	1	ITH3_MESAU
10	161	3.0	1829	1	DPOL_THEST
11	159	3.0	1956	1	ATX1_PLAFA
12	157.5	2.9	575	1	YFBK_ECOLI
13	154.5	2.9	946	1	ITH2_HUMAN
14	152	2.8	1290	1	BXC1_CLOBO
15	151.5	2.8	420	1	Y103_SNY3
16	150.5	2.8	921	1	ITH4_PIG
17	150	2.8	654	1	MCPC_BACSU
18	149	2.8	930	1	ITH4_HUMAN
19	148	2.8	964	1	DPOL_CBEPT
20	144	2.7	1087	1	YXNK_CLOTM
21	143	2.7	946	1	ITH2_MESAU
22	142.5	2.7	382	1	YLJ0_CAEEL
23	142	2.7	1169	1	SMC_METJA
24	141	2.6	1251	1	RB22_PLAVB
25	140.5	2.6	935	1	ITH2_PIG
26	140	2.6	2710	1	TOXA_CLODI
27	140	2.6	3305	1	APLP_MANSE
28	139.5	2.6	764	1	PAG_BACAN
29	139	2.6	1513	1	STUI_YEAST
30	138	2.6	1180	1	C4AA_BACTI
31	137	2.6	984	1	HYSA_STRAG
32	136.5	2.6	3063	1	CAIC_HUMAN
33	135.5	2.5	946	1	ITH2_MOUSE

#### ALIGNMENTS

RESULT 1  
CIC2\_HUMAN  
ID CIC2\_HUMAN STANDARD; PRT; 1091 AA.  
AC P54289;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta subunits precursor.  
DE subunits precursor.  
GN CACNA2D1 OR CACNL2A OR CCHL2A.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP MEDLINE=92110010; PubMed=1309651;  
RA Williams M.E., Feldman D.H., McCue A.F., Brenner R., Velicelebi G., Ellis S.B., Harpold M.M.;  
RT "Structure and functional expression of alpha 1, alpha 2, and beta subunits of a novel human neuronal calcium channel subtype.";  
RL Neuron 8:71-84(1992).  
CC -!- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN EXCITATION-CONTRACTION COUPLING.  
CC -!- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS: ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: CENTRAL NERVOUS SYSTEM, SKELETAL MUSCLE AND AORTA TISSUES.  
CC -!- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM A PRECURSOR FORM (BY SIMILARITY).  
CC -!- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.  
CC -!- SIMILARITY: CONTAINS 1 VMFA DOMAIN.  
-----  
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EMBL; M76559; AAA51903.1; -  
Genew; HGNC:1399; CACNA2D1.  
MTM; 114204; -  
DR InterPro; IPR004010; Cache.  
DR InterPro; IPR002035; VWF\_A.  
DR Pfam; PF00092; vwa; 1.  
DR Pfam; PF02743; Cache; 1.  
DR SMART; SM00327; VWA; 1.  
DR PROSITE; PS50234; VWF; 1.  
DR Ionic channel; Transmembrane; Ion transport; Voltage-gated channel; Calcium channel; Glycoprotein; Signal.  
FT SIGNAL 1 24 POTENTIAL.  
CHAIN 25 944 L-TYPE CALCIUM CHANNEL ALPHA-2 SUBUNIT

34 134.5 2.5 2077 1 TEGU\_HSV6U  
35 133 2.5 862 1 MUTS\_BORBU  
36 133 2.5 1323 1 ADRI\_YEAST  
37 132.5 2.5 547 1 SYM\_BUCAL  
38 132.5 2.5 929 1 CALC\_NOTVI  
39 132.5 2.5 1679 1 Y109\_YEAST  
40 132 2.5 697 1 YE9C\_SCHPO  
41 131 2.5 1634 1 DPOL\_METJA  
42 130.5 2.4 987 1 YD94\_METJA  
43 130.5 2.4 1018 1 YC14\_METJA  
44 129.5 2.4 1658 1 YM67\_YEAST  
45 129 2.4 1244 1 Y307\_MYCPN

P52340 human herpe  
O51737 borrelia bu  
P07248 saccharomyc  
P57210 buchnera ap  
O91145 notophthalm  
P40457 saccharomyc  
O13773 schizosacch  
Q58295 methanococc  
Q58789 methanococc  
O58611 methanococc  
Q03661 saccharomyc  
P75342 mycoplasma

Tue Feb 11 13:47:57 2003

us-10-090-827-14.rsp

Page 16

Db 369 TALQMGDKNGATILQINA---TRLQSGEDLSEGDRLKTRVSKTTLOP 413

Search completed: February 10, 2003, 14:19:45  
Job time : 15.5046 secs





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QY 93 RSKALVSLALEAEKVOAAHQWRE-----DFASN-----EV 122
Db 81 ITSRMATTMIQSKVNNNSPQNVVDVQIPKGAFLNSFMSVTDCGKTFRSSIKKTVGCA 140
QY 123 VYVNAK-----DDLDPKNDSE-----PGSQRTKPFVIEDANGROISVQH----- 163
Db 141 LQAARAKGKTAGLVRSASSLNDENFRTEVNVLPFGAKVQFELHYQEVKVRKLGSEHRIYL 200
QY 164 ----AAVHIPTDIYEGSTIVLNLNWTSALE-----EVEKKNREE-----DPSLLMOVF 208
Db 201 QFGLRLAKHLEVDWVIEQGLRFLHVPDTFEGHFGVGVPIVSKGQQAHVSKFPIVAQO-- 258
QY 209 GSATGLARYYPASPWNVNSRTPNKIDLYDVRRP-----WYIQGAAS-----PK 252
Db 259 -----RICPSCR--ETAVDGLVLYDVVREKAGELEVNGYFVHFAPDNLDPK 309
QY 253 DMLILVDVSGSVGLTKLIRTSVSEMLETSLDDDFVNVVAFNSNAQDVSCFQHLVQANV 312
Db 310 NILFVIDVSGSMGVKMKQTVKAMTKIILDDRAEDHFDVDFNQNR--TWRNOLISATK 367
QY 313 RNKKVLKDAVNITAKGITDYKGF---SFAPEQLNLYNVRANCKLIMLFTDG-----G 365
Db 368 TOVADAKRYEIKIOPSGGTNINEALLRAIFILNEANNLGLLDPNSVSLIILVSGDPTVG 427
QY 366 ERAQEIEFNKYNKKVRFRFSVGQ-----HNYERGFIQW-----ACENK 407
Db 428 ELKLSKIQKNVKNQDNISLFSLGWGFVDVDFLKLNSNHNHGAQRIYGNQDTSOLK 487
QY 408 GYVEI--PSIGAIRN--TQEYLDVL-----GRPMVLG--DKAKQVQWNTVYLD 452
Db 488 KYNVSTPLLRNVQFNPHTSVTDVQNNFHNFGSGSEIVVAGKFDPAK-----LD 539
QY 453 ALEGLVITGTLPVFNITQGFENKTNLKNLILGMVGDVLSLEDI-----KRLTFRFTLCP 508
Db 540 QIE--SVITA-----TSANTQLVLETLAQWDLQFSLDKDKADDFTR-K 582
QY 509 NGYFFAIDPNGVVLHPNLOPNKPSQEPVTLDFDLDAELENDIKVEIRKNKIDGESGKT 568
Db 583 LWAYLTIN--QLLAERSLAP--TAAAKRRITRSILQMSLDHHTVPLTSLVIENAGDGR 638
QY 569 FRTLKVSOD 577
Db 639 MLADAPPQD 647

RESULT 14
BXCL_CLOBO
ID BXCL_CLOBO STANDARD; PRT; 1290 AA.
AC P18640;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Botulinum neurotoxin type C1 precursor (EC 3.4.24.69) (BoNT/C1)
DE (Bontoxilysin C1)
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90370487; PubMed=2204031;
RA Hauser D., Eklund M.W., Kurazono H., Binz T., Niemann H., Gill D.M.,
RA Boquet P., Popoff M.R.;
RT "Nucleotide sequence of Clostridium botulinum C1 neurotoxin.";
RL Nucleic Acids Res. 18:4924-4924(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Type C Stockholm / C-ST;
RX MEDLINE=91024998; PubMed=222445;
RA Kimura K., Fujii N., Tsuzuki K., Murakami T., Indoh T.,
RA Yokosawa N., Takeshi K., Syuto B., Oguma K.;
*RT "The complete nucleotide sequence of the gene coding for botulinum

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RT type C1 toxin in the C-ST phage genome.";
RL Biochem. Biophys. Res. Commun. 171:1304-1311(1990).
RN [3]
RP SEQUENCE OF 2-25.
RC STRAIN-type C Stockholm / C-ST;
RX MEDLINE=88153072; PubMed=2450068;
RA Tsuzuki K., Yokosawa N., Syuto B., Ohishi I., Fujii N., Kimura K.,
RA Oguma K.;
RT "Establishment of a monoclonal antibody recognizing an antigenic site
common to Clostridium botulinum type B, C1, D, and E toxins and
RL Infect. Immun. 56:898-902(1988).
RN [4]
RP IDENTIFICATION OF SUBSTRATE.
RX MEDLINE=94038966; PubMed=7901002;
RA Blasi J., Chapman E.R., Yamasaki S., Binz T., Niemann H., Jahn R.;
RT "Botulinum neurotoxin C1 blocks neurotransmitter release by means of
RL cleaving HPC-1/syntaxin.";
EMBO J. 12:4821-4828(1993).
CC -1- FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED
AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD
WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT
INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
CC ENDOPEPTIDASE THAT CLEAVES SYNTAXIN.
CC -1- CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the
neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No
detected action on small molecule substrates.
CC -1- SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L) AND A
HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVITY,
WHILE THE N-AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHANNEL
FORMATION AND TOXIN BINDING, RESPECTIVELY.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MISCELLANEOUS: THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS OF
BOTULINUM NEUROTOXIN: TYPES A, B, C1, D, E, F, AND G.
CC -1- MISCELLANEOUS: BOTULINUM TYPE C1 NEUROTOXIN IS SYNTHESIZED BY C
STRAIN OF CLOSTRIDIUM BOTULINUM WHICH CARRY THE APPROPRIATE
BACTERIOPHAGE.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27.
CC -----
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CC -----
EMBL; X56433; CAA47060.1; -
DR EMBL; X72793; CAA51313.1; -
DR EMBL; X53751; CAA37780.1; -
DR EMBL; D90210; BAA14235.1; -
DR EMBL; X62389; CAA44263.1; -
DR PIR; S11291; S11291.
DR PIR; A35396; A35396.
DR PIR; A43503; A43503.
DR HSP; P10845; 3BTA.
DR MEROPS; M27.002; -.
DR InterPro; IPR000395; Bontoxilysin.
DR InterPro; IPR000130; Zn_Mtpeptidse.
DR Pfam; PF01742; Peptidase_M27; 1.
DR PRINTS; PR00760; BONTOXILYSIN.
DR PRODOM; PD001963; Bontoxilysin; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc.
FT INIT_MET 0 0
FT CHAIN 1 448 BOTULINUM NEUROTOXIN C1, LIGHT-CHAIN.
FT CHAIN 449 1290 BOTULINUM NEUROTOXIN C1, HEAVY-CHAIN.
FT METAL 228 228 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 229 229 BY SIMILARITY.
FT METAL 232 232 ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID 436 452 INTERCHAIN (PROBABLE).
FT CONFLICT 84 84 P -> T (IN REF. 2).

```

of heavy (H) chain cDNA clones coding for a 383 amino-acid sequence of the H chain.";

Biol. Chem. Hoppe-Seyler 369:15-18(1988).

[4]

PARTIAL SEQUENCE FROM N.A.

TISSUE=Liver;

CDNA-88024442; PubMed-3663330;

Schreitmüller T., Hochstrasser K., Resinger P.W.M., Wächter E., Gebhard W.;

"CDNA cloning of human inter-alpha-trypsin inhibitor discloses three different proteins.";

Biol. Chem. Hoppe-Seyler 368:963-970(1987).

[5]

SEQUENCE OF 55-74; 116-127; 224-246; 295-307 AND 365-385.

Enghild J.J., Thøgersen I.B., Pizzo S.V., Salvesen G.;

"Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-alpha-trypsin inhibitor, from human plasma.";

Polypeptide chain stoichiometry and assembly by glycan.";

J. Biol. Chem. 264:15975-15981(1989).

[6]

SEQUENCE OF 55-64.

TISSUE=plasma;

MEDLINE-93039735; PubMed-1384548;

Malik N., Balduyck M., Maes P., Capon C., Mizon C., Han K.K., Tartar A., Fournet B., Mizon J.;

"The heavy chains of human plasma inter-alpha-trypsin inhibitor: their isolation, their identification by electrophoresis and partial sequencing. Differential reactivity with concanavalin A.";

Biol. Chem. Hoppe-Seyler 373:1009-1018(1992).

[7]

SEQUENCE OF 55-64 AND 681-702, CROSS-LINK STRUCTURE, AND CARBOHYDRATE-LINKAGE SITES T-691.

MEDLINE-93232026; PubMed-7682553;

Enghild J.J., Salvesen G., Thøgersen I.B., Valnickova Z., Pizzo S.V., Hefta S.A.;

"Presence of the protein-glycosaminoglycan-protein covalent cross-link in the inter-alpha-inhibitor-related proteinase inhibitor heavy chain 2/bikunin.";

J. Biol. Chem. 268:8711-8716(1993).

[8]

SEQUENCE OF 67-101, AND HYALURONAN BINDING.

TISSUE=Serum;

MEDLINE-94075371; PubMed-7504674;

Huang L., Yoneda M., Kimata K.;

"A serum-derived hyaluronan-associated protein (SHAP) is the heavy chain of the inter alpha-trypsin inhibitor.";

J. Biol. Chem. 268:26725-26730(1993).

[9]

SEQUENCE OF 699-702, AND COVALENT LINKAGE WITH CHONDROITIN SULFATE.

TISSUE=Plasma;

MEDLINE-94229087; PubMed-7513643;

Morelle W., Capon C., Balduyck M., Sautiere P., Kouach M., Michalski C., Fournet B., Mizon J.;

"Chondroitin sulphate covalently cross-links the three polypeptide chains of inter-alpha-trypsin inhibitor.";

Eur. J. Biochem. 221:881-888(1994).

[10]

CARBOHYDRATE-LINKAGE SITES, AND MASS SPECTROMETRY.

MEDLINE-98343966; PubMed-9677337;

Flahaut C., Capon C., Balduyck M., Ricart G., Sautiere P., Mizon J.;

"Glycosylation pattern of human inter-alpha-inhibitor heavy chains.";

Biochem. J. 333:749-756(1998).

[11]

CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.

MEDLINE-98087700; PubMed-9425062;

Olsen E.H.N., Rahbek-Nielsen H., Thøgersen I.B., Roepstorff P., Enghild J.J.;

"Posttranslational modifications of human inter-alpha-inhibitor: identification of glycans and disulfide bridges in heavy chains 1 and 2.";

Biochemistry 37:408-416(1998).

-1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A

BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES.

-1- SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN.

BIKUNIN, INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2 AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.

-1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN 4-SULFATE BRIDGE TO THEIR C-TERMINAL ASPARTATE.

-1- MASS SPECTROMETRY: MW=76508; METHOD=MALDI; RANGE=55-702.

-1- SIMILARITY: BELONGS TO THE ITIH FAMILY.

-1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.

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-----

EMBL; X07173; CAA30160.1; ALT\_SEQ.

EMBL; M18193; AAA60558.1; -

EMBL; M33033; AAA59195.1; -

PIR; S00346; IYH02.

PIR; B34245; B34245.

GlycoSuiteDB; P19823; -

Genew; HGNC:6167; ITIH2.

MIM; 146640; -

InterPro; IPR002035; VWF\_A.

Pfam; PF00092; vwa; 1.

SMART; SM00327; VWFA; 1.

PROSITE; PS0234; VWFA; 1.

Serine protease inhibitor; Repeat; Signal; Multigene family;

Glycoprotein. 1 18

POTENTIAL.

PROPEP 19 54

CHAIN 55 702

INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2.

VWFA.

N-LINKED (GLCNAC. . .) (COMPLEX).

/FTid-CAR\_000140.

O-LINKED (GALNAC. . .) (PARTIAL).

/FTid-CAR\_000214.

N-LINKED (GLCNAC. . .).

O-LINKED (GALNAC. . .).

/FTid-CAR\_000215.

O-LINKED (GALNAC. . .).

/FTid-CAR\_000216.

O-LINKED (GALNAC. . .).

/FTid-CAR\_000217.

CARBOXYLATION.

CHONDROITIN 4-SULFATE, CROSS-LINK SITE.

K -> L (IN REF. 5).

P -> A (IN REF. 2 AND 3).

F -> S (IN REF. 2 AND 3).

N -> D (IN REF. 2 AND 3).

V -> A (IN REF. 2 AND 3).

SEQUENCE 946 AA; 106436 MW; 1478CF3E8F3BA776 CRC64;

Query Match 2.8%; Score 154.5; DB 1; Length 946;

Best Local Similarity 19.9%; Pred. No. 0.13;

Matches 133; Conservative 106; Mismatches 259; Indels 171; Gaps 29;

QY 33 IKSVDKQEDLVYIAKTASGVNQLDIYEKYQDLYTVEPNNAQLVEIAARDIEKLNS 92

DB 26 LSEFVD--YEDLVEL---APGKQFLVAENRRYQSRPSGESEEMMEVDQVLTYSYKQVST 80







DR SMART: SM00327: VWA: 1.  
DR PROSITE: PS0234: VWFA: 1.  
KW Serine protease inhibitor; Repeat; Signal; Multigene family;  
KW Glycoprotein.  
FT SIGNAL 1 21 POTENTIAL.  
FT PROPEP 22 33 BY SIMILARITY.  
FT CHAIN 34 647 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN  
H3.  
FT PROPEP 648 887 BY SIMILARITY.  
FT DOMAIN 282 442 VWFA.  
FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 580 580 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT BINDING 647 647 CHONDROITIN 4-SULFATE, CROSS-LINK SITE  
(BY SIMILARITY).  
SQ SEQUENCE 887 AA: 99097 MW: 389F0FF96D514096 CRC64;  
Query Match 3.3%; Score 180.5; DB 1; Length 887;  
Best Local Similarity 18.5%; Pred. No. 0.0034;  
Matches 173; Conservative 139; Mismatches 350; Indels 275; Gaps 39;  
QY 27 FPSAVTIKSWDKMDELVTAKTASGVNOLVDIYKQDLYTVFPPNARQLVEIAARDI 86  
Db 101 YPGSVKEVAQYKAVSQGTAG---LVKASGRKLEKFTVSVNVAAGSKVIPELY 156  
QY 87 EKLISNESKALVSLAEAKVQAQHWRED---FASNEVYVYNAKDDLDPEKNDSEPSQ 143  
Db 157 EELL-KRKNKGYEMLVKQPKQLVRHFEIDAHIFEQGISMLDA----- 199  
QY 144 RIKPVFTEDANFQRIQSYQAAVHIPTDIYEGSTIVINELNWTLSALDEVFKKREEDPSL 203  
Db 200 -----DASF-----ITNDL-LGSALTKEF----- 217  
QY 204 LMQVFGATGLARYYPASPWVDSRT-PNKID-----LVYVRRP-----WY 244  
Db 218 -----SGKHGVSPKPSLDQORSCPTCTDILLNGDEFTIVYDVNRESPPGVQIVNGYF 269  
QY 245 I-----QG-AASPKMLILVDSVSGSLTKLIRTSVSEMLETLSDDDFVNVAESNSA 298  
Db 270 VHFAPQGLPVVPKNTAFVLDVSGSGRKGKIQOTREALUKLDMDKEEDYLNLFESTGV 329  
QY 299 QDVSCFOHLVQANVRNKKVLKDAVNINIAKIGITDYKKGFSFAPEQLNLYNVRAN----- 353  
Db 330 --TWKDHVKATPANLEEARAFVKNIKDRSMNTINDGLLGIEML---NKAREDLHVP 384  
QY 354 -CNKIIMLFTDG-----GEERAQEIFPNKDKKVRFRFSVG--QHYVERGPQWACENK 407  
Db 385 RSTSVILVMDGDANTGESPEKIQENVRNAIRGKPLYNLGFNNLNTNFLESALENH 444  
QY 408 GYVEIPSIGAIRNTQEVLDVLRPMVLGAKQVQWTVNYDLALELGL--VITGTLTP 465  
Db 445 GFARRIYEDSDASIQLOGFEEVANPLL-----TNVELEVPENAILDLTRNSYP 493  
QY 466 VFNITGOFENKTLNKLILGVNGVDVSLDLEIKLTPRETLCPNGYFFAIDPNGYVLLHP 525  
Db 494 HF-----YDG-----SEIVVAGRLVDRNVDN-----FRADVKHGHALN- 526  
QY 526 NLPKPNKPSQEPVTLDFDLAELENDIKVEIRNKMIDGESKEKTF-----RLVKSQDER 579  
Db 527 -----DLTFTEEDVMDKEMDAALK-----EQGIYIFGDIYERLWAYLTTEQLLEKRNAR 574  
QY 580 YIDKGRNTYTWTPVNGTDVSLA--LVLPVTSFYIYKAKLEETIQARSKKGMKDSSET-- 635  
Db 575 GDEKENT-----AAELESLKHFVTLPTLSVMTVPENEDQATADKPGEAISASTA 629  
QY 636 -LKPDPNFEESGYTFIAPRDYCNLIKISDNNTEFLNF---NEFIDRKTPNPNPSCNADLIN 691  
Db 630 YLTSQSSSHSPYIV-----DGDPHFIQVPGKNDTICFNIDEKPGTVLSLQ 677  
QY 692 RVLIDAGFTNELVQVWTSQKNKIKGVKARFVTDGGITRVYKPEAGENQENPEYEDSF 751  
Db 678 DPTVTGIATVGOIIT-----GEKGNASSRTGKT----- 704  
QY 752 YKRSLDNDNYVFTAPVFNKSGPGAYESGIMVSKAVEIYIQGLKLPVAVGKIDVNSWTE 811

Db 705 -----YFGKLGIANAWMDFRIVETTERILGN-----GDALSTFSWLD 742  
QY 812 NPTKTSIRDPCAGPYCDCKRNSDVMCDVILDDG-CFLLMAN-----HDDYTNQIGRF 862  
Db 743 TVTVTQ-----TGLSVTINRKNMV--VSFEDGISFVILHVQVKKKHPHQDFLG----- 790  
QY 863 FGEIDPSLMRLHLVNTSVYAFNKSVDYQSV-CEPGAAP 898  
Db 791 FYVVDSHRMSAQTHGLLGOFTQPEDEKVFVDVRPGSDP 827  
RESULT 9  
ITH3\_MESAU  
ID ITH3\_MESAU STANDARD; PRT; 886 AA.  
AC P97280;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Inter-alpha-trypsin inhibitor heavy chain H3 precursor (ITI heavy  
DE chain H3) (HC3).  
GN ITH3.  
OS Mesocricetus auratus (Golden hamster).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
OC Mesocricetus.  
OX NCBI\_TaxID=10036;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver.  
RX MEDLINE=97420688; PubMed=9276673;  
RA Nakatani T., Suzuki Y., Yamamoto T., Sinohara H.;  
RT "Molecular cloning and sequencing of cDNAs encoding three heavy-chain  
RT precursors of the inter-alpha-trypsin inhibitor in Syrian hamster:  
RT implications for the evolution of the inter-alpha-trypsin inhibitor  
RT heavy chain family".  
RL J. Biochem. 122:71-82(1997).  
RN [2]  
RP SEQUENCE OF 31-50; 446-472 AND 504-523, AND SUBUNITS.  
RC TISSUE=Plasma;  
RX MEDLINE=97018241; PubMed=8864857;  
RA Yamamoto T., Yamamoto K., Sinohara H.;  
RT "Inter-alpha-trypsin inhibitor and its related proteins in Syrian  
RT hamster urine and plasma".  
RL J. Biochem. 120:145-152(1996).  
RN [3]  
RP FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A  
RP BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,  
RP INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE  
RP LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE  
RP ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY  
RP SIMILARITY).  
CC [1] SUBUNIT: I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM  
CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN.  
CC BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2  
CC AND BIKUNIN. INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND  
CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.  
CC [1] PM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN  
CC 4-SULFATE BRIDGE TO THEIR C-TERMINAL ASPARTATE (BY  
CC SIMILARITY).  
CC [1] SIMILARITY: BELONGS TO THE ITH FAMILY.  
CC [1] SIMILARITY: CONTAINS 1 VWFA DOMAIN.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
DR EMBL; D89287; BAAL3940.1; -.  
DR InterPro: IPR002035; VWFA\_A.  
DR Pfam; PF00092; vwa; 1.

\*Chondroitin 4-sulfate covalently cross-links the chains of the human blood protein pre-alpha-inhibitor.\*;  
 J. Biol. Chem. 266:747-751(1991).  
 -!- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES.  
 -!- SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN, BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2 AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.  
 -!- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE.  
 -!- SIMILARITY: BELONGS TO THE ITIH FAMILY.  
 -!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.  
 -----  
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 -----

EMBL: X67055; CAA47439.1; -;  
 EMBL: X14690; CAA32821.1; -;  
 Genew: HGNC:6168; ITIH3.  
 MIM: 146650; -;  
 InterPro: IPR002035; VWFA\_A.  
 Pfam: PF00092; vwa; 1.  
 SMART: SM00327; VWFA; 1.  
 PROSITE: PS0234; VWFA: 1.  
 Serine protease inhibitor; Repeat; Signal; Multigene family;  
 Glycoprotein. 1 17 POTENTIAL.  
 SIGNAL 18 30  
 PROPEP 31 647  
 CHAIN 31 647  
 INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3.  
 VWFA.  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CHONDROITIN 4-SULFATE, CROSS-LINK SITE.  
 R -> K (IN REF. 2).  
 N -> G (IN REF. 2).  
 Q -> H (IN REF. 2).  
 Q -> H (IN REF. 2).  
 885 AA; 99121 MW; BC63856F8F5E4A1B CRC64;  
 Query Match 3.3%; Score 182; DB 1; Length 885;  
 Best Local Similarity 20.2%; Pred. No. 0.0028;  
 Matches 132; Conservative 107; Mismatches 243; Indels 170; Gaps 33;

QY 27 FPSAVTIKSWDKQEDLVTLAKTASGVNQLVDIYKQDLYTVPPNARQLVEIARDI 86  
 DB 97 YPGNVKEVAKQYKAVSGKTAG-----LVKASGRKL 131  
 QY 87 EKLNSRKSAL---VSLALEAEKQAAHQWREDFASNEVVYNAKODLPDKNDSPEGSQ 143  
 DB 132 EKFTSVNVAAGSKVTLEYELLKHKGK-----YEMLVKQPK-----Q 173  
 QY 144 RIKPVFIEDANFGROIYQHAHVHPTDIYEGSTIVNELNWTLSALDEVFKKNREDPDL 203  
 DB 174 LVKHFETE-----VDIFEQGISMLDAEASFTNDLL-----GSA 208  
 QY 204 LWQVFGSTGLARYPPASPVWDSRT-PNKID-----LYDVRRRP-----WY 244  
 DB 209 LTKFSGKKGVSRKPS---LDQQRSCPTCTDLSLLNGDFTITVDVNRSPCNQIVNGYF 265  
 QY 245 I-----QG-AAAPKMLITDVSGVSGLTLLKIRTSVSEMMLETLSDDDFVNVASFNSNA 298  
 DB 266 VHFAPQGLPVPPNVAFVIDISGMAGRKLEQTKALLRILEDKMEEDYINFLFSG-- 323

QY 299 QDVSCF-QHLVQANVRNKKVLKDAVNNITAKGIDTYKKGFSFAFQQLLNVVSR----- 351  
 DB 324 -DVTWKHELVAQENLEQARTFVKSMEDKGMTINDGLRGISML--NKAREEHRIP 379  
 QY 352 ANCKNIIMLFTDG-----GEERAQEIFNKNYK--DKKVRVRFPSVGOHNYRGPTQWMA 405  
 DB 380 ERSTISIVIMLTDGDANVGESRPEKIQENVRNAIGKGFPLYNLGFG--NNLNTNFLENMALE 438  
 QY 406 NKGYVEEIPSGAIRINTQEVLDVLGRPMVLADGKAKQVQMTNVYLDAL-----L 456  
 DB 439 NIGCFARRIYEDSDADLQOGFYEEVANPL-LTGVEWEPE--NAILDTQNTYQHFDYGS 495  
 QY 457 GLVITGTLPVFVNITCOFENKTNLK-----NQLILGVMGVDVSLDKRLTPRFTICPNY 511  
 DB 496 EIVWAGRL-VDEDMNSF--KADVKGHGATNDL---TFTEEVDMKEMK-----ALQERDY 544  
 QY 512 YFAIDPN-----GYVLLHPNLOPK---NPKSOEPTVLDLDAELENDIKVEIRKNMIDG 562  
 DB 545 IFG---NYIERLWALYITQELLEKKRNAHGEKENLTARALDSLKYHFVTPLTSMVVTK 601  
 QY 563 ESGETFTLVKSQDERYT-DKGNRTYTPVN-GTDYSLALVLTPTSYFYII 612  
 DB 602 PE-----DNEDERALADRGEDAEATVPSPAMSYLTQVPPQNPYYV 644

## RESULT 8

ITIH3 RAT  
 ID ITIH3 RAT STANDARD; PRT; 887 AA.  
 AC Q63416;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Inter-alpha-trypsin inhibitor heavy chain H3 precursor (ITI heavy chain H3).  
 DE chain H3).  
 GN ITIH3.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Sprague-Dawley; TISSUE=Liver;  
 RA Blom A.; Fries E.;  
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY SIMILARITY).  
 CC -!- SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN, BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2 AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.  
 CC -!- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE ITIH FAMILY.  
 CC -!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.  
 -----

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 -----

EMBL: X83231; CAA58233.1; -;  
 InterPro: IPR002035; VWFA\_A.  
 Pfam: PF00092; vwa; 1.

CC 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY  
CC SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE ITH3 FAMILY.  
CC -!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; X70393; CAA49843.1; .

DR MGD; MG1:96620; itih3.

DR InterPro; IPR002035; VWFA\_A.

DR Pfam; PF00092; vwa; 1.

DR SMART; SM00327; VWA; 1.

DR PROSITE; PS00234; VWFA; 1.

KW Serine protease inhibitor; Repeat; Signal; Multigene family;

KW Glycoprotein. 1 18

FT SIGNAL 19 30

FT PROPEP 31 646

FT CHAIN 31 646

FT PROPEP 647 886

FT DOMAIN 279 439

FT CARBOHYD 88 88

FT CARBOHYD 577 577

FT BINDING 646 646

FT SEQUENCE 886 AA; 98977 MW; 15955308C7F5030A CRC64;

Query Match 3.68; Score 194.5; DB 1; Length 886;

Best Local Similarity 19.94; Pred. No. 0.0005;

Matches 185; Conservative 138; Mismatches 347; Indels 261; Gaps 44;

QY 27 FPSAVTIKSWDKMEDLVTLAKTAGVNLVDIYEQDLYTVEPNAROLVELIARDI 86

DB 98 YPGNKEKEVAQKYEKAVSOKTAG-----LVKASGRKLEAFTVSNVAGSKVTFELTY 153

QY 87 EKLLNSRKALVSLALEAEKQVAAHQWREDFASNEVYVYNAKDLDPEKNDSEPGSORIK 146

DB 154 BELL-KRNKGYEMLYKQPKQLVRHFEID-----AHIFEP-----Q 189

QY 147 PVFIEDANFGQISQVQAAVHIPDIDYEGSTIVINELNWTLSALDEVFKKNEEDPSLLWQ 206

DB 130 GLSMDAE-----ASFITNDL-LGSALTQSF----- 214

QY 207 VFGSATGLARYYPASPWPVDSNRT-PNKID-----LYDVRRRP-----WVI-- 245

DB 215 -----SGKKGHVSKPSLDQORSCTCTDLSLLNGDFTIVDVNRESQGVQVNGYFVHF 269

QY 246 ---QG-AASPKDMLILVDVSGVSGLTCLKLRTSVSEMLETSLDDDFVNVASFNSNAQDV 301

DB 270 FAPQGLPVVPKNIVFIDVSGMSGRKIQTREALLKLDVKKEDDYDLNFTLEST---DV 326

QY 302 SCFO-HLVQAVNRKKVYLKDAVNNTAKGTIDYKKGSAFEQQLLNVSAN-----C 354

DB 327 TTKDHLVQATPAMLKEAKTEVKNHDOQSMNTINDGLLKGIEML---NKAREDHVTPERS 383

QY 355 NKIIIMFTDG-----GEERAQEIFKNYK--DKKRVRFVSQGHYNERGPIQWACENKG 408

DB 384 TSIIMLTGDANTGESRPEKIQENVRNAGGKFPPLNLGFG-NLNLYNLEFLALENHG 442

QY 409 YYYEIPSGAIRITQYDVLGRPMVLADGKAKQVQWNTVYLDALDELGL-VITGLPLV 466

DB 443 LARRIEDSDANLQGFYEAVANPLL-----TNVEYEPENAILDLTRNSYPH 491

QY 467 FNITQFQENKTNLKNQILGVMGVDVSLSDIKRLTPRTCLPCNGYFAIDPNCVLLHPN 526

DB 492 F-----YDG-----SEIVVAGRLVDRNNDN-----FKADVKGHGALN-- 523

QY 527 LQKNPKSQEPTVLDLFLDAELNDIKVEIRNKMIDSGEKK--TFRTLKVSQDERYIDKG 584

DB 524 ---DLFTTEVDMEEMDAALK-----EGYIFGDYIERLWAYLTIEQLLEKRNKAG 572

QY 585 NRTVTWTPVNCYDYSLA--LVLPYTSYYIKAKLEETITQARSKKGMKDSSET-----LK 637

DB 573 DEKENIT-ARALDLSLKYHFVTLTSMVVTKPEDNEDQTSIADNAGEAFAETTTWSFLT 631

QY 638 PDNPEESGYTFIAPRDYCNLDKLSIDNTEFLANFEFIDRKTNNPNSCNADLINRVLLDA 697

DB 632 TQSSQSPYYV-----DGDPHFIQI-----PKNDISCFNIDKPK 668

QY 698 GFTNELVONYWSKOKNIKGVKARFVVDGGITRVYKPEAGENMQENPETYEDSFYKRSLD 757

DB 669 GTVLRLIQD-----PVT--GIT-VTQGIIGD-----KRS-- 694

QY 758 NDNVVFTAPYFNKSGPGAYESGIMVSKAVELYIQGKLLKPAVGIKIDVNSWIENFTKTS 817

DB 695 NASSRTGKTYFGKLGITNAWMDRFEVTEKIIILG-----TGAELSTFSLDVTVTQ 747

QY 818 IRDPCAGPVCDCKRNSDVMCDVILDDG-GFLLMAN-----HDDYTNQIGRFFGEIDP 868

DB 748 -----TGLSVTINRKNMV--VSFGDGISFVILHQQWKKHPVHQDFLG-----FYVDS 795

QY 869 SLMRHLVNISVYAFNKSVDYQSV-CEPGAAP 898

DB 796 HRMSAOTHGLLGQFFQFPDFKVFQIRPGSDP 826

RESULT 7

ITH3\_HUMAN STANDARD; PRT; 885 AA.

ID ITH3\_HUMAN AC Q06033; Q99085;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Inter-alpha-trypsin inhibitor heavy chain H3 precursor (ITI heavy

DE chain H3) (Serum-derived hyaluronan-associated protein) (SHAP).

GN ITIH3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=93215656; PubMed=7681778;

RA Bourguignon J., Diarra-Mehrpour M., Thiberville L., Bost F.,

RA Sesboue R., Martin J.P.;

RT "Human pre-alpha-trypsin inhibitor-precursor heavy chain. cDNA and

RT deduced amino-acid sequence."

RL Eur. J. Biochem. 212:771-776(1993).

RN [2]

RP SEQUENCE OF 341-885 FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=89137072; PubMed=2465147;

RA Diarra-Mehrpour M., Bourguignon J., Sesboue R., Mattei M.-G.,

RA Passage E., Salier J.P., Martin J.P.;

RT "Human plasma inter-alpha-trypsin inhibitor is encoded by four genes

RT on three chromosomes."

RL Eur. J. Biochem. 179:147-154(1989).

RN [3]

RP SEQUENCE OF 30-49; 463-477 AND 497-515.

RX MEDLINE=89380192; PubMed=2476436;

RA Enghild J.J., Thøgersen I.B., Pizzo S.V., Salvesen G.;

RT "Analysis of inter-alpha-trypsin inhibitor and a novel trypsin

RT inhibitor, pre-alpha-trypsin inhibitor, from human plasma."

RL J. Biol. Chem. 264:15975-15981(1989).

RN [4]

RP SEQUENCE OF 631-647, AND CROSS-LINKAGE SITE TO BIKUNTIN.

RX MEDLINE=91093267; PubMed=1898736;

RA Enghild J.J., Salvesen G., Hefta S.A., Thøgersen I.B.,

RA Rutherford S., Pizzo S.V.;







SEQUENCE OF 961-975; 992-1000 AND 1033-1050.  
 MEDLINE=90368635; PubMed=2168391;  
 de Jongh K.S., Warner C., Catterall W.A.;  
 "Subunits of purified calcium channels. Alpha 2 and delta are encoded  
 by the same gene.";  
 J. Biol. Chem. 265:14738-14741(1990).  
 CC -!- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN  
 EXCITATION-CONTRACTION COUPLING.  
 CC -!- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:  
 ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS  
 HETERODIMERS THAT ARE DISULFIDE-LINKED.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS: 2 isoforms are produced BY ALTERNATIVE  
 SPLICING.  
 CC -!- TISSUE SPECIFICITY: SKELETAL MUSCLE.  
 CC -!- PFM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM  
 A PRECURSOR FORM.  
 CC -!- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.  
 CC -!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.  
 CC -----  
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 the European Bioinformatics Institute. There are no restrictions on its  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 EMBL; M21948; AAA81562.1; -;  
 DR PIR; S10579; CHRA2.  
 DR InterPro; IPR004010; Cache.  
 DR InterPro; IPR002035; VWF\_A.  
 DR Pfam; PF00092; vwa; 1.  
 DR Pfam; PF02743; Cache; 1.  
 DR SMART; SM00327; WVA; 1.  
 DR PROSITE; PS0234; VWFA; 1.  
 DR Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;  
 KW Calcium channel; Glycoprotein; Phosphorylation; Signal;  
 KW Alternative splicing.  
 FT SIGNAL 1 26  
 FT CHAIN 27 960  
 FT CHAIN 961 1106  
 FT TRANSMEM 448 471  
 FT TRANSMEM 921 945  
 FT TRANSMEM 1082 1101  
 FT DOMAIN 255 432  
 FT CARBOHYD 94 94  
 FT CARBOHYD 138 138  
 FT CARBOHYD 186 186  
 FT CARBOHYD 326 326  
 FT CARBOHYD 350 350  
 FT CARBOHYD 477 477  
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 FT CARBOHYD 678 678  
 FT CARBOHYD 784 784  
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 FT CARBOHYD 891 891  
 FT CARBOHYD 898 898  
 FT CARBOHYD 988 988  
 FT CARBOHYD 1001 1001  
 FT MOD\_RES 503 503  
 FT MOD\_RES 848 848  
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Query Match 96.0%; Score 5224.5; DB 1; Length 1106;  
 Best Local Similarity 94.7%; pred. No. 4.2e-304;  
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 Db 1 MAAGRPLAWTLTQAWLILIGPSSEPPSPSAVTKSWVDKMQEDLVTLAKTASGVNQLV 60

QY 59 DIYEKYQDLYTTEPNNAQOLVEIAARDIEKLLSNRSKALVSLALEAEKQVAAHQWREDA 118  
 Db 61 DIYEKYQDLYTTEPNNAQOLVEIAARDIEKLLSNRSKALVSLALEAEKQVAAHQWREDA 120  
 QY 119 SNEVYVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFNGRQISYQHAHVHPTDIYEGSTI 178  
 Db 121 SNEVYVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFNGRQISYQHAHVHPTDIYEGSTI 180  
 QY 179 VLNELNWTSLADLVFKKREDEPSLLQVFGSATGLARYYPASPDVNSRTNPKIDLYDV 238  
 Db 181 VLNELNWTSLADLVFKKREDEPSLLQVFGSATGLARYYPASPDVNSRTNPKIDLYDV 240  
 QY 239 RRRPWYIQGAASPKDMLILVDVSGVSGSLTLKLRISVSEMLETSLDDDDFVNVASFNSNA 298  
 Db 241 RRRPWYIQGAASPKDMLILVDVSGVSGSLTLKLRISVSEMLETSLDDDDFVNVASFNSNA 300  
 QY 299 QDVSCFQHLVQAVNRNKKVYLKDAVNNTAKGIDYKKGFSAFQELLNNTVNSRANCNKII 358  
 Db 301 QDVSCFQHLVQAVNRNKKVYLKDAVNNTAKGIDYKKGFSAFQELLNNTVNSRANCNKII 360  
 QY 359 MLFTDGGEEAQAEIFNKYNKDKKRVFRFSVGOHNYERGPIONMACENKGYEYEPSIGA 418  
 Db 361 MLFTDGGEEAQAEIFNKYNKDKKRVFRFSVGOHNYERGPIONMACENKGYEYEPSIGA 420  
 QY 419 IRTNQEYLDVLGRPMVLADGAKAQVQWTVNYLDLDELGLVITGLTPVFNITQGFENKTN 478  
 Db 421 IRTNQEYLDVLGRPMVLADGAKAQVQWTVNYLDLDELGLVITGLTPVFNITQGFENKTN 480  
 QY 479 LKNQLILGVMGVDVSLIEDIKRLTPFTLCPNGYFFAIDPNGYVLLHPNLPQK----- 530  
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 QY 531 -----NPKSQBPVTLDFLDAELENDIKVEIRNKMIDGSEKTFRLTVLSQDER 579  
 Db 541 INLRKRPNVQNPQSQBPVTLDFLDAELENDIKVEIRNKMIDGSEKTFRLTVLSQDER 600  
 QY 580 YIDKGNRTYTWTPVNGTDY--SLALVLPYTFYVYKAKLEETITQAKSKGKMKMDSFTLKP 638  
 Db 601 YIDKGNRTYTWTPVNGTDYSSALVLPYTFYVYKAKLEETITQARY-----SETLKP 653  
 QY 639 DNFEEGYTFIADRYCNDLKIISDNTFLLNFNEFIDRTPNPNPCNADLINRVLLDAG 698  
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 QY 699 FTNELVQNYWSKQNIKGVKAREVVTDDGGITRVYKPEAGENWQENPETEDSFYKRSLDN 758  
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 QY 759 DNYVFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVGIKIDVNSWIENFTKTSI 818  
 Db 774 DNYVFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVGIKIDVNSWIENFTKTSI 833  
 QY 819 RDCAGPVCCKRNSDVMDCVILDDGGFLMANHDDYTNOIGRFGEIDPSLMRHLVNLIS 878  
 Db 834 RDCAGPVCCKRNSDVMDCVILDDGGFLMANHDDYTNOIGRFGEIDPSLMRHLVNLIS 893  
 QY 879 VYAFNKSVDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGMWATAAASILQOFLSLT 938  
 Db 894 VYAFNKSVDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGMWATAAASILQOFLSLT 953  
 QY 939 FPRILLEAVEMEDDDFTASLSKQSCITTEQTYFFDNDKSKFSFVLDGCGNCSRIHPGKLMN 998  
 Db 954 FPRILLEAVEMEDDDFTASLSKQSCITTEQTYFFDNDKSKFSFVLDGCGNCSRIHPGKLMN 1013  
 QY 999 TNLIFIMVESKGTCPDTRLLIOAEOITSDGPNPCDMVK 1036  
 Db 1014 TNLIFIMVESKGTCPDTRLLIOAEOITSDGPNPCDMVK 1051  
 RESULT 4  
 YLJ9\_CABEL STANDARD; PRT; 1205 AA.  
 ID YLJ9\_CABEL  
 AC P34372;

DR InterPro: IPR004010; Cache.  
 DR InterPro: IPR002035; VWF\_A.  
 DR Pfam: PF00092; vwa; 1.  
 DR Pfam: PF02743; Cache; 1.  
 DR SMART: SM00327; VWA; 1.  
 DR PROSITE: PS50234; VWFA; 1.  
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;  
 KW Calcium channel; Glycoprotein; Phosphorylation; Signal;  
 FT SIGNAL 1 24  
 FT CHAIN 25 944  
 FT FT  
 FT CHAIN 945 1091  
 FT FT  
 FT TRANSMEM 445 468  
 FT TRANSMEM 906 930  
 FT TRANSMEM 1067 1086  
 FT DOMAIN 252 429  
 FT CARBOHYD 92 92  
 FT CARBOHYD 136 136  
 FT CARBOHYD 184 184  
 FT CARBOHYD 323 323  
 FT CARBOHYD 347 347  
 FT CARBOHYD 474 474  
 FT CARBOHYD 584 584  
 FT CARBOHYD 593 593  
 FT CARBOHYD 663 663  
 FT CARBOHYD 769 769  
 FT CARBOHYD 812 812  
 FT CARBOHYD 876 876  
 FT CARBOHYD 883 883  
 FT CARBOHYD 973 973  
 FT CARBOHYD 986 986  
 FT MOD\_RES 500 500  
 FT MOD\_RES 833 833  
 SQ SEQUENCE 1091 AA; 123822 MW; 7054907D9D343B34 CRC64;

Query Match 96.2%; Score 5234; DB 1; Length 1091;  
 Best Local Similarity 95.7%; Pred. No. 1.1e-304;  
 Matches 992; Conservative 24; Mismatches 19; Indels 2; Gaps 2;

QY 1 MAAGCLLALTTLTQSLIGSPSEPPSPVATIKSWDKMQEDLVITLAKTASGVNQLVDI 60  
 DB 1 MAAGCLLALTTLTQSLIGSPSEPPSPVATIKSWDKMQEDLVITLAKTASGVNQLVDI 60  
 QY 61 YEKYQDLYTEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKYQAAHQRDEFSN 120  
 DB 61 YEKYQDLYTEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKYQAAHQRDEFSN 120  
 QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIYQHAHVHIPTDIYEGSTIVL 180  
 DB 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIYQHAHVHIPTDIYEGSTIVL 180  
 QY 181 NELNWTSAIDLVFKKNEEDPSLLWQVGSATGLARYYPASPPVDNSRTNPKIDLYDVR 240  
 DB 181 NELNWTSAIDLVFKKNEEDPSLLWQVGSATGLARYYPASPPVDNSRTNPKIDLYDVR 240  
 QY 241 RPWYIOGAASPKMLILVDVSGVSGLTLLKLRISVSEMLETISDDDFVNVAFNSNAQD 300  
 DB 240 RPWYIOGAASPKMLILVDVSGVSGLTLLKLRISVSEMLETISDDDFVNVAFNSNAQD 300  
 QY 301 VSCFQHLVQANVRNKKVKDAVNNITAKGTDYKKGFSAFEQLLNVNSRANCKIIML 360  
 DB 300 VSCFQHLVQANVRNKKVKDAVNNITAKGTDYKKGFSAFEQLLNVNSRANCKIIML 360  
 QY 361 FTDCGEERAQEIFNKYKDKKVRFRFSVQCHNVRGPIQWMAKNGYYEIPISGAIR 420  
 DB 360 FTDCGEERAQEIFNKYKDKKVRFRFSVQCHNVRGPIQWMAKNGYYEIPISGAIR 420  
 QY 421 INTQYLDLVGRPMVLADGAKAKQVQNTVYLDALGLGLVITGLPVENITGQFENKTNLK 480  
 DB 420 INTQYLDLVGRPMVLADGAKAKQVQNTVYLDALGLGLVITGLPVENITGQFENKTNLK 480

QY 481 NQLILGVMGVDVSLIEDIKRLTPRTLCPCNGYFAIDPBGVYLLHPNLQPNKPSQBPVTL 540  
 DB 480 NQLILGVMGVDVSLIEDIKRLTPRTLCPCNGYFAIDPBGVYLLHPNLQPNKPSQBPVTL 539  
 QY 541 DFLDAELENDIKVEIRNMKIDGESGEKTFRTLVKSQDERYIDKGNRTYTTWTPVNGTDYS - 599  
 DB 540 DFLDAELENDIKVEIRNMKIDGESGEKTFRTLVKSQDERYIDKGNRTYTTWTPVNGTDYR 599  
 QY 600 LALVLPITYSEYYIKAKLEETITQARSKKGMKQSEYLKPDNFESGYTFIAPRDYCNDLK 659  
 DB 600 LALVLPITYSEYYIKAKLEETITQARSKKGMKQSEYLKPDNFESGYTFIAPRDYCNDLK 659  
 QY 660 ISDNTEFLNFEFIDRKTPNPNPCNADLINRVLLDAGFTNELVONYWSKQNIKGVKA 719  
 DB 660 PSDNTEFLNFEFIDRKTPNPNPCNADLINRVLLDAGFTNELVONYWSKQNIKGVKA 719  
 QY 720 RFVVTGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESC 779  
 DB 720 RFVVTGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESC 779  
 QY 780 IMYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTSIRDPGAGVCDCKRNSDVMDCV 839  
 DB 780 IMYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTSIRDPGAGVCDCKRNSDVMDCV 839  
 QY 840 ILDDGGFLLMANHDDVTNQLGRFFGETDPSLMRHLVNIWYAFNKSYDYOSVCEPGAAPK 899  
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 QY 900 QGAGHSAYVPSVADILQIGWATAAAWSILQOFLLSLTFPRLEAVEDEDDFTASLSK 959  
 DB 900 QGAGHSAYVPSVADILQIGWATAAAWSILQOFLLSLTFPRLEAVEDEDDFTASLSK 959  
 QY 960 QSCITEQTQYFFDNDSEKSGVLDGNCGRIFHGEKLMNTNLFIMVESKGCPCDTRL 1019  
 DB 960 QSCITEQTQYFFDNDSEKSGVLDGNCGRIFHGEKLMNTNLFIMVESKGCPCDTRL 1019  
 QY 1020 IQAEQTSQSDGNPCDMVK 1036  
 DB 1020 MQAEQTSQSDGNPCDMVK 1036  
 RESULT 3  
 C1C2\_RABIT  
 ID C1C2\_RABIT STANDARD; PRT; 1106 AA.  
 AC P13806;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta subunits precursor.  
 GN CACNA2D1 OR CACNL2A OR CCHL2A.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88336904; PubMed=2458626;  
 RA Ellis S.B., Williams M.E., Ways N.R., Brenner R., Sharp A.H., Leung A.T., Campbell K.P., McKenna E., Koch W.J., Hui A., Schwartz A., Harpold M.M.;  
 RA "Sequence and expression of mRNAs encoding the alpha 1 and alpha 2 subunits of a DHP-sensitive calcium channel.";  
 RL Science 241:1661-1664(1988).  
 RN [2]  
 RP SEQUENCE OF 961-973.  
 RX MEDLINE=91131638; PubMed=1847144;  
 RA Jay S.D., Sharp A.H., Kahl S.D., Vedvick T.S., Harpold M.M., Campbell K.P.;  
 RA "Structural characterization of the dihydropyridine-sensitive calcium channel alpha 2-subunit and the associated delta peptides.";  
 RL J. Biol. Chem. 266:3287-3293(1991).  
 RN [3]

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FT CHAIN 945 1091 (BY SIMILARITY).
FT L-TYPE CALCIUM CHANNEL DELTA SUBUNIT (BY
FT SIMILARITY).
FT TRANSMEM 446 469 POTENTIAL.
FT TRANSMEM 906 930 POTENTIAL.
FT TRANSMEM 1067 1086 POTENTIAL.
FT DOMAIN 253 430 VWFA.
FT CARBOHYD 92 92 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 184 184 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 324 324 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 348 348 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 585 585 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 594 594 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 663 663 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 986 986 N-LINKED (GLCNAC. .) (POTENTIAL).
FT MOD_RES 501 501 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
FT MOD_RES 833 833 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
SQ SEQUENCE 1091 AA: 123183 MW: 254E13EE29A47837 CRC64;

Query Match 100.0%; Score 5443; DB 1; Length 1091;
Best Local Similarity 100.0%; Pred. No. 3.7e-317;
Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 YEKQDLYTVEPNAROLVIAARDTEKLSNRKSKALVSLALEAEKVAQAHOHREDFASN 120
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DB 121 EVVYNAKDDLDPKNDSEPGSQRIKPVFIEDANFGQISYQHAHVHPIDYEGSTIVL 180
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QY 241 RPWYIOGAASPDKMLILVDYSGVSGTLTKLIRTSVSEMLETSLDDDFNVNVSFNSNAOD 300
DB 241 RPWYIOGAASPDKMLILVDYSGVSGTLTKLIRTSVSEMLETSLDDDFNVNVSFNSNAOD 300
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DB 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDTYKKGFSAFEQLLNNVNSRANCNKIIML 360
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DB 361 FTDCGERAEQIEFNKDKKVRFRFSVGOHNYERGPQIOWACENKGYIYEIPSGAIR 420
QY 421 INTQEYLDVLRPMVLADGAKAQVQNTNVDLALGLVITGTLPVFNITGQFENKTNLK 480
DB 421 INTQEYLDVLRPMVLADGAKAQVQNTNVDLALGLVITGTLPVFNITGQFENKTNLK 480
QY 481 NQLILGVMGVDVSLIEDIKRTPRTPLCPNGYYPFAIDPNGVYLLHPNLQPNKPSQEPVTL 540
DB 481 NQLILGVMGVDVSLIEDIKRTPRTPLCPNGYYPFAIDPNGVYLLHPNLQPNKPSQEPVTL 540
QY 541 DFLDAELNDIKVEIRNKMIDGESGEKFTFLVKSQDERVIDKGNRTYTWTPNGYDYSL 600
DB 541 DFLDAELNDIKVEIRNKMIDGESGEKFTFLVKSQDERVIDKGNRTYTWTPNGYDYSL 600
QY 601 ALVLPYTSFYIKAKLEETITQARSKKGMKDSITLKPONFEESGYFTFAPRYCNDLKI 660
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QY 721 FVYTOGGITRVYPKRAGENWQENPETYEDSFYKRSLDNDNTVFTAPYFNKSGPGAYESGI 780
DB 721 FVYTOGGITRVYPKRAGENWQENPETYEDSFYKRSLDNDNTVFTAPYFNKSGPGAYESGI 780
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPGAGVPCDKRNSDVMDCVI 840
DB 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPGAGVPCDKRNSDVMDCVI 840
QY 841 LDGCGFLMANHDDYTNOIGRFFGEIDPSLMRHLNINISVYAFNKSYSYQSVCEPGAAPKQ 900
DB 841 LDGCGFLMANHDDYTNOIGRFFGEIDPSLMRHLNINISVYAFNKSYSYQSVCEPGAAPKQ 900
QY 901 GAGHSAYVPSVADILQIGWATAAANSILOQFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960
DB 901 GAGHSAYVPSVADILQIGWATAAANSILOQFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960
QY 961 SCITETQTOYFFONDSEKSFSGVLDGCGNCSRIHFGEKMLNTLIFIMVESKGTCPDTRLLI 1020
DB 961 SCITETQTOYFFONDSEKSFSGVLDGCGNCSRIHFGEKMLNTLIFIMVESKGTCPDTRLLI 1020
QY 1021 QAEQTSDDGPNPCDMVK 1036
DB 1021 QAEQTSDDGPNPCDMVK 1036

RESULT 2
CIC2_RAT
ID CIC2_RAT STANDARD; PRT; 1091 AA.
AC P54290;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta
DE subunits precursor.
OS CACNA2D1 OR CACNL2A OR CCHL2A.
GN Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92228762; PubMed=1314383;
RA Kim H.L., Kim H., Lee P., King R.G., Chin H.;
RT "Rat brain expresses an alternatively spliced form of the
RT dihydropyridine-sensitive L-type calcium channel alpha 2 subunit.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:3251-3255(1992).
CC -!- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN
CC EXCITATION-CONTRACTION COUPLING.
CC -!- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:
CC ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS
CC HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -!- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM
CC A PRECURSOR FORM (BY SIMILARITY).
CC -!- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.
CC -!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DB EMBL; M86621; AAA41088.1; -

```

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2003, 14:13:50 ; Search time 9.50459 Seconds  
(without alignments)  
4520.920 Million cell updates/sec

Title: US-10-090-827-14

Perfect score: 5443

Sequence: 1 MAGCLLALTLFLQSLIG.....RLLIQAEQTSQGNPCDMVK 1036

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5443	100.0	1091	1	CIC2_HUMAN
2	5234	96.2	1091	1	CIC2_RAT
3	5224.5	96.0	1106	1	CIC2_RABIT
4	739.5	13.6	1205	1	YLJ9 CAEEL
5	607	11.2	734	1	UN36 CAEEL
6	194.5	3.6	886	1	ITH3_MOUSE
7	182	3.3	885	1	ITH3_HUMAN
8	180.5	3.3	887	1	ITH3_RAT
9	164.5	3.0	886	1	ITH3_MESAU
10	161	3.0	1829	1	DPOL_THEST
11	159	2.9	1956	1	ATX1_PLAFA
12	157.5	2.9	575	1	YFBK_ECOLI
13	154.5	2.8	946	1	ITH2_HUMAN
14	152	2.8	1290	1	BXC1_CLOBO
15	151.5	2.8	420	1	Y103_SYNY3
16	150.5	2.8	921	1	ITH4_PIG
17	150	2.8	654	1	MCPC_BACSU
18	149	2.7	920	1	ITH4_HUMAN
19	148	2.7	964	1	DPOL_CHEPV
20	144	2.6	1087	1	YXNK_CLOTH
21	143	2.6	946	1	ITH2_MESAU
22	142.5	2.6	382	1	YLJ0_CAEEL
23	142	2.6	1169	1	SMC_METJA
24	141	2.6	1251	1	RB22_PLAVB
25	140.5	2.6	935	1	ITH2_PIG
26	140	2.6	2710	1	TOXA_CLODI
27	140	2.6	3305	1	APLP_WANSE
28	139.5	2.6	764	1	PAG_BACAN
29	139	2.6	1513	1	STUI_YEAST
30	138	2.5	1180	1	C4AA_BACTI
31	137	2.5	984	1	HYSA_STRAG
32	136.5	2.5	3063	1	CAIC_HUMAN
33	135.5	2.5	946	1	ITH2_MOUSE

## RESULT 1

ID	CIC2_HUMAN	STANDARD;	PRT; 1091 AA.
AC	P54289;		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta subunits precursor.		
DE	subunits precursor.		
GN	CACNA2D1 OR CACNA2A OR CCHL2A.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=92110010; PubMed=1309651;		
RA	Williams M.E., Feldman D.H., McCue A.F., Brenner R., Velicelebi G., Ellis S.B., Harpold M.M.;		
RT	Structure and functional expression of alpha 1, alpha 2, and beta subunits of a novel human neuronal calcium channel subtype.;		
RL	Neuron 8:71-84(1992).		
CC	FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN EXCITATION-CONTRACTION COUPLING.		
CC	SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS: ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).		
CC	SUBCELLULAR LOCATION: Integral membrane protein.		
CC	TISSUE SPECIFICITY: CENTRAL NERVOUS SYSTEM, SKELETAL MUSCLE AND AORTA TISSUES.		
CC	PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM A PRECURSOR FORM (BY SIMILARITY).		
CC	SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.		
CC	SIMILARITY: CONTAINS 1 VWFA DOMAIN.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announcement/">http://www.isb-sib.ch/announcement/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).		
CC	EMBL; M76559; AAA51903.1; -		
DR	Genew; HGNC:1399; CACNA2D1.		
DR	MIM; 114204; -		
DR	InterPro; IPR004010; Cache.		
DR	InterPro; IPR002035; VWF_A.		
DR	Pfam; PF00092; vwa; 1.		
DR	Pfam; PF02743; Cache; 1.		
DR	SMART; SM00327; VWA; 1.		
DR	PROSITE; PS50234; VWFA; 1.		
DR	Ionic channel; Transmembrane; Ion transport; Voltage-gated channel; Calcium channel; Glycoprotein; Signal.		
KW	SIGNAL		
FT	CHAIN 1 25 944 L-TYPE CALCIUM CHANNEL ALPHA-2 SUBUNIT		

P52340 human herpe  
O51737 borrelia bu  
P07248 saccharomyc  
P57210 buchera ap  
Q91145 notophthaim  
P40457 saccharomyc  
O13773 schizosacch  
Q58295 methanococc  
O03661 saccharomyc  
Q58789 methanococc  
Q58611 methanococc  
P75342 mycoplasma

## ALIGNMENTS

34 134.5 2.5 2077 1 TEGU\_HSV60  
35 133 2.4 862 1 MUTS\_BORBU  
36 133 2.4 1323 1 ADRI\_YEAST  
37 132.5 2.4 547 1 SYM\_BUCAL  
38 132.5 2.4 929 1 CALC\_NOTVI  
39 132.5 2.4 1679 1 YIO9\_YEAST  
40 132 2.4 697 1 YB9C\_SCHPO  
41 131 2.4 1634 1 DPOL\_METJA  
42 131 2.4 1658 1 YM67\_YEAST  
43 130.5 2.4 987 1 YD94\_METJA  
44 130.5 2.4 1018 1 YC14\_METJA  
45 129 2.4 1244 1 Y307\_MYCPN



QY 780 IMVSKAVEIYIOCKLL-----KPVVVGIKIDVNSWIENFTKTSIRDPCAG 824  
::|| : : |  
Db 563 VVSKKITNFKKDVLFDQYRRYFDENDHFHRAIALTTKMRNEFIK----- 610  
QY 825 PVCDCRNSDV 835  
: | : | :  
Db 611 -IVDARENDL 620

Search completed: February 10, 2003, 14:22:24  
Job time : 25.7185 secs



Db 628 KEYTYNTYCNLDHINDSTCSSYLLNSETKDAYCEYINIDH-----LCD-----INKKND 678  
QY 697 AGFTNELVQVNSKOKNIKGVARFVYTDGITRVYPKEAGENQENPETYEDSFYKRSI 756  
Db 679 INSKNELMGKYSKNELMGKTIKHELM-----GKYSKNEL 712  
QY 757 DNDNYVFTAPYFNKSGPGAYESGIMYSKAVEIYIOGKLLKPAVVG-----IKIDVNSWI 810  
Db 713 -----MGKYSKNELMGKYSKNELMGKYSKNELMGKTIKNOVGVDNIYH 765  
QY 811 ENFTKTSIRD-PCAGPVCDCRNSDWDV-----ILDDGFLLMANHDDYTNOIGRF--- 862  
Db 766 MNCNDNDYDPCD---YNCNNDNTYHRLXYHNINKDNSFNPPKKNKSYNNISHIKI 822  
QY 863 -----FGBIDPSLMHRLVNSIVAF-----NKSYDYO 889  
Db 823 NYPLLFALACHTLSKVNKNKMGVLEILMFNFTNCDMLNNSFIIEKKKNCYSDFQ 882  
QY 890 SVCEPGAAPKOGAGHRSAYVPSVADILQIGWATAAASWILQOFLLSLTPFRLLEAVEME 949  
Db 883 KI---DGDKNIGANDERCHLNN-----NLVSYNLKRF----- 912  
QY 950 DDFTASLSKOSCITEQTYFFNDSDKS 977  
Db 913 --EFQSLQRMSVIVKST-YGNNDNDNN 937  
  
RESULT 14  
D64998  
hypothetical protein b270 - Escherichia coli (strain K-12)  
C:Species: Escherichia coli  
C>Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002  
C:Accession: D64998  
A: Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; C  
A: Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617; PMID:9278503  
A:Accession: D64998  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-575 <BLAT>  
A:Cross-references: GB:AE000317; GB:U00096; NID:gl788605; PIDN:AAC75330.1; PID:gl788606;  
A:Experimental source: strain K-12, substrain MG1655  
  
Query Match 2.9%; Score 157.5; DB 2; Length 575;  
Best Local Similarity 21.6%; Pred. No. 0.1;  
Matches 111; Conservative 93; Mismatches 206; Indels 105; Gaps 25;  
  
QY 71 EPNAROLVEIAARDIEKLLSNRSKALVSLALEBAEKVQAAHQWREDFASNEVYVYNAKDD 130  
Db 22 OPENKESQOQPSPTTEQVLAQAQAIAK---EAEQSA---AKALAAQEQVQYSDKQA 75  
QY 131 LDPEKND-----SEPGSORLKPVFIEDANFGROISYOHAA---VHLPD 172  
Db 76 LQRLQCAPTARAAKAKATHIANPGTARYQQF---DNDVPKVAQNPLATFSLDVTGS 132  
QY 173 YEGSTIVINE-----LNWTSALDEVFKKREDEPSLWQVFGSGATGLARY 218  
Db 133 YANVRRELNQGLLPPPDVAVRVEEVNYPSPDWDI--KDKQSIKASPIPPAMRYELA--- 187  
QY 219 PASPWVNSRTPNKLIDYVRRRPWYIQGAASPKDMLILVDVSGS-VSGTLTKLIRTSVS 277  
Db 188 PA-PW-NEQRTLLKVDILAKDRKSEELPAS-----NLVFLDTSGMSIDRLPLIQSSLK 241  
QY 278 EMLFTSLDDPPVNVASFNSNAQDVSCFQHLVQANVRNKKVYLKAVNNITAKGLTDYKKG 337  
Db 242 LVLRELQDDNIALVYAGSRIA-----LPSTGSGSHKAEINAIASIDDAEGSTNGAGL 296  
QY 338 SFAFEQLNLYNVRANCKIIMLTG-----GEERAQEIFNKYKDKKRVFRFSVQG 391  
Db 297 ELAYQOATK-GFIKGINR-ILLATDGDENVGIDDPKSIEMVKQKQESVGLTSTTCVGN 354

QY 392 HNYERGPQIOWMACENKGYEIPISGAIIRINTQYLDVLRPMVL--AGDKAKQVQ----- 445  
Db 355 SINEAMVRIADVGNVGYIDTLS-----EAKVNLSEMRQMLITVAKDKAQIEFNPA 410  
QY 446 WTNVYLDALGLVLTGTLTPVFNITGQFENKTNLKNQILGVMGVD-VSLEDI---KRLT 501  
Db 411 WYTEY---RQIG-----YE-----KROLRVEHFNNNDYDAGDIGAGKHIT 447  
QY 502 PRFTLCPNGYFAIDPNGYVLLHPNLQPKPKSQE 536  
Db 448 LLFELTLNGQASIDKLRYA--PDNKLAKSKTKKE 480  
  
RESULT 15  
E90542  
lipoprotein [imported] - Mycoplasma pulmonis (strain UAB CTIP)  
C:Species: Mycoplasma pulmonis  
C>Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 03-Aug-2001  
C:Accession: E90542  
R:Chambaud, I.; Hellig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer,  
Nucleic Acids Res. 29, 2145-2153, 2001  
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma p  
A:Reference number: A99512; MUID:21267165; PMID:11353084  
A:Accession: E90542  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-918 <KUR>  
A:Cross-references: GB:AL445566; PID:gl4089658; PIDN:CAC13418.1; GSPDB:GN00153  
A:Experimental source: strain UAB CTIP  
C:Genetics:  
A:Gene: MYPU\_2450  
A:Genetic code: SGC3  
  
Query Match 2.9%; Score 156.5; DB 2; Length 918;  
Best Local Similarity 20.0%; Pred. No. 0.25;  
Matches 122; Conservative 99; Mismatches 229; Indels 161; Gaps 29;  
  
QY 305 OHLVQANVANKV---LKDVANNITAKGIDYKKGFSFAPFOLLNLYNVRANCKIIML 360  
Db 91 KRILPSNVVNNELDFNSLKLITKNTLIGEKIPKNTVAFSIDPN-SVENASADN--- 145  
QY 361 FTDGGEERAQEIFNKYNKDKV---RVPRFSVGOHNERGPIOWMACENKGYEIPISG 417  
Db 146 -TDG-----SMNIIVSLKDGNGVLEKVKFIT-----GLLSELEYIS 181  
QY 418 AIRINTQYLDVLRPMVLGDKAKQVQVNTVYLDALGLVITGLP-----VF 467  
Db 182 DQNLK---VDVPKNENILASSIVEVEQITNE-----KISLSTQCKVPSTFDLTXYDISF 232  
QY 468 NITGQFENKTNLKNQILGVMG-----VDVSLEDIKR--LTPRFTL-CPNGYVYFAIDPN 518  
Db 233 HVLSHDDEKGSILKIRVSLSAKSKTSKDPDYTIEGFKQSFLIEDRISLAKAQGVNKTAD- 291  
QY 519 GYVLLHPNLQPKPKSQEPVTLDFDALENDIKVEIRKNKIDGSGEKFTTLVKSODE 578  
Db 292 ---IISLQLDPSASSED---KLVLSAYDISVPDGLKFNFSVFEAKOGTF----- 338  
QY 579 RYDKGNRTYTPVNGTDYSLALVLPYTFYIYIAKLEETITTOARSKGKMDSETLK- 637  
Db 339 ---DKGVLYFTLQINGTRTRTEEVKLDIQFTNIKKRYLDETILKIDSV--VLKENSNLN 393  
QY 638 ---PDNPEESGYFIAPRDCNDLKISDNTTEFLNFNEF-IDRKTPNPNNSCNADLNRLV 694  
Db 394 SLPSELVENKEI---ENWQNEIELDSSKAKINVKNEFQVSVSTSANPEYN-----L 442  
QY 695 LDAGFTNE-----LVONYWSKQKNIKGVKARF--VYTDGGITRVYP---KEAGENMOE 742  
Db 443 ICGLNVFVRISRDGLIVQVTRLSGLTKLDANLFDVAKANVSNQLPGLNKLAKDTNFRF 502  
QY 743 NPETYE-DSF-----YKRSLDN-----DNYVFTAPY---FNKSGPGAYESG 779  
Db 503 GEKTFSTDSFELKFNKAKENNSILNLYKLSLENVKNLKNFSGOVSDVFKTRKGTCKEN 562

A:Residues: 1-2706 <ROW>  
A:Cross-references: EMBL:Y13402; PIDN:CAA73831.1  
A:Experimental source: strain IT 4/25/5  
C:Genetics:  
A:Introns: 2493/3  
A:Note: R29R+var1

Query Match 3.0%; Score 161; DB 2; Length 2706;

Best Local Similarity 18.2%; Pred. No. 0.74;

Matches 183; Conservative 137; Mismatches 345; Indels 338; Gaps 46;

```
QY 36 WDKMOEDLVLTAKTAGVGNOLVDIYEKYQDLYTVEPNA-----RQL 78
   : : : : : : : : : : : : : : : : : : : : : : : :
Db 308 WEDEAEFCIRKI-----KLENNKKECD-----ENNKYCSGDHCKRYLKDNWIF 358
   : : : : : : : : : : : : : : : : : : : : : : : :
QY 79 VEIARDIEKLSNRSKALVSALAEKQAAHQWRDEFASNEVYVYNAKDDLDPEKNS 138
   : : : : : : : : : : : : : : : : : : : : : : : :
Db 359 IDLNCPRCENACSNYTK-----WIEIQKQFDKQKR--YNEI---KIKTINSNENDK 408
   : : : : : : : : : : : : : : : : : : : : : : : :
QY 139 E-----PGSQRIKPFVIEDANFGRQISYQHAHVHIPTDIYEGSTIVLNELNWSALDE 191
   : : : : : : : : : : : : : : : : : : : : : : : :
Db 409 EYENLKKGGYSTIN-TFELSNHGKQCO-----DN 438
   : : : : : : : : : : : : : : : : : : : : : : : :
QY 192 VFKNREEDPSLLMQVFGSAGLARYYPASP-----WVDNSRTPNKI 233
   : : : : : : : : : : : : : : : : : : : : : : : :
Db 439 IDKKNKTFFKNL-ETGP-----SGYCEADPIYGVKSNCKPTPTENENSNRLPTDT 493
   : : : : : : : : : : : : : : : : : : : : : : : :
QY 234 DLYDVRRPWTYIOGAASPKDMLILVDVSGVSGLTGLKLI RTSVSEMLETLSDDDDFVNVA 293
   : : : : : : : : : : : : : : : : : : : : : : : :
Db 494 STKNLN-----ATNIDMLVNDGIGNAI-----515
   : : : : : : : : : : : : : : : : : : : : : : : :
QY 294 FNSNAODVSCFOHLVQAVNRKK-----VLKDAVNNITAKGITYKGFSEAFQQL 345
   : : : : : : : : : : : : : : : : : : : : : : : :
Db 516 ---DNELEKNCTYGLLGKIKQKQWCOYLANNIDOCKINNMVNSGYFONKATFNVLFORWL 573
   : : : : : : : : : : : : : : : : : : : : : : : :
QY 346 NYNYSRANCKNIIIMFTDGGERAQAEIFKNYKDKKVRVFSVGOHNERGPTQWMAE 405
   : : : : : : : : : : : : : : : : : : : : : : : :
Db 574 RYFVRDHNRLK-----EKIDVCIKKENINENICIRKCTN-----CE 610
   : : : : : : : : : : : : : : : : : : : : : : : :
QY 406 NKGYEYIETPSICAIRI-----NTQBYLDVLRPMVLADKAKQVQWTVNVLDALEGLVIT 461
   : : : : : : : : : : : : : : : : : : : : : : : :
Db 611 CVGWLEKKEAEWDKINOHYNQKNHIMFILPYITWITGYEK-ITFPNDFKALE-----DV 665
   : : : : : : : : : : : : : : : : : : : : : : : :
QY 462 GTLPVFNITGOFENKTLNKLILGVGVDSLEIDKRLTPRTLCPNGYIFALDPNGYV 521
   : : : : : : : : : : : : : : : : : : : : : : : :
Db 666 DTINVLOTLEKQD-THCKIEKIRSI-DVDLKEIISWLNQKIEVCKS---HHDEDKHEYC 721
   : : : : : : : : : : : : : : : : : : : : : : : :
QY 522 LLHPNLPQKPKSQEPVTLDFDLAELENDIKVEIRNKMIDGESKPT-----FRT 571
   : : : : : : : : : : : : : : : : : : : : : : : :
Db 722 C---DILPKSVDDDEDD-EVDDEKEESSQTTKRN--ISQKGTKSASCVKGACAIKVG 775
   : : : : : : : : : : : : : : : : : : : : : : : :
QY 572 LVKSODERYID---KGNRYTW-----TPVNGTD-----YSLALVLPYISF 609
   : : : : : : : : : : : : : : : : : : : : : : : :
Db 776 VLOOKSGSIDNCNAKRNKNWOCNDKNTFVDNEGVCMPPRKKSICIHNLTLLEEQTNNK 835
   : : : : : : : : : : : : : : : : : : : : : : : :
QY 610 Y-----YIKALEET-ITQARSKGKMKDSETLK---PDNFEF-SGYTFIAPRDYC--N 656
   : : : : : : : : : : : : : : : : : : : : : : : :
Db 836 YQLREAFIKCAAKETNLWDKYNDKNEAEELKKGKIPEDFRIMFYTFGDFRDFCLEN 895
   : : : : : : : : : : : : : : : : : : : : : : : :
QY 657 DL-----KISDNTEFLNNEFIDRK-----TPNPNPC--NADLINRVLLDAGFTNEL 703
   : : : : : : : : : : : : : : : : : : : : : : : :
Db 896 DMGRDVKVKKINKVFNNSKRGFKKIDPENWNWNGPOIWMGMLCALIHADTKDSIKN 955
   : : : : : : : : : : : : : : : : : : : : : : : :
QY 704 VQNY-----W-----SKONIKGVKARFVV 723
   : : : : : : : : : : : : : : : : : : : : : : : :
Db 956 KDNTYKEKVTILAKROGSGMWTSEFAKPKFLRWFEVWYDDYCKERQKYLTEVASTCKS 1015
   : : : : : : : : : : : : : : : : : : : : : : : :
QY 724 TDGGITRV-----YPREAGENQENPETEDSFYKRSLDN-----DNVY- 762
   : : : : : : : : : : : : : : : : : : : : : : : :
Db 1016 IDGGLCDRGCKNNKCDYKKYKRRKKKEWNLDQYKQKRENGIDKGPGLIIVKDYVL 1075
   : : : : : : : : : : : : : : : : : : : : : : : :
QY 763 -----FTAPYFNKSPGAYESIMVSKAVEIYIOGKLLKPAVVGKIDVNSWI--810
   : : : : : : : : : : : : : : : : : : : : : : : :
```

```
Db 1076 ANAKEYLKKKFTASCVTSSGKAQNSATEEYKKNIELLSEEQY-----YDADQYCGC 1126
QY 811 -----ENFTKTSIRDPACAGPVCDCR-----RNSDVMDCVIL 841
   : : : : : : : : : : : : : : : : : : : : : : : :
Db 1127 TKFIHDDKYSKISGRSNCCLNSDAKKNKIKWRNSDEKDYAF 1169
   : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 13

A44396

P-type cation translocating ATPase - malaria parasite (Plasmodium falciparum)

C:Species: Plasmodium falciparum

C:Date: 10-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jun-2000

C:Accession: A44396

R.Krishna, S.; Cowan, G.; Meade, J.C.; Wells, R.A.; Stringer, J.R.; Robson, K.J.  
J. Cell Biol. 120, 385-398, 1993

A:Title: A family of cation ATPase-like molecules from Plasmodium falciparum.

A:Reference number: A44396; MUID:93132070; PMID:8421054

A:Accession: A44396

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-1984 <KRI>

A:Note: sequence extracted from NCBI backbone (NCBIP:122678)

Query Match 2.9%; Score 159; DB 2; Length 1984;

Best Local Similarity 17.1%; Pred. No. 0.6;

Matches 179; Conservative 144; Mismatches 359; Indels 366; Gaps 45;

```
QY 58 VDIYEKYQDLYTVEPNAQRLVEIAARDLEKLLSNR-----SKALVSLAEARK 106
   : : : : : : : : : : : : : : : : : : : : : : : :
Db 128 INVY-RYNTSYIIS--ELVPGDIYEIKNNWTPCDTIILSGVSTMSEHMLTGES 180
   : : : : : : : : : : : : : : : : : : : : : : : :
QY 107 VQAAHQWRDEFASNEVYVYNAKDDLDPEKND-----SEPGSQRIKPFVIEDANFGRQTS 160
   : : : : : : : : : : : : : : : : : : : : : : : :
Db 181 V-PIHKERLPFEGNATINKNNKYDSNDEKDYLRIVNNHASINMIKRNHLIETLGKKDR 239
   : : : : : : : : : : : : : : : : : : : : : : : :
QY 161 YQAAVHIPTDIYEGSTIVLNELN--TSALDEVFKNREEDPSLLQWFGSATGLARYYP 219
   : : : : : : : : : : : : : : : : : : : : : : : :
Db 240 EYKSNTH-----DLCSMNKLCTYINNTYDDVHKNNKMD-----272
   : : : : : : : : : : : : : : : : : : : : : : : :
QY 220 ASPVDNSRTPNKRIDLYDVRRPWTYIOGA-ASPKDMLILVDVSGVSGLTGLKLI RTSVSE 278
   : : : : : : : : : : : : : : : : : : : : : : : :
Db 273 ---YNNNNNNKKKKINNLN---FVKGYIYNSNLLY-----303
   : : : : : : : : : : : : : : : : : : : : : : : :
QY 279 MLETSLDDDFVNVASFNSNAQDVSCFOHLVQAVNRNKKVKLDAVNNITAKGITYKKGFS 338
   : : : : : : : : : : : : : : : : : : : : : : : :
Db 304 -----DDKIGVNIPE--DDVNNMKH--KFNQRNINYNKDTNNL-----EYNNKHR 345
   : : : : : : : : : : : : : : : : : : : : : : : :
QY 339 FAFEOQLNYSRANCKIIMLFTDGGERAQAEIFKNYKDKKVRVFSVGOHNERGP 398
   : : : : : : : : : : : : : : : : : : : : : : : :
Db 346 YIYDCLLKKVEAISQNKIY-----SNEDINKY-----374
   : : : : : : : : : : : : : : : : : : : : : : : :
QY 399 IOWMAECENKGYEYIETPSICAIRINTQYLDVLRPMVLAG-----DKAQV 444
   : : : : : : : : : : : : : : : : : : : : : : : :
Db 375 ---MLYGYTVLSLVNINIKYNNKEENRIGL-VIKGTFTTKGKIVNNLIYHKREL 429
   : : : : : : : : : : : : : : : : : : : : : : : :
QY 445 QWTVNVLDALEGLVITGTLPVFNITGQFENKTNLKNOLIG-----V 487
   : : : : : : : : : : : : : : : : : : : : : : : :
Db 430 NINDSYKFLIT-LIYALFSVFILLYITLSNNEYTHIIKCLDIITDIPALPTILT 488
   : : : : : : : : : : : : : : : : : : : : : : : :
QY 488 MGVDVSLIEDIKRLTPRTLCPNGYVFA-----IDPNGYVLLHPNLO-----PKPKSO 535
   : : : : : : : : : : : : : : : : : : : : : : : :
Db 489 VGISIAISRLKKKFSISCLCPHKINIAQINTWVFDKGT-ILTENNLOFIIQITQNNKK 547
   : : : : : : : : : : : : : : : : : : : : : : : :
QY 536 EPTVLDLDAELENDIKVEIRNKMIDSGSEKTFETLVKSDERYIDKGNRTYTPVNG 595
   : : : : : : : : : : : : : : : : : : : : : : : :
Db 548 NMLS-DFIHK-----EMNTESIYHSKDDNMIHNK-----577
   : : : : : : : : : : : : : : : : : : : : : : : :
QY 596 TDYSLALVLPYTFYFYIKAKLEETITQARSKGKMKD-----SETLKPONFESG 645
   : : : : : : : : : : : : : : : : : : : : : : : :
Db 578 -----SIISEYIYKDNMKNLHTSSK-KKSITKERSNLFVQTIKCLLDHYIKKK 627
   : : : : : : : : : : : : : : : : : : : : : : : :
QY 646 YTFIAPRDYCNLKDSDNN-TEFLLN-----FNEF--IDRKTPNPNPCNADLINRVLLD 696
   : : : : : : : : : : : : : : : : : : : : : : : :
```



## RESULT 9

S30350  
inter-alpha-trypsin inhibitor heavy chain 3 precursor - human  
N:Alternate names: HC3; inter-alpha-trypsin inhibitor chain H3; pre-alpha-inhibitor heavy chain H3  
C:Species: Homo sapiens (man)  
C:Date: 03-May-1994 #sequence\_revision 20-Feb-1995 #text\_change 04-Feb-2000  
C:Accession: S30350; S34123; S02141; D34245; A39079; S50133; B53642; A59167  
R:Bourguignon, J.; Diarra-Mehrpour, M.; Thiberville, L.; Bost, F.; Sesbouee, R.; Martin, Eur. J. Biochem. 212, 771-776, 1993  
A:Title: Human pre-alpha-trypsin inhibitor-precursor heavy chain cDNA and deduced amino-acid sequence  
A:Reference number: S30350; MUID:93215656; PMID:7681778  
A:Accession: S30350  
A:Molecule type: mRNA  
A:Residues: 1-885 <BOU1>  
A:Cross-references: EMBL:X67055; NID:g288562  
R:Bourguignon, J.  
submitted to the EMBL Data Library, June 1992  
A:Reference number: S34123  
A:Accession: S34123  
A:Molecule type: mRNA  
A:Residues: 1-310, 'K', 312-343, 'R', 345-885 <BOU2>  
A:Cross-references: EMBL:X67055; NID:g288562; PIDN:CAA47439.1; PID:g288563  
R:Diarra-Mehrpour, M.; Bourguignon, J.; Sesbouee, R.; Mattei, M.G.; Passage, E.; Salier, Eur. J. Biochem. 179, 147-154, 1989  
A:Title: Human plasma inter-alpha-trypsin inhibitor is encoded by four genes on three chromosomes  
A:Reference number: S02141; MUID:89137072; PMID:2465147  
A:Accession: S02141  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 341-356, 'G', 358-845, 'H', 847-885 <DIA1>  
A:Cross-references: EMBL:X14690; NID:g35464; PIDN:CAA32821.1; PID:g35465  
R:Englund, J.J.; Thøgersen, I.B.; Pizzo, S.V.; Salvesen, G. J. Biol. Chem. 264, 15975-15981, 1989  
A:Title: Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-alpha-1-trypsin inhibitor  
A:Reference number: A92736; MUID:89380192; PMID:2476436  
A:Accession: D34245  
A:Molecule type: protein  
A:Residues: 30-49 <ENG1>  
R:Englund, J.J.; Salvesen, G.; Hefta, S.A.; Thøgersen, I.B.; Rutherford, S.; Pizzo, S.V. J. Biol. Chem. 266, 747-751, 1991  
A:Title: Chondroitin 4-sulfate covalently cross-links the chains of the human blood protein alpha-1-trypsin inhibitor  
A:Reference number: A39079; MUID:91093267; PMID:1898736  
A:Accession: A39079  
A:Molecule type: protein  
A:Residues: 631-647 <ENG2>  
R:Diarra-Mehrpour, M.; Bourguignon, J.; Sarafan, N.; Bost, F.; Sesbouee, R.; Muschio-Boncompagni-Ondis, V. Biochim. Biophys. Acta 1219, 551-554, 1994  
A:Title: Tandem orientation of the inter-alpha-trypsin inhibitor heavy chain H1 and H3 genes  
A:Reference number: S50132; MUID:95002176; PMID:7522574  
A:Accession: S50133  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-27 <DIA2>  
A:Cross-references: EMBL:X75318  
R:Wisniewski, H.G.; Burgess, W.H.; Oppenheim, J.D.; Vilcek, J. Biochemistry 33, 7423-7429, 1994  
A:Title: TSG-6, an arthritis-associated hyaluronan binding protein, forms a stable complex with inter-alpha-trypsin inhibitor  
A:Reference number: A53642; MUID:94271799; PMID:7516184  
A:Accession: B53642  
A:Molecule type: protein  
A:Residues: 30-34, 'X' <WIS>  
R:Jessen, T.E.; Faarvang, K.L.; Ploug, M. FEBS Lett. 230, 195-200, 1988  
A:Title: Carbohydrate as covalent crosslink in human inter-alpha-trypsin inhibitor: a novel crosslink  
A:Reference number: S02431; MUID:88167187; PMID:2450785  
A:Accession: A59167  
A:Molecule type: protein  
A:Residues: 30-32, GEKEQAVDT' <JES>  
C:Comment: As pre-alpha-inhibitor, this protein is covalently cross-linked by chondroitin-6-sulfate  
C:Genetics:  
A:Gene: GDB:ITIH3  
A:Cross-references: GDB:120109; OMIM:146650

## A:Map position: 3p13-3p12

C:Superfamily: inter-alpha-trypsin inhibitor complex component II  
C:Keywords: chondroitin sulfate proteoglycan; glycoprotein; heterodimer; proteinase I  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-29/Domain: propeptide #status predicted <PRO>  
F:30-647/Product: inter-alpha-trypsin inhibitor heavy chain 3 #status experimental <M>  
F:648-885/Domain: carboxyl-terminal propeptide #status predicted <CTP>  
F:87,576/Binding site: carbonyl site: carbonyl (Asn) (covalent) #status predicted  
F:647/Modified site: chondroitin sulfate ester carboxyl end (Asp) (in mature form) #s

Query Match 3.4%; Score 185; DB 2; Length 885;

Best Local Similarity 20.4%; Pred No. 0.0045;

Matches 133; Conservative 106; Mismatches 243; Indels 170; Gaps 33;

QY 27 FPSAVTIKSWDKMQEDLVTLAKTAGSVNQLVDIYEKYQDLYTFEPNNAQLVEIAARDI 86  
Db 97 YPGNVKEVAKQYKAVSQGKTAG-----LVKASGRKL 131  
QY 87 EKLLSNRSKAL---VSLALEAEKQVAAHQWRDFASNEVVYNAKDDLDPEKNDSEPGSQ 143  
Db 132 EKPTVSVNVAAGSKVTFELTYELLKRHKG-----YEMLYKVQPK-----Q 173  
QY 144 RIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVLNLNWTSDALDEVKKKNEEDPSL 203  
Db 174 LVKHFELE-----VDIFEQGISMLDAEASFINDLL-----GSA 208  
QY 204 LMQVFGSATGLARYPASPWVDNSRT-PNKID-----LYDVRRRP-----WY 244  
Db 209 LTKSFGKKGHVSKFPS---LQQRSCPTCTDLSLLNGDFTITYDVNRSPGNVQIVNGYF 265  
QY 245 I-----QG-AASPDKMLILVDVSGSVSGTLKLRITVSEMLETSSDDFVNVASFNSA 298  
Db 266 VHFAPQGLPVVPKNVAFVIDISGSMAGRKLEQTKKALLRILEDQDEEDYLLFILFSG-- 323  
QY 299 QDVSCF-OHLVQANVKNKVLKADVNNTAKITDYTKGFSFAPQLLNYSR----- 351  
Db 324 -DVSTWKEHLVQATPENLOEATFKVSMEDKGMTINDGLLGISML---NKAREHRIP 379  
QY 352 ANCNKIIMLFTDG----GEERAQEIFNKYNK--DKKRVRFVSQVGHNYERGPIDQWACE 405  
Db 380 ERSTSVIMITDGDANVGSRPEKIQENRNAIGGKFPYLNLFQF--NLLNYNFLENMALE 438  
QY 406 NKGYEIEFSIGAIRINTQYLDVLRPMVLADGKAKQVQWNTNYLDAL-----L 456  
Db 439 NHGFARIIYEDSDADLQLOGFYEEVANPL-LTCVEMEXPE--NAILDLTQNTYQHFYDGS 495  
QY 457 GLVITITLVPFNITGQFNKTNLK-----NQLILGVMGVDVSLDITKRLTPRTLCPNGY 511  
Db 496 EIVVAGRL-VDEDMNSF--KADVKGHGATNDL---TTFEEVDMKEMEK-----ALQERYD 544  
QY 512 YFAIDPN-----GYVLLHPNLOPK---NPKSQEPVTLDFDLDAELENDIKVEIRKMKIDG 562  
Db 545 IFG---NYIERLWAYLTIEQLLEKRNKNAHEKENLTARALDLSLKYHFTVPLTSMVVK 601  
QY 563 ESSEKTFRLVKSQDERYI-DKGNRTYTPVN-GTDYSIALVLPTYSFYI 612  
Db 602 PE-----DNEDERADAPGEDAEATVPSPAMSYLTSYQPPONPYIV 644

## RESULT 10

D97033  
uncharacterized protein, probably surface-located [imported] - Clostridium acetobutyli  
C:Species: Clostridium acetobutylicum  
C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001  
C:Accession: D97033  
R:Nolling, J.; Breton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L  
J. Bacteriol. 183, 4823-4838, 2001  
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium  
A:Reference number: A96900; MUID:21359325; PMID:21359325  
A:Accession: D97033  
A:Status: preliminary  
A:Molecule type: DNA

QY 271 LRTSVSEMLETSLDD---DFVNV---ASFNSNAODVSCFQHLVQANVRNKKVLKD---A 321  
Db 345 AVRGVSDFLSTQNTAVADYVNVGLVGYSSPCNTVTOGASGITVPI---DKVSSSHVKS 402  
QY 322 VNNITA---KGIDYKKGFSFAFEQLLNVNVRANKIIMLFTDGGPERAQEIPFNKYNK 378  
Db 403 INQALAPQSGGFTQLGLRKGTEML---EQDSSDNOKMMILMTDG---VPTFSYKVN 455  
QY 379 DKVR---VPRFVGQUNYERG---PIQ---WMACENKGYEYEL---PSGAIINTOE 425  
Db 456 ASKVDNVIYQSGFAESRDEPGNTSKIQSPYVYKINGGNSIEIRDTWAATLGEAEISKOE 515  
QY 426 YLDVLRPMVLGD-----KAKOVOMTNYVLDALGLVITGTLPVFNITGOFE 474  
Db 516 ISIHTLGLQNGDGYLSQEEVKSRTSLIATGLYQDANSAN-----DITDYLK 565  
QY 475 NKTN-----LKNOLILGVGVDSLEDIKRLTPRFTLPCNGYVFAIDPNGYVLLHPN 526  
Db 566 NOANVLSRFNTITGLILDPLGAQPEYKDTK-----FEITSVG----- 604  
QY 527 LQPNKPSQEPVTLDFDAELENDIKVEIRNKMIDGSEKTFRTLKVSQDERYIDKGNR 586  
Db 605 -----EDSIDNLTGKINEKLEISNLNI---GKNOEVOIHQVRLNTTDDFKNY 653  
QY 587 TY-----TWTPVNGT---DYSIALVPLTYSFYIKAKLE-----ETIQARSK 627  
Db 654 WYOMNGETTLTP---NGSPDNKNVFGVPSAKSSGINLTLEKQWLANSENIPENVELLIGRR 712  
QY 628 GKMKDSE---TLKPDNFEESGYTPIAPRDYCNLDUKISDNTEFLLNNEFIDRKTNN 682  
Db 713 SAQISSDWTVTVLKEDDEWRSQLENLPKYSILGEEFYIEIKDEIVLN---SEIYDWTIGE 771  
QY 683 PSNADLINRVLDD---AGFTNELVONYWSKOKNKGKARFVVDGGITRVYKPEAGE 738  
Db 772 DKTIANIEKRLQIKTSNHDNEPISEVEFVLKNSQGEIDKAVIN-----EKGE 822  
QY 739 -NQENPETEYDFYKRLSDNDNYVTAPYFNKSGPGAYESGIMWSK-----AVEIYIQ 791  
Db 823 ILFDKTRLYGEEYQLHEIKSPGSLGEPWKIKT---EPENGPIIKVDGEQIALDEHYN 879  
QY 792 GKLLKPAVGIKIDVNSWIENFTKTSIRDPKAGVCDCKRNSDVMDCVILD-----DG-- 844  
Db 880 KFMIS---LNTINDIN---VEEF-----RNSVTIDKRAVDSEKLDGAV 917  
QY 845 -GFLLMANHDYTNQIRGFEIDPISLMRHLVNIISVYAFNKSQDYQVCEPAGAPKQAG 903  
Db 918 FNLQIESVDDELTLQKPL---EITNLLPGL-----YALQESVSPNGYVRDDEV 964  
QY 904 H--RSAYVPSVADILQIGWATAAANSILOOFL-----LSLTF- 939  
Db 965 HFRVFKNGSIVATGSEB-----IDIPFLDENESGKNGILVNLBEENGDIJHLTIFY 1015  
QY 940 ---PRLEAVEMDDDDFTASLQSCQ---ITEQYQFPDNDQ---KSFSGVLDCGNCRI 990  
Db 1016 NOAVPPLQLEVDKIDDDFTSLAGVSEFELTRGKSTDSVVRINSFDRILKTFN---NE 1073  
QY 991 FHGEKL-MNTNL 1001  
Db 1074 FTGETIALKSNL 1085

RESULT 8  
S54355  
inter-alpha-trypsin inhibitor heavy chain 3 precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 04-Feb-2000  
C:Accession: S54355  
R:Chan, P.; Risler, J.L.; Raguenez, G.; Salier, J.P.  
Biochem. J. 306, 505-512, 1995  
A:Title: The three heavy-chain precursors for the inter-alpha-inhibitor family in mouse  
A:Reference number: S54353; MUID:95194326; PMID:7534067  
•A:Accession: S54355  
A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA  
A:Residues: 1-886 <CHA>  
A:Cross-references: EMBL:X70393; NID:g695635; PIDN:CAA49843.1; PID:g695636  
C:Superfamily: inter-alpha-trypsin inhibitor complex component II

Query Match 3.6%; Score 194.5; DB 2; Length 886;  
Best Local Similarity 19.9%; Pred. No. 0.0012;  
Matches 185; Conservative 138; Mismatches 347; Indels 261; Gaps 44;

QY 27 FPSAVTIKSWVDKMQEDLVTLAKTASGVNOLVDIYEKYQDLYTVEPNNAQLVEIAARDI 86  
Db 98 YPGNVKKEVAQKQYKAVSQGKTAG---LVKASGRKLEKFTVSVNVAAGSKVTFFELTY 153  
QY 87 EKLISNRSKALVSLALEAEKQAAHOMREDPASNEVYVYNAKDDLDPKNDSEPGSORIK 146  
Db 154 EELL-KRNKGYEMLVKQPKQLVRHFEID-----AHIFED-----Q 189  
QY 147 PVFTEDANFGRIQISYQHAANVHIPTDIYEGSTIVLNELNWTLSALDEVFKKNEEDPSLLWQ 206  
Db 190 GISMLDAE-----ASFITNDL-LGSALTAKSF----- 214  
QY 207 VFGSATGLARYYPASPVVDNSRT-PNKID-----LYDVRRRP-----WYI-- 245  
Db 215 -----SGKKGHVSTKPSLDQORSCPTCTDLSLLNGDFTIYDVNRESQNVQIVNGYFVHF 269  
QY 246 ---QG-AASPKDMLILVDVSGSVSGLTLKLI RTSVSEMLETSLDDDFVNVASFNSNAQDV 301  
Db 270 FAPQGLPVVVKNIYFVIDVSGSMGRKIQQTRALLKILDDVKEDDYLNFLTST---DV 326  
QY 302 SCFQ-HLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFEQLLNVNVRAN-----C 354  
Db 327 TTWKDLHVOATPANLKEAKTFVKNIHQDSMTNINDLGLKGIEML---NKASEDHTVPEPS 383  
QY 355 NKIIMLETDG---GEERAQEIFNKYNK---DKKVRVFRFSVQGHNYERGPQIWMACENKG 408  
Db 384 TSIILMLDGDANTGESREPKIQENVRNAIGKPLYNLFGF-NLNLNFTLETALENHG 442  
QY 409 YVEYTPSGAIRINTQEVLDVLRPMVLGAKQVQNTVYLDALGLL---VTGTLPV 466  
Db 443 LARRIYEDSDANLQGFVEEVANPLL-----TNVEVEYPENAILDLTRNSYPH 491  
QY 467 FNIQGFENKTNLKNQILGVGVDSLEDIKRLTPRFTLPCNGYVFAIDPNGYVLLHPN 526  
Db 492 F-----YD-----SEIVVAGRLVDRNDN-----FKADYKGHGALN-- 523  
QY 527 LQPNKPSQEPVTLDFDAELENDIKVEIRNKMIDGSEK---TPRTLKVSQDERYIDK 584  
Db 524 ---DLTFTTEVDMEEMDAALK-----EQGYIFGDVIERLWAYLTIEQLLEKKNAG 572  
QY 585 NRTYTWTPVNGTDYSLA-LVLPYTSFYIKAKLESETITQARSKKMKDSET-----LK 637  
Db 573 DEKENIT-AEALDLSLKYHFVTPLTSMVVTKPEDNEDQTSIADNAGEAPAFETTTMSFLT 631  
QY 638 PDNFEESGYTPIAPRDYCNLDKISDNTEFLLNNEFIDRKTNNPNSNADLINRVLDA 697  
Db 632 TQSSGSPYIV-----DGDPHFIQI-----PGKNSICFNIDEKP 668  
QY 698 GFTNELVONYWSKQKNIKGVKARFVVDGGITRVYKPEAGENWQENPETEYDFYKRLSD 757  
Db 669 GTVRLRIQD-----PVT--GIT-VTGQIIIGD-----KRS-- 694  
QY 758 NDNYVFTAPYFNKSGPGAYESGIMVSKAVEIYIQGLKLPVAVGIKIDVNSWIENFTKTS 817  
Db 695 NASSRTGKTYFGKLGITNAWMDFRVEVTEKIIIG-----TGAEISTFSLDVTVTQ 747  
QY 818 IRDPCAGVCDCKRNSDVMDCVILDG-GFLLMAN-----HDDYTNQIRGFEIDP 868  
Db 748 -----TGLSVTINRKNMV--VSFGDGISFVILLHQVKKHVPHQDFLG-----FVWDS 795  
QY 869 SLMRHLVNIISVYAFNKSQDYQVYQSV-CEPAGAP 898  
Db 796 HRMSAQTHGLLGQFQFPDFKVFGRPGSDP 826

submitted to the EMBL Data Library, June 1995

A:Reference number: Z19019

A:Accession: T18770

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1148 <WIL>

A:Cross-references: EMBL:Z49007; PIDN:CAA90091.1; GSPDB:GN00020; CESP:T24F1.6

A:Experimental source: clone B0491

R:Chui, C.

submitted to the EMBL Data Library, June 1995

A:Reference number: Z20004

A:Accession: T25249

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1148 <WIL>

A:Cross-references: EMBL:Z49912; PIDN:CAA90141.1; GSPDB:GN00020; CESP:T24F1.6

A:Experimental source: clone T24F1

C:Genetics:

A:Gene: CESP:T24F1.6

A:Map position: 2

A:Introns: 91/2; 131/3; 170/3; 283/1; 322/2; 410/3; 487/1; 563/1; 602/3; 654/3; 683/3; 7

Query Match 10.5%; Score 572; DB 2; Length 1148;

Best Local Similarity 21.2%; Pred. No. 3.2e-26;

Matches 238; Conservative 213; Mismatches 424; Indels 248; Gaps 41;

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QY 37 VDKMOEDLVTLA-----KTASGVNQLVDIYKQDYVPEPNARQLVEIAARDI 86
Db 99 VDTTEAPASIAQSANILDFQTSFSLVQEEFKLPDIKSKKEDAAEKLRAVEHL 158
QY 87 EKLNSRKSALVSLAEAKVQAARQWRDFASNEVVYNAKDOLDPEKNDSEPGSOR-- 144
Db 159 DRLVTRVDAKKLASSAEASNAVF-----DEYDDOAYAVPQADKRCE 201
QY 145 --IKPVIEDANFRQISYQH--AAVHIPTDIYEGSTIVLNELNWTSA--LDEVEFKNR 197
Db 202 AYMKKNESDMHFYSNM--VEHNSKSGIHITVESYQCDPRVMRDFDWTGTHLEKTSNDK 260
QY 198 EEDPSLWQVFGSATGLARYPPASPDVNSRTNPKLDLYVRRPWPYIOGAASPKMLIL 257
Db 261 EKAPEMGHQIYGYSGLTRAPRHH--KVEPTPIIDLPFRFPWPFVNAESVPKDIVFL 319
QY 258 VDVSGSVSGUTLKLIFTSVSEMLTSDDDFVNVAFSNSNAOD--VSCFOH--LVOANVRNK 315
Db 320 LDYSGSVGKPTMLIKITMYLSTLSPNDYFVGYNFNNHFNPIISCANFTMPATTSNK 379
QY 316 KVLKDAVNNTAKGITDYKKGFSAPEQL---LNYNVS-----RANCNKIIMLFTDGEE 367
Db 380 KVFEEGLMLEEKQAHFATPLKFSLDVLKGNLDSNOSLFADYRSGHKLIIIFTDGVDE 439
QY 368 RAQEIFN---KYNKDKKRVRFRESVSGHNYVERGPIQWACENKGYIYIIPSGAIRINTQ 424
Db 440 WPHQILDEEFOTRNSSELIRIFGSMGYGTSLLPLQOYMACKSHGGYSEIDSMVVKPQR 499
QY 425 EYLDVLGRPMVLADKAK-----QVQWTVNYLDALEGLVITGLPVPFNITGOFENKT 477
Db 500 TIQNVLSQ---VRGDELKGTNAEKREPSWTQLYMETQGTGPIVTLSPILT-----SEQR 551
QY 478 NLKNQILTVGMGVDSLEIDIKRTPRLTFCPCNGYFAIDPNGVYLLHPNLO--PKNPK--- 533
Db 552 IWRDQKLAGVADISIKETKHP--TSSEQMYGIYVDNNGMLYHPQLIPKTEVHCV 609
QY 534 -----SQEPV-----TILDFDALELENDIKVEIRN 557
Db 610 RRSACYDAQOVKOKAGSLRVHVGFSDEVRYRLVGLDISIPTLDMDYLDGSDTAIDLRR 669
QY 558 KMIDGESGKTFPTLVKSQDERYIDKGNRTYTWTPVNGYDYSIALV--LPTYSFYIKAK 615
Db 670 -----RITTKTCYEAIKDINSKEYCHSHIKDSPFTLVIVNNIQLKTVTYDDSV 717
QY 616 LEETITQ-----ARSKKGKMKDSETLKPDNFEESGYTFETAPRDYC--NDLKISDNT 665
Db 718 QELGLDNLKLVTFYPRRDVCQWKLDEYAAHDFRV--WSDISEKEICAQDDMDRLPRAFT 775
```

```
QY 666 EFLINFEFIDRKTNNPNSCNADLINRVLLDAGETNELVQYWSKQKNIKGVKAREVVD 725
Db 776 KGLGSWTQSWPKSDIEHTC-----LLAQYEPNASTPHYVNS-----FVHTR 817
QY 726 GGTRVYPRKAGNMGQNPETYEDSYKRSLDNDNTVFTAPFNKSGPGAYESGIMVSKA 785
Db 818 SKLTAFYPTCSSHDMKAVNKKFDEET--KLTDDNDEV---QFSMR-----SESLIYRT 866
QY 786 VEYIOGKLLKPAVGVKIDVN---SWIENFYKTSRDCPCAGVCDCKRNSD-----VMD 837
Db 867 IADYDNNRL---AVGTQWKENFFDQYDFNFT-----RQNPWKICKRQOE 908
QY 838 CVILDDGGFLMANHDDYTNQIRFFGEIDPSLMRHLVNISVYAFNKSVDYQSVCRPGAA 897
Db 909 CSIITRNHGVIIASSAHRAHAKLF---DPQLFESLVKVLNLSVNSWTEVSECK---- 960
QY 898 PKOGACHRSAYVPSVADIIQIGWNATAA--AWSIIQQFLLSLTFFRLLEBAVEMDDDTFA 955
Db 961 -----AKRVAPWSSAAPGSSSILRYFVTSI-----FKLAKTSEWR 995
QY 956 SLKSQSCITEQTQYFFDNDKSKFSGLDCGNC--SRIFHGEKLMNTNLIPIWVESKGTG--- 1012
Db 996 NLLESALTIVDAQPSMTGNTCTFQKIKPPERCFMKFFHYRMTLNTTK--OLQLTGMSTCSR 1054
QY 1013 -----PCDTRLIIQAEQTSQGNP-----CDMV 1035
Db 1055 YAKLYVPVHTTLLIADACRACQYRKRFESEPRKLEKCDVV 1097
```

RESULT 7  
C6880  
hypothetical protein yvcc [imported] - Lactococcus lactis subsp. lactis (strain IL140  
C:Species: Lactococcus lactis subsp. lactis  
C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001  
C:Accession: C96880  
R:Boletini, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Eh  
Genome Res. 11, 731-753, 2001  
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis  
A:Reference number: A86625; MUID:21235186; PMID:11337471  
A:Accession: C96880  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1450 <STO>  
A:Cross-references: GB:A8005176; PID:g12725093; PIDN:AAK06141.1; GSPDB:GN00146  
A:Experimental source: strain IL1403  
C:Genetics:  
A:Gene: yvcc

Query Match 3.6%; Score 198; DB 2; Length 1450;  
Best Local Similarity 21.0%; Pred. No. 0.0016;  
Matches 242; Conservative 149; Mismatches 439; Indels 322; Gaps 56;

```
QY 37 VDKMOEDLVTLAKVAGVNLVDIYKQDYVPEPNARQLVEIAARDIEK-----L 89
Db 69 INKTENDELKLFSEFCNQPIETEE--NESWTLKEKNT-----IISDFEKEGKIVL 120
QY 90 LSNRSKALVSLAEAKVQAARQWR---EDFA-----SNEWVYNA 127
Db 121 RANNSISLLNLEIQADAKLIENDQEVISEDILAKKSTIFSLYIPENKADSKEDKNKT 180
QY 128 KDDLDPEKNDSEPGSORIKP---VFIEDANFGROISVQHAHV----- 167
Db 181 BEVLNNESSQETVSQKKOSQLAFSPNSFGIKASPNDLAQNENISPEYRODETGISP 240
QY 168 ----IPTDIYEGSTIVLNELNWTSALEDPFKKNEEDPSLLWQVFGSATGLARYPPASPW 223
Db 241 NHSWIPT---GNTVVNHCQWNSF-----SSQWGVNSWN--GEATNLNLSYIYAG 287
QY 224 VDN-----SRTPNKIDLY--DVRRPWTYIOGAASPKMLILVDYSGVSGITLK 270
Db 288 VNPVDFALRYAKETETPGLYDYLNVGRN---VQNPVKPVDIVLVIDMSGSGQAKET 344
```

Db 72 EYKDAIEIDGLQVKKLAKIMEEFHKKSEAVRRLVEAAEEAHLKHEFDADL--QY 128  
QY 123 VYINAK--DDLDPKNDSPGSGRIKVFIEDANFGR-QISYQHAHVHPTDIYEGSTIV 179  
Db 129 EYFNAVILNERDKGNFLGKEFI--LAPNDHFNNLPVNLSDVQVPTWYKNDPAI 185  
QY 180 LNELNWTLSALDEVFKKRRDEDSLLWQVCGSATGLARYYPASPWVDNSTRPKIDLYVR 239  
Db 186 VNGVYSESLNKVYDFNDFORSLIMIQYFSGAKFFRQYPGIKWEPDE---NGVIAFDCR 242  
QY 240 RRPWYIQAASPKDMLILVDVSGVSLTKLIRTSVSMLETLSDDDFVNVSNSNAQ 299  
Db 243 NRKWIQAATSPKDVVILVDVSGSKGLRLTAKQTVSSILDTLGGDDFFNIITNEELH 302  
QY 300 DVS-CFQ-HLVQANVKNKVLDAVNNITAKGIDYKKGFSFAFQLLNNVSRAN--CN 355  
Db 303 YVBPCLNGTLVQADRTNKEHREHLDKLPKAGIGMLDIALNEAPNLSDFNHTGSGICS 362  
QY 356 KIIMLPDTCGGEERAQIFNKYN-KDKKRVFRFVSGQHNRYERGPIOWMACENKGYIYEP 414  
Db 363 QAIMLTIDGAVTDYTFIFAKYNWPKRKRIFTYILIGREAAFAADNLKMACANKGFEFTQIS 422  
QY 415 SIGAIRINTQEYLDVLGRPMVLGAKAKOVQWNTVYLD-----ALEGLVI--TCT 463  
Db 423 TLADQENWYELHVLSPKVI--DOEHVWVTEAYIDSTLPQAOGLADQGLVMTTVA 480  
QY 464 LPVFNITGOFENKTNLKNOLILGVMDVSDLEDIKRLTPRETLCNPGYFYFAIDPNGVLL 523  
Db 481 MPVFS---KONETRSG-ILLGVVGTDPVKELKLTTPKYKLGIGHYAFATINNGYILT 535  
QY 524 HNLQOP--KNPKSQEP--VTLDLDAELENDIKVEIENKMDIGSGSKTFTLVKSODE 578  
Db 536 HPELRPLYEEGKRRKPNYSVDLSEVEDREDDDY-LRNAMVNRKTGK--FSMEYK---- 588  
QY 579 RYIDKGNRT-----YTWPVNGTDSLALVLT--YSFYIKAKLEETITQARSKKGMK 631  
Db 589 KTVDKGRVLTWNTDYIIDTNGTFFSLGVALSRCHGYFF-----RGNTV 634  
QY 632 DSETLKPDNFESGVTFIAPRDYCN-DLKISDNNTFEFLNFEIDRTKTPNPNCSNADLI 690  
Db 635 IEEGL--HOLEHPDVSLADEWSYCNLTLPEHRLHSQLEAIKLYLKKEP-LLOCDKELI 691  
QY 691 NRVLIDAGFTNELVQNYWS-----KKNKIKVKARFVVTGGITRVYP----- 733  
Db 692 QEVLFDA-VSAPIEAYTSLANKSENKSDKGVEAFGLTGLSRINLIFYGAELTNQD 750  
QY 734 -KEAGENMQENPTYEDGFYKRSLDN--DNYVFTAPY----FNKSGPGAYESGIMVSKAV 786  
Db 751 FLKAGDKENIFNADHFWLWYRAAQAQIAGSFYISIPFSTGTVNS-----NVVTASTSI 804  
QY 787 EYIYOGKLLKPAVGIIKIDVNSWIENFTKTSIRDPGAGVCDCKRNSDVMDCVILDGGF 846  
Db 805 QLLDERKSPVVAAGVIGOMKLEFFORKEFTWASRQCASLDGKCSISODDVTVCYLIDNNGF 864  
QY 847 LLMAHNDYTNIGIRGFEIDPSLMRLHVLNLSVYAFNKSIDYQSVCEPCAAPKOGAHR 906  
Db 865 ILVS--EDIT-OTGDFEGEVAGVANKLITMGSEKRTILYDQAMCR---ANKESDSAH 918  
QY 907 AYVPSVADILQIGWATAAASLIQOFLLSLTFPRLLFAVEMEDDDFTASLSK-----OS 961  
Db 919 GLLDYKAPL-----SAAKWIMTELVLFLVEF-----NLCSWHSDMTAKAKLQTLLEP 968  
QY 962 CITEQTQTFDNDKSFSGVLDGCGNSRIFHGEKLMNTNLIIFIMVSKGTGCPDPT 1016  
Db 969 CDTEYPAFVSERTIKETTGNIACEDCKSFVIQIIPSSNLPWVVDV--SCLCES 1021

## RESULT 5

S44617

C50C3.11 protein - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 30-Jun-2001

C:Accession: S44617

R:Favvello, A.D.

submitted to the EMBL Data Library, May 1993

A:Description: Sequence of the C. elegans cosmid C50C3.

A:Reference number: S44627

A:Accession: S44617

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-734 &lt;FAV&gt;

A:Cross-references: EMBL:L14433; NID:g289649; PID:g289650

C:Genetics:

A:Introns: 24/2; 87/3; 175/1; 259/1; 290/3; 346/3; 460/3; 538/3

Query Match 11.2%; Score 607; DB 2; Length 734;

Best Local Similarity 26.6%; Pred. No. 1.2e-28;

Matches 180; Conservative 127; Mismatches 258; Indels 112; Gaps 20;

QY 47 LAKTAGVQNLVDIYKQDYVTEPNARQLVETPAIAARDIEKLSNRS----KALVSLAL 102

Db 36 MKETFSKISHETILKQYKLVBEQEPRAELKKSHRIEDYLKRSQFAYKAKIS--L 93

QY 103 EAEKVOAAHQWREDFASNEVYVYNAKDDLPEK--NDSEPGSQRIKP-----VFIEDANF 155

Db 94 EARSVRNDSTVNDPQSKSFIRMSAKOGNDGTTIYESNHLGKRLKVNNETKSNFLTQANF 153

QY 156 -GROISYQHAHVHPTDIYEGSTIVLNLNWTLSALDVEFKKKNREDPSSLWQVFGSATGL 214

Db 154 YTLPTSSVSSAVHPTPLYDRNEDLLPKIDW--SDIDAVYTRNEETKDLAFQFCSEAGY 212

QY 215 ARYPASPFW--DNRSTPNKIDLYDVRRPWYIOGAAPKMDLILVDVSGVSGITLKLIR 273

Db 213 MRYYPAAAFWEDNQ--DEHLDLDFCRNTEWYINSATSKNVLIMLDMSGSMLQRYEVAK 270

QY 274 TSVSEMLETISDDDFVNVAFSNSNA---QDVSCFQHLVQAVNRKKNKVLKDAVNNTAKGI 330

Db 271 OTTEAILLETSHNDYFNIMTFPSKNTFLLLDGCNGTNGLLQATMRNKKALRRKMDTYQSEG 330

QY 331 TDYKKGFSFAFQOLLNYN-----VSRANCNKIIMLFTDGGEEAQAETFNKYNKDKKVRVF 385

Db 331 AEYEKALPLAFSLVDLDINNGGDNNGACENVIMLTDGAPNAYKKIFDMYNADKKVRVF 390

QY 386 RFSVGQNYERGPLOWMACENKGYIYEPISGAIRINTQEYL----DVLGRPMVLGADKA 441

Db 391 TELVGEAIDFNEVREMACNNRGYVHVANNADVDEKIHYYIRMSRVVGRHYKESGQLS 450

QY 442 KQVQWTVNYLDALDELGL--VITGLPVFNITGQFENKTN----- 478

Db 451 ---WWTGVYERLYLPRPEFAPVPVITNOSFVAMNKMASRRKIRLOKSEARSMEFVTIV 507

QY 479 ---LKNQLILGVMDVSDLEDIKRLTPRETLCNPGYFYFAIDPNGVYLLHPNLPQKNP-- 532

Db 508 SYPVIVNETPMGVAANVPLTEVAQKSHPANIGSKSYFFMLDQNGFQVMTHPQLRPIDPPT 567

QY 533 --KSQEPVTLDFLD-----AELENDIKVEIRNKMID 561

Db 568 KYHKQNTNNMDLLEVEYQNGQNVRSQKSOAVSDLVCEGANTAECDVLLKRAVRKMIID 627

QY 562 GESGEKTFRTLVKSQDERY---IDK---GNRTYTWTPVNGTDSLALVLPYTSFYIKA 614

Db 628 CDNSD-----VQQLDVLYATELLDRVYPTNTYAEICINHANFVLGLAVAKGDDYRVVK 681

QY 615 KLEETITQARSKKGMK 631

Db 682 K-----QKKYDFGRVK 692

## RESULT 6

T18770

probable calcium channel protein - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 29-Oct-1999

C:Accession: T18770; T25249

R:Sulston, J.





||||| 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNNVSRANCKNIIML 360  
QY 361 FTDGGERAQEIENKYNKDKKVRFRFSVQGHNYERGPQIOMMACENKGYEYIPIPSIGAIR 420  
Db 361 FTDGGERAQEIENKYNKDKKVRFRFSVQGHNYERGPQIOMMACENKGYEYIPIPSIGAIR 420  
QY 421 INTOEYLDVLCRPMVLADGAKAKOVQWTVNYLDALGLVITGTLPVFNITGPENKTNLK 480  
Db 421 INTOEYLDVLCRPMVLADGAKAKOVQWTVNYLDALGLVITGTLPVFNITGPENKTNLK 480  
QY 481 NOLLILGVMGVDVLSLEDIKRLTPRTFLCPNGYFAIDPNGVYLLHNPQLPKNPKSQBPVTL 540  
Db 481 NOLLILGVMGVDVLSLEDIKRLTPRTFLCPNGYFAIDPNGVYLLHNPQLPKNPKSQBPVTL 540  
QY 541 DFLDAELNDIKVEIRNKMIDGESGKFTFTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
Db 541 DFLDAELNDIKVEIRNKMIDGESGKFTFTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
QY 601 ALVLPTYSFYIYKAKLEETITQARSKKGMKDSSETLKPDPNFEESSGYTFIAPRDYCNLDKI 660  
Db 601 ALVLPTYSFYIYKAKLEETITQARSKKGMKDSSETLKPDPNFEESSGYTFIAPRDYCNLDKI 660  
QY 661 SDNTEFLLNPNFIDRKTPNPNPCNADLNRVLLDAGFTNELVQNWYSKQKNIKGVKAR 720  
Db 661 SDNTEFLLNPNFIDRKTPNPNPCNADLNRVLLDAGFTNELVQNWYSKQKNIKGVKAR 720  
QY 721 FVVTDDGGITRVYPKEAGENWQENPETEYDSFYKRSNDNDNYVTAPYFNKSGPGAYESGI 780  
Db 721 FVVTDDGGITRVYPKEAGENWQENPETEYDSFYKRSNDNDNYVTAPYFNKSGPGAYESGI 780  
QY 781 MVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDCCKRNSDVMDCVI 840  
Db 781 MVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDCCKRNSDVMDCVI 840  
QY 841 LDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYAFNKSIDYQSVCEPGAAPK 900  
Db 841 LDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYAFNKSIDYQSVCEPGAAPK 900  
QY 901 GAGHRSAYVPSVADIQIGWATAAASIIQQFLLSLTFFPRLLFAVEMEDDDFTASLSK 960  
Db 901 GAGHRSAYVPSVADIQIGWATAAASIIQQFLLSLTFFPRLLFAVEMEDDDFTASLSK 960  
QY 961 SCITEQTOYFFDNDKSFSGVLDGCGNCSRIHFHGEKLMNTNLIIFIMVESKGTGCPDTRLLI 1020  
Db 961 SCITEQTOYFFDNDKSFSGVLDGCGNCSRIHFHGEKLMNTNLIIFIMVESKGTGCPDTRLLI 1020  
QY 1021 QAEQTSQDGNPCDMVK 1036  
Db 1021 QAEQTSQDGNPCDMVK 1036

## RESULT 2

A44147

calcium channel protein alpha-2 chain precursor - rat

N:Alternate names: dihydropyridine-sensitive L-type

N:Contains: calcium channel alpha-2 chain

C:Species: Rattus norvegicus (Norway rat)

C:Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 20-Aug-1999

C:Accession: A44147

R:Kim, H.L.; Kim, H.; Lee, P.; King, R.G.; Chin, H.

Proc. Natl. Acad. Sci. U.S.A. 89, 3251-3255, 1992

A:Title: Rat brain expresses an alternatively spliced form of the dihydropyridine-sensitive

A:Reference number: A44147; MUID:92228762; PMID:1314383

A:Accession: A44147

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1091 &lt;Kim&gt;

A:Cross-references: GB:W86621; NID:g203954; PIDN:AAA41088.1; PID:g203955

C:Superfamily: calcium channel alpha-2 chain

C:Keywords: calcium; glycoprotein; ion channel; transmembrane protein

Query Match

96.2%; Score 5234; DB 2; Length 1091;

Best Local Similarity 95.7%; Pred. No. 3e-307;  
Matches 992; Conservative 24; Mismatches 19; Indels 2; Gaps 2;  
QY 1 MAAGCLLALTTLTFLPSLLIGSPSEEPFSAVITIKSWVDKMQEDLVTLAKTAGVNNOLYDI 60  
Db 1 MAAGCLLALTTLTFLPSLLIGSPSEEPFSAVITIKSWVDKMQEDLVTLAKTAGVNNOLYDI 60  
QY 61 YEKYQDLYTVEPNNAQQLVEIAARDIEKLLSNRSLALSLAEAEKVAQAQHWREDFASN 120  
Db 61 YEKYQDLYTVEPNNAQQLVEIAARDIEKLLSNRSLALSLAEAEKVAQAQHWREDFASN 120  
QY 121 FVYVYNAKDDLDPEKNDSEPSQRIKPVFIEDANFGRQISQHAHAHPTDIYEGSTIVL 180  
Db 121 FVYVYNAKDDLDPEKNDSEPSQRIKPVFIEDANFGRQISQHAHAHPTDIYEGSTIVL 180  
QY 181 NELNWTLSALDEYFKKRNREDPSLLMQVFGSAGTLARYYPASPWVDSNRTPNKIDLYDVR 240  
Db 181 NELNWTLSALDEYFKKRNREDPSLLMQVFGSAGTLARYYPASPWVDSNRTPNKIDLYDVR 240  
QY 241 RPYIIGAAAPKMDLILVDVSGVSGLTLLKIRTSVSEMLETSDDDDFVNVASFNSNAQD 300  
Db 241 RPYIIGAAAPKMDLILVDVSGVSGLTLLKIRTSVSEMLETSDDDDFVNVASFNSNAQD 300  
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNNVSRANCKNIIML 360  
Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNNVSRANCKNIIML 360  
QY 361 FTDGGERAQEIENKYNKDKKVRFRFSVQGHNYERGPQIOMMACENKGYEYIPIPSIGAIR 420  
Db 361 FTDGGERAQEIENKYNKDKKVRFRFSVQGHNYERGPQIOMMACENKGYEYIPIPSIGAIR 420  
QY 421 INTOEYLDVLCRPMVLADGAKAKOVQWTVNYLDALGLVITGTLPVFNITGPENKTNLK 480  
Db 421 INTOEYLDVLCRPMVLADGAKAKOVQWTVNYLDALGLVITGTLPVFNITGPENKTNLK 480  
QY 481 NOLLILGVMGVDVLSLEDIKRLTPRTFLCPNGYFAIDPNGVYLLHNPQLPKNPKSQBPVTL 540  
Db 481 NOLLILGVMGVDVLSLEDIKRLTPRTFLCPNGYFAIDPNGVYLLHNPQLPKNPKSQBPVTL 540  
QY 541 DFLDAELNDIKVEIRNKMIDGESGKFTFTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
Db 541 DFLDAELNDIKVEIRNKMIDGESGKFTFTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
QY 600 LALVLPTYSFYIYKAKLEETITQARSKKGMKDSSETLKPDPNFEESSGYTFIAPRDYCNLDK 659  
Db 600 LALVLPTYSFYIYKAKLEETITQARSKKGMKDSSETLKPDPNFEESSGYTFIAPRDYCNLDK 659  
QY 660 ISDNTEFLLNPNFIDRKTPNPNPCNADLNRVLLDAGFTNELVQNWYSKQKNIKGVKAR 719  
Db 660 ISDNTEFLLNPNFIDRKTPNPNPCNADLNRVLLDAGFTNELVQNWYSKQKNIKGVKAR 719  
QY 720 RFVVTDDGGITRVYPKEAGENWQENPETEYDSFYKRSNDNDNYVTAPYFNKSGPGAYESG 779  
Db 720 RFVVTDDGGITRVYPKEAGENWQENPETEYDSFYKRSNDNDNYVTAPYFNKSGPGAYESG 779  
QY 780 IMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDCCKRNSDVMDCV 839  
Db 780 IMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDCCKRNSDVMDCV 839  
QY 840 ILDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYAFNKSIDYQSVCEPGAAPK 899  
Db 840 ILDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYAFNKSIDYQSVCEPGAAPK 899  
QY 900 QGAGHRSAYVPSVADIQIGWATAAASIIQQFLLSLTFFPRLLFAVEMEDDDFTASLSK 959  
Db 900 QGAGHRSAYVPSVADIQIGWATAAASIIQQFLLSLTFFPRLLFAVEMEDDDFTASLSK 959  
QY 960 QSCITEQTOYFFDNDKSFSGVLDGCGNCSRIHFHGEKLMNTNLIIFIMVESKGTGCPDTRLLI 1019  
Db 960 QSCITEQTOYFFDNDKSFSGVLDGCGNCSRIHFHGEKLMNTNLIIFIMVESKGTGCPDTRLLI 1019  
QY 1020 IQAEQTSQDGNPCDMVK 1036  
:|||||:|||||

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 10, 2003, 14:13:54 ; Search time 19.7185 Seconds  
(without alignments)  
5050.861 Million cell updates/sec

Title: US-10-090-827-14  
Perfect score: 5443  
Sequence: 1 MAAGCLLALTTLFQSLILG.....RLLIQAQTSDGPNPCDMVK 1036

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues  
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_73:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	5443	100.0	1091	2	JH0565	calcium channel al
2	5234	96.2	1091	2	A4147	calcium channel pr
3	5224.5	96.0	1106	1	CHRA2	calcium channel al
4	1085	19.9	1091	2	T30256	calcium channel al
5	607	11.2	734	2	S44617	C50C3.11 protein -
6	572	10.5	1148	2	T18770	probable calcium c
7	198	3.6	1450	2	C86880	hypothetical prote
8	194.5	3.6	886	2	S54355	inter-alpha-trypsi
9	185	3.4	885	2	S30350	inter-alpha-trypsi
10	175.5	3.2	1819	2	D97033	uncharacterized pr
11	164.5	3.0	889	2	JC5576	inter-alpha-trypsi
12	161	3.0	2706	2	T28155	variant-specific s
13	159	2.9	1984	2	A44396	p-type cation tran
14	157.5	2.9	375	2	D64998	hypothetical prote
15	156.5	2.9	918	2	E90542	lipoprotein (impor
16	155.5	2.9	680	2	A97331	membrane associate
17	155	2.8	1516	2	E71619	RAD2 endonuclease
18	155	2.8	2364	2	I40884	cytotoxin L - Clos
19	154.5	2.8	946	1	IYH02	inter-alpha-trypsi
20	154.5	2.8	1315	2	J28679	fibrinogen-binding
21	153	2.8	932	2	JC5953	inter-alpha-inhibi
22	152	2.8	1291	2	S46431	botulinum neurotox
23	152	2.8	1291	2	A49777	botulinum neurotox
24	151.5	2.8	420	2	S76691	hypothetical prote
25	151.5	2.8	1426	2	A95580	hypothetical prote
26	150.5	2.8	921	2	JC4625	inter-alpha-trypsi
27	150.5	2.8	1385	2	D89824	hypothetical prote
28	150	2.8	654	2	A69656	methyl-accepting c
29	150	2.8	1027	2	B90527	atp-binding protei

ALIGNMENTS

RESULT 1

JH0565  
calcium channel alpha-2b chain precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 20-Aug-1999  
C:Accession: JH0565  
R:Williams, M.E.; Feldman, D.H.; McCue, A.F.; Brenner, R.; Velicelebi, G.; Ellis, S.B  
Neuron 8, 71-84, 1992  
A:Title: Structure and functional expression of alphas, alpha2, and beta subunits of  
A:Reference number: JH0564; MUID:92110010; PMID:1309651  
A:Accession: JH0565  
A:Molecule type: mRNA  
A:Residues: 1-1091 <WIL>  
A:Cross-references: GB:M76559; MID:g179761; PIDN:AAA51903.1; PID:g179762  
A:Experimental source: basal ganglia  
A:Note: Several conflicts are found between GenBank submission, authors' translation  
C:Comment: This protein is a subunit of the voltage dependent calcium channel.  
C:Superfamily: calcium channel alpha-2 chain  
C:Keywords: glycoprotein; phosphoprotein  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-1067/Product: calcium channel alpha-2b chain #status predicted <CAL>  
F:32-268,326,539,635,1087/Binding site: phosphate (Thr) (covalent) (by protein kinase  
F:91,142,250,625,817/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #  
F:92,136,184,324,348,468,475,585,594,663,682,769,812,876,883,973,986/Binding site: ca  
F:501/Binding site: phosphate (Thr) (covalent) #status predicted  
F:833/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status pre

Query Match 100.0%; Score 5443; DB 2; Length 1091;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAAGCLLALTTLFQSLILGSPSPFPFSAVTIKSWDKMDEDLVTAKTAGVNLVDI	60
Db	1	MAAGCLLALTTLFQSLILGSPSPFPFSAVTIKSWDKMDEDLVTAKTAGVNLVDI	60
Qy	61	YEKYODLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLAEAEKVAQAHHQWREDFASN	120
Db	61	YEKYODLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLAEAEKVAQAHHQWREDFASN	120
Qy	121	EVVYNNAKDDLDPKENDSEPSQRIKPVFIEDANFGROIHQHAAVHIPTDIYEGSTIVL	180
Db	121	EVVYNNAKDDLDPKENDSEPSQRIKPVFIEDANFGROIHQHAAVHIPTDIYEGSTIVL	180
Qy	181	NELNWTSSALDEVFKNRREDPSLLWQVFGSATGLARYYPASPDWNSRTPNKIDLYDVR	240
Db	181	NELNWTSSALDEVFKNRREDPSLLWQVFGSATGLARYYPASPDWNSRTPNKIDLYDVR	240
Qy	241	RPWYIQGAASPKDMLILVDVSGVSGLTFLKIRTSVSEMLETLLSDDDFVNVASFNQAQD	300
Db	241	RPWYIQGAASPKDMLILVDVSGVSGLTFLKIRTSVSEMLETLLSDDDFVNVASFNQAQD	300
Qy	301	VSCFQLVQANVRNKKVLKDAVNNTAKITDYYKGSFAFEQLLNYSRANCKIIML	360

Db 310 SDPLPLTIO-VOTQOPSTDVQVOESILTLAKYRQTOIAETKLGDRQGAATMLQTAAK 368  
QY 591 TPVNGTDYSLALVLPYTFYVYKAKLEETITQARSKKGKMDSETLKP 638  
Db 369 TALQMGDKNGATILQOTNA---TRLOSGEDLSEGDKKTRMVSKTTLQP 413

Search completed: February 10, 2003, 14:19:51  
Job time : 15.7523 secs

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FT ACT_SITE 229 229 BY SIMILARITY.
FT METAL 232 232 ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID 436 452 INTERCHAIN (PROBABLE).
FT CONFLICT 84 84 P -> T (IN REF. 2).
SQ SEQUENCE 1290 AA; 148734 MW; 71FBE379F97129E8 CRC64;

Query Match
Best Local Similarity 20.3%; Score 152; DB 1; Length 1290;
Matches 205; Conservative 125; Mismatches 346; Indels 334; Gaps 54;

QY 106 KVAQAQHWREDFASNEWYNAKDDLPKNDSEPSQRIK---PVFIEDANFGR----- 157
Db 138 KTRGNNWVKTSINPSVIITG-----PRENIIDPTSTFKLTNTNTFAAQEGFALSIIIS 192
QY 158 -----QISYQHAHAHVHTDIYEGS-----TIVNELNWTLSALDEVEFK---KNRE 198
Db 193 ISPREMLTYSNAT---NDVGEGRFSKSEFCMDPILILMHELN---HAMINLYGIAIPNDQ 246
QY 199 EDPSSLWQVGSATGLARYYP-----ASPVDNSTRPNKIDLYDVRRRPWYIQGAASPKD 253
Db 247 TISSVTISNIFYQYNVKLEYAETAYFGGPTID--LIPKSARKYFEFKALDYRKSIAKRLN 304
QY 254 MLILVDVSG---SVSGLTLKLIIR-----TSVSEMLETSLDDDFVNVASFNSNAQDVSCF 304
Db 305 SITANPSSPNKYIGEKYOKLIRKYPVVESSGEV--TVNRNKFVEL--YNELTQIFTEF 360
QY 305 QHLVQAVNRNKKV-LKDVAVNITAK-----GITDYKKGFSAFEQL-----LNTNVSR--- 351
Db 361 NYAKIYNVQRKYLNSVYTPVTANILDDNVYDIQNGFNIPKSNLNVLFMGQNLSPAL 420
QY 352 --ANCKIIMLFT-----DGEEARAQEIFNK-----YNKD-----KKVRVPR 386
Db 421 RKVNPNMLYLFKFKHAIDG-----RSLYNTKLTDCRELLVKNKTDLPFIGDISDKTDI 475
QY 387 FSVQGHVYRGPIQWACENKGYEYTPSIGAJRI--NQEY--LDVL----- 430
Db 476 FLKRDINEETEV-----YYPNVSVQVILSKNTSEHQDLQLPSPIDSESEIILP 526
QY 431 GRPMVLADGAKAKOVWNT--VYLDALLEGIVITGLTPVFNITQFENKTN----- 478
Db 527 GENQVFDNRTQNVLYNSYYLESQKL-----SDNVEDFTFRSIEALDNSAKVYTYFP 582
QY 479 -LNKOLLGVWG-----VDVSELEIKRLTPFTLCPNGYFAIDPNGVYLLHPNLQPK 530
Db 583 TLANKVNAVQGGFLMWANDVVEDEFTNLRKDTLTKDISVSAIIP-----YIGPALNIS 638
QY 531 NPKSOEPTLDF-----LDAELENDI-----KVEIRNKMIDGESGEKTFRTL 572
Db 639 NSVRGNTFAFVATGVITLLEAPPETIPALGAFVLYSKVQERNEII-----KTIDNC 692
QY 573 VKSODERYIDKGNRTYTW-----TPVNGTDSLALVLPYTFYFIKAKLEETITQ 622
Db 693 LEQRIKRWKD-----SYEMMGWTLRSIITQFNISYQMYDSL-NYQAGAIIKAKID----- 742
QY 623 ARSKGKWKDSEITLP--DNFESGYTFIAPRDYCNDLKISDNNTTELLNFNEFI----- 675
Db 743 LEYKSGSKENIKSQVENLKNS-----LDVKIS-----EAMNINKFIRECSV 787
QY 676 -----DRKTPNPNPCNADLINRVLLDA----- 697
Db 788 TYLFKNMLPKVIDELNEFDRT-----KAKLIN--LIDSHNILLYGEVDKLKAKVNNNSF 839
QY 698 -----GFTN-----ELVQNYW-----SKOKNTGKVKARFVTDGGITRVYPKEAGE 738
Db 840 QNTIPNIFSYTNLSLKKDIINEYFNNDISKILSLQNRKNTLVDTSG-----YNAEVSE 894
QY 739 --NQENPEYEDSFYKRSLDNDNYVTPAFYFNKSGPGVAGESIMYSKAVEIYLOGKLK 796
Db 895 EGDVOLAP-----IP--PFDFKLGGSGGEDRGKVIQVTONENIVYNSMYE 935
QY 797 PAVVGIKIDVNSWTENFTKTSIRDPCAGPVCDCKRNSDVMDCVILDGGFLLMANHD--- 853
Db 936 SFSISFWIRINKWVSNLPGYTIID-----SVKNNSGWSIGIISNPLVFTLQNEDESEQ 988
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QY 854 -----DYTNQIGR-----FFGEIDPSLMRHLVNIISVYAFNKSYSYQSVCE 893
Db 989 SINFSDISNAPGYNKWFVTVTNMMG---NMKIYINGKLIDITKVKKE 1035

RESULT 15
Y103_SYNY3
ID Y103_SYNY3 STANDARD; PRT; 420 AA.
AC Q55874;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein sll0103.
GN SLL0103.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=96127529; PubMed=8590279;
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA Sugitara M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT region from map positions 64% to 92% of the genome.";
RL DNA Res. 2:153-166(1995).
CC 1- SIMILARITY: TO E.COLI YFBR.
CC 1- SIMILARITY: CONTAINS 1 VMAF DOMAIN.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D64004; BAA10635.1; -
DR InterPro; IPR002035; VMAF_A.
DR Pfam; PF00092; vma; 1.
DR SMART; SM00327; VMA; 1.
DR PROSITE; PS0234; VMAF; 1.
KW Hypothetical protein; Complete proteome.
FT DOMAIN 43 215 VMAF.
SQ SEQUENCE 420 AA; 45849 MW; E711B51478E74F3 CRC64;

Query Match
Best Local Similarity 20.8%; Score 151.5; DB 1; Length 420;
Matches 85; Conservative 85; Mismatches 183; Indels 55; Gaps 16;

QY 251 PKDMLILVDVSGSVSGLTLKLIITSVSEMLETSLDDDFVNVASFNSNAQDVSCFQHLVQA 310
Db 41 PLNLGLVLDHSGSDGQPLETVKSAALGLIDRLDEDDRLSVIAPDRAKIV-----IENQ 95
QY 311 NVRNKKVLKDVANNITAGITDYKKGFSAFEQLLYNVNVRANCKIIMLTFDGGEERAQ 370
Db 96 QVRNGAATAKATLERLKAEGTAIDEGKLIGTQEAARKGEDRVY---HFLITDGENEHD 152
QY 371 E-----IFNKYNKDKKVRFRFSVGOHNYERGPIOWMACENKG--YYEIPISGAIIRNTQ 424
Db 153 NDRCLKLTGVASDYKLTVHTLFGDGH--WNQDVLEAIAASAQGSLSYIENPS-EALHTFRQ 210
QY 425 EYLDVLGRPMVLADGAKAKOVWNTNYLDALLEG-----LVITGTLPVFNITQFENKTNLK 480
Db 211 LF-----QRMNSVNGVLTNAHL-LLELAPOAHLAI--VKPVAQVSPETMDLT-VQ 254
QY 481 NQLILLCVMGVDSVLEDIKRLTPFTLCPNGYFAIDPNCYVLLHNPKNPKSOF----- 536
Db 255 NOGAEEVEELGDMTLDQERV-----LLNLYLDQLLPQGHVIGVQVIRYDDPASGQTNLL 309
QY 537 ----PVTLDLDAELENDIKVEIRNKMIDGESGEKT--FRTLKVSQDERYIDKGNRTYTW 590
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RT RX MEDLINE=89076497; PubMed=2462430;  
RA Salier J.P., Diarra-Mehrpour M., Sesboue R., Bourguignon J.,  
RA Martin J.P.;  
RT "human inter-alpha-trypsin inhibitor. Isolation and characterization  
RT of heavy (H) chain cDNA clones coding for a 383 amino-acid sequence  
RT of the H chain.";  
RL Biol. Chem. Hoppe-Seyler 369:15-18(1988).  
RN [4]  
RP PARTIAL SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=88024442; PubMed=3663330;  
RA Schrettmueller T., Hochstrasser K., Resinger P.W.M., Wachter E.,  
RA Gebhard W.;  
RT "cDNA cloning of human inter-alpha-trypsin inhibitor discloses three  
RT different proteins.";  
RL Biol. Chem. Hoppe-Seyler 368:963-970(1987).  
RN [5]  
RP SEQUENCE OF 55-74; 116-127; 224-246; 295-307 AND 365-385.  
RX MEDLINE=89380192; PubMed=2476436;  
RA Enghild J.J., Thøgersen I.B., Pizzo S.V., Salvesen G.;  
RT "Analysis of inter-alpha-trypsin inhibitor and a novel trypsin  
RT inhibitor, pre-alpha-trypsin inhibitor, from human plasma.  
RT Polypeptide chain stoichiometry and assembly by glycan.";  
RL J. Biol. Chem. 264:15975-15981(1989).  
RN [6]  
RP SEQUENCE OF 55-64.  
RC TISSUE=Plasma;  
RX MEDLINE=93039735; PubMed=1384549;  
RA Malki N., Balduyck M., Maes P., Capon C., Mizon C., Han K.K.,  
RA Tartar A., Fournet B., Mizon J.;  
RT "The heavy chains of human plasma inter-alpha-trypsin inhibitor: their  
RT isolation, their identification by electrophoresis and partial  
RT sequencing. Differential reactivity with concanavalin A.";  
RL Biol. Chem. Hoppe-Seyler 373:1009-1018(1992).  
RN [7]  
RP SEQUENCE OF 55-64 AND 681-702, CROSS-LINK STRUCTURE, AND  
RP CARBOHYDRATE-LINKAGE SITES T-691.  
RX MEDLINE=93232026; PubMed=7682553;  
RA Enghild J.J., Salvesen G., Thøgersen I.B., Valnickova Z.,  
RA Pizzo S.V., Hefta S.A.;  
RT "Presence of the protein-glycosaminoglycan-protein covalent cross-link  
RT in the inter-alpha-inhibitor-related proteinase inhibitor heavy chain  
RT 2/Dikunin.";  
RL J. Biol. Chem. 268:8711-8716(1993).  
RN [8]  
RP SEQUENCE OF 67-101, AND HYALURONAN BINDING.  
RC TISSUE=Serum;  
RX MEDLINE=94075371; PubMed=7504674;  
RA Huang L., Yoneda M., Kimata K.;  
RT "A serum-derived hyaluronan-associated protein (SHAP) is the heavy  
RT chain of the inter alpha-trypsin inhibitor.";  
RL J. Biol. Chem. 268:26725-26730(1993).  
RN [9]  
RP SEQUENCE OF 699-702, AND COVALENT LINKAGE WITH CHONDROITIN SULFATE.  
RC TISSUE=Plasma;  
RX MEDLINE=94229087; PubMed=7513643;  
RA Morelle W., Capon C., Balduyck M., Sautiere P., Kouach M.,  
RA Michalski C., Fournet B., Mizon J.;  
RT "Chondroitin sulphate covalently cross-links the three polypeptide  
RT chains of inter-alpha-trypsin inhibitor.";  
RL Eur. J. Biochem. 221:881-888(1994).  
RN [10]  
RP CARBOHYDRATE-LINKAGE SITES, AND MASS SPECTROMETRY.  
RX MEDLINE=98343966; PubMed=9677337;  
RA Flahaut C., Capon C., Balduyck M., Ricart G., Sautiere P., Mizon J.;  
RT "Glycosylation pattern of human inter-alpha-inhibitor heavy chains.";  
RL Biochem. J. 333:749-756(1998).  
RN [11]  
RP CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.  
RX MEDLINE=98087700; PubMed=9425062;  
RA Olsen E.H.N., Rahbek-Nielsen H., Thøgersen I.B., Roepstorff P.,  
RA Enghild J.J.;  
RT "Posttranslational modifications of human inter-alpha-inhibitor:

identification of glycans and disulfide bridges in heavy chains 1 and 2.";  
Biochemistry 37:408-416(1998).  
-!- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A  
BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,  
INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE  
LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE  
ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES.  
-!- SUBUNIT: I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM  
ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,  
BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2  
AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND  
BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.  
-!- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN  
4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE.  
-!- MASS SPECTROMETRY: MW=76508; METHOD=MALDI; RANGE=55-702.  
-!- SIMILARITY: BELONGS TO THE ITIH FAMILY.  
-!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.  
-----  
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EMBL; X07173; CAA30160.1; ALT\_SEQ.  
DR EMBL; M18193; AAA60558.1; -.  
DR EMBL; M33033; AAA59195.1; -.  
DR PIR; S00346; IYHU2.  
DR PIR; B34245; B34245.  
DR GlycoSuiteDB; P19823; -.  
DR Genew; HGNC:6167; ITIH2.  
DR MIM; 146640; -.  
DR InterPro; IPR002035; VWF\_A.  
DR Pfam; PF00092; vwa; 1.  
DR SMART; SM00327; vwa; 1.  
DR PROSITE; PS50234; VWFA; 1.  
KW Serine protease inhibitor; Repeat; Signal; Multigene family;  
Glycoprotein.  
FT SIGNAL 1 18 POTENTIAL.  
FT PROPEP 19 54  
FT CHAIN 55 702 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN  
H2.  
FT PROPEP 703 946 VWFA.  
FT DOMAIN 308 468  
FT DISULFID 261 264  
FT DISULFID 650 651  
FT CARBOHYD 118 118  
FT CARBOHYD 666 666 N-LINKED (GLCNAC. . .) (COMPLEX).  
FT CARBOHYD 671 671 /FTID-CAR\_000140.  
FT CARBOHYD 673 673 O-LINKED (GALNAC. . .) (PARTIAL).  
FT CARBOHYD 673 673 /FTID-CAR\_000214.  
FT CARBOHYD 675 675 N-LINKED (GLCNAC. . .).  
FT CARBOHYD 675 675 O-LINKED (GALNAC. . .).  
FT CARBOHYD 691 691 /FTID-CAR\_000215.  
FT CARBOHYD 691 691 O-LINKED (GALNAC. . .).  
FT CARBOHYD 691 691 /FTID-CAR\_000216.  
FT CARBOHYD 691 691 O-LINKED (GALNAC. . .).  
FT CARBOHYD 691 691 /FTID-CAR\_000217.  
FT MOD\_RES 282 282 CARBOXYLATION.  
FT MOD\_RES 283 283  
FT BINDING 702 702 CHONDROITIN 4-SULFATE, CROSS-LINK SITE.  
FT CONFLICT 374 374 K -> L (IN REF. 5).  
FT CONFLICT 674 674 P -> A (IN REF. 2 AND 3).  
FT CONFLICT 705 705 F -> S (IN REF. 2 AND 3).  
FT CONFLICT 729 729 N -> D (IN REF. 2 AND 3).  
FT CONFLICT 731 731 V -> A (IN REF. 2 AND 3).  
SQ SEQUENCE 946 AA; 106436 MW; 1478CF3E8F3BA776 CRC64;  
Query Match 2.8%; Score 154.5; DB 1; Length 946;  
Best Local Similarity 19.9%; Pred. No. 0.13;  
Matches 133; Conservative 106; Mismatches 259; Indels 171; Gaps 29;

600	Db	KEYTNTNYCNDLHINDSTCSSYLLNSETKDAYCEYYNIDH-----LCD----	INKKND	650
697	Qy	AGFTNELVQNWSKQKNIKGVKAREVVTDGITRVYPKEAGENWQENPETYEDSPYKRSL	756	
651	Db	INSKNELMGKYSKNELMGKTIKNELM-----GKYSKNEL	684	
757	Qy	DNDNYVETAPYFNKSGPGAYESGIMYSKAVEIYIOGKLLKPAVVG-----IKIDVNSWI	810	
685	Db	-----MGKYSKNELMGKYSKNELMGKYSKNELMGKTIKNOVCVDTNIYH	737	
811	Qy	ENFTKSIRD-PCAGPVCDOCKRNSVMDCV-----ILDDGGFLLMANHDDYTNOIGRF----	862	
738	Db	MNCNDNYNDYPCD-----YNCNCDNTYHRLYEHNINKDSFNIPPEKNKSYNNISEHIKI	794	
863	Qy	-----FGEIDPSLMRHLVNLVSVAF-----	NKSYDYQ	889
795	Db	NYPLPEALACCHTSLSKVNKNKMGDVLIELMFNTNCDMLNNSFIITEKKKNGSYDFQ	854	
890	Qy	SVCEGAAPKQAGHRSAYVSVADILQIGWATAAAWSILOOFLSLSTFFPLLEAVEVE	949	
855	Db	KI---DGDKNIGANDERCHLNN-----NLVSYNILKRF-----	884	
950	Qy	DDDFTSLSKQSCITEQTQYFFDNDSKS	977	
885	Db	--EFQSLRQARMSVIVKST--YGNNDNDNN	909	

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RESULT 12
YFBK_ECOLI
ID YFBK_ECOLI STANDARD; PRT; 575 AA.
P76481;
AC DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein yfbk.
YFBK OR B2270.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia
OX NCBI_TaxID=562;
[1]
SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
!- SIMILARITY: TO SYNECHOCYSTIS PCC 6803 SLL0103.
!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
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CC EMBL; AE000317; AAC75330.1; --
CC EcoGene; EG14095; yfbk.
CC InterPro; IPR002035; VWF_A.
CC Pfam; PF00092; vwa; 1.
CC SMART; SM00327; VWA; 1.
CC PROSITE; PSS0234; VWFA; 1.
CC Hypothetical protein; Complete proteome.
DOMAIN 216 394 VWFA.
SEQUENCE 575 AA; 63634 MW; 7B56A1A77A2BE11 CRC64;

Query Match 2.8%; Score 157.5; DB 1; Length 575;
Best Local Similarity 21.6%; Pred. No. 0.043;

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Query Match	2.8%;	Score 157.5;	DB 1;	Length 575;
Best Local Similarity	21.6%;	Pred. No. 0.043;		

Matches	111;	Conservative	93;	Mismatches	206;	Indels	105;	Gaps	25;
Qy	71	EPNNARQVELTAARDIEKLLNSRKALVSLALEAEKVKQAAHQWRDFASNEWVYNAKDD	130						
Db	22	QPKESQOOQPSPTTEQOVLAAQAAATK---EAEQSAAA---AKALAAQEVQOYSDKQA	75						
Qy	131	LDPEKND-----SEFGSQRIPKVTIEDANFGRIQISYQAA---VHIPTDI	172						
Db	76	LQGRLOEAPTFAAAKAKATHIANPGTARYQQF---DDNPVKVQAQNPLATFSLDVTGS	132						
Qy	173	YEGSTIVLNE-----LNTSALDEVFKKNREDDPSLLMQVFGSATGLARYY	218						
Db	133	YANVRRELNOGLPPPPDAVRVEEIVNFPSPDWDI--KDKQISPAKPIPFAMRYELA---	187						
Qy	219	PASPVDONSRTPKIDLYDVRRRPWYTOGAASPKDMLLLVDVSGS--VSGLTCLKLIRSVS	277						
Db	188	PA-PW-NFQRTLLKVDILAKDKSEELPAS-----NLVFLIDTSGMSIDERLPIQSSLK	241						
Qy	278	EMLETLSDDDFPVNVASFNSNAQDYSCEPHLVQAQNRVKNKVLKDAVNNTAKGIDYKKGF	337						
Db	242	LLVKELREQDNIATVTVAGDSRIA-----LPSISGSHKAEINAAISLDAGSTNGAGL	296						
Qy	338	SFAFEQLLNIVNSRANCKNIIMLETDG-----GEERAQEIFNKYNDKKYRVFRFSVGQ	391						
Db	297	ELAYQQATK-GFTKGGINR-ILLATDGFNVGIDDPKSIESWYVKQRESGYTLSTFGVGN	354						
Qy	392	HNVERGPIQWACENGYVEIISIGAIRINTQEYLDVLRPVMVL--AGDKAKOVQ----	445						
Db	355	SNYNEAMWRIADVGNNGYSYIDTLS---EAKVLNSEMROMLITVAKDVKAQIENPA	410						
Qy	446	WTNYILDALGLVITGTLPVFNITGOFENKTNLKNOLILGVMGVD--VSLEDI---	501						
Db	411	WVTEY---RQIG-----YE-----KQRLRVEHFNNNDVADGIGAGKHIT	447						
Qy	502	PRFTLPCNGYFAIDPNGYVLLHPNLQPKPKSQE	536						
Db	448	LLFELTNGKASIDKLRYA--PDNKLAKSDKTKE	480						

RESULT 13

ID	ITH2_HUMAN	STANDARD;	PRT;	946 AA.
AC	P19823; Q15484; Q14659;			
CD	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DE	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy			
DE	chain H2) (Inter-alpha-trypsin inhibitor complex component II)			
DE	(Serum-derived hyaluronan-associated protein) (SHAP).			
GN	ITI1H2 OR IGHEP2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RP	[1]			
RN	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RX	MEDLINE=88152237; PubMed=2450046;			
RA	Gebhard W., Schreitmuller T., Hochstrasser K., Wachter E.;			
RT	"Complementary DNA and derived amino acid sequence of the precursor			
RT	of one of the three protein components of the inter-alpha-trypsin			
RT	inhibitor complex.";			
RL	FEBS Lett. 229:63-67(1988).			
RN	[2]			
RP	SEQUENCE OF 384-865 FROM N.A.			
RX	MEDLINE=88068576; PubMed=2446322;			
RA	Salier J.P., Diarra-Mehrpour M., Sesboue R., Bourguignon J.,			
RA	Benarous R., Ohkubo I., Kurachi S., Kurachi K., Martin J.P.;			
RT	"Isolation and characterization of cDNAs encoding the heavy chain of			
RT	human inter-alpha-trypsin inhibitor (I alpha TI): unambiguous			
RT	evidence for multipolypeptide chain structure of I alpha TI.";			
RL	proc. Natl. Acad. Sci. U.S.A. 84:8272-8276(1987).			
RN	[3]			
RP	SEQUENCE OF 384-766 FROM N.A.			

QY 388 SV-----GOHNYRGPIQWACENKGY---YYEIPSTGAIKINTQBYLDVGLRPMVLGDK 440  
 DB 643 TIVVTOGNNKKIDIVAKLLDSLGIPYSRYEKYIENGKELTKHILEITGRD-----695  
 QY 441 AKOVQNTVYLDALGLVITGLPVFNITQGF-----NKTNLUKNQILGLVGMVD 491  
 DB 696 -----GLIFOTLVGFISSEKNEALEKAEIVREMRNLKNSFYNLSTFE 739  
 QY 492 VSLIEDIKRLTPRTLCPCNGYFAIDPBGVYLLHPNLOPKPKSQBPVTLDFLDAELENDI 551  
 DB 740 VSSEYKGEYDUTLEGNPIYFA---NG-ILTHNSIIPSIIVTHN-VSPDTLRE-----789  
 QY 552 KVEIRNMIDGEGEKTFRTLVKSQDERYIDKGNRTYTWTPVNGDYSIALVLPYTSFY 611  
 DB 790 -----GCKNYDVAPIVG--YKFCCKDFPG---F 811  
 QY 612 IKAKLETTQARSKGKKKQSDSETLKPDPNFESGY-----TFIAPRDYCNLDKISD 562  
 DB 812 IPSILGELITMROEIKKKMK--ATIDPIEKKMLDYQRAVKLLANSILPNW---LPIIE 866  
 QY 663 NNTFEELNFEETDRKTPNNPSCNADLINRVLLDAGFTNELVQNYWSKOKNIKGVKAREV 722  
 DB 867 NGEVKKVKGIEFDTRMEQOKVRIVDTEVLEVDNIFAFSLNKSSEIKKVKAL---924  
 QY 723 VTDGITRVYPKEAGE 738  
 DB 925 -----IRHKYGEAYE 935

RESULT 11  
 ATX1\_PLAFA STANDARD; PRT; 1956 AA.  
 AC Q04956;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Probable cation-transporting ATPase 1 (EC 3.6.3.-).  
 OS Plasmodium falciparum.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=5833;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=TS/96;  
 RX MEDLINE=93132070; PubMed=8421054;  
 RA Krishna S., Cowan G., Meade J.C., Wells R.A., Stringer J.R.,  
 RA Robson K.J.;  
 RT "A family of cation ATPase-like molecules from Plasmodium  
 falciparum.";  
 RL J. Cell Biol. 120:385-398(1993).  
 CC -|- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.  
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -|- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2  
 ATPASES). SUBFAMILY V.  
 CC  
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 CC  
 CC EMBL; X65738; CAA46646.1; -.  
 DR InterPro; IPR001757; ATPase\_E1-E2.  
 DR Pfam; PF00122; E1-E2\_ATPase; 1.  
 DR PROSITE; PS00154; ATPASE\_E1\_E2; 1.  
 KW Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding.  
 FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 36 58 POTENTIAL.  
 FT DOMAIN 59 61 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 62 80 POTENTIAL.  
 FT DOMAIN 81 407 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 408 427 POTENTIAL.  
 FT DOMAIN 428 440 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 441 462 POTENTIAL.  
 FT DOMAIN 463 481 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 482 500 POTENTIAL.  
 FT DOMAIN 501 519 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 520 538 POTENTIAL.  
 FT DOMAIN 539 557 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 558 576 POTENTIAL.  
 FT DOMAIN 577 595 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 596 614 POTENTIAL.  
 FT DOMAIN 615 633 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 634 652 PHOSPHORYLATION (BY SIMILARITY).  
 FT METAL 1760 1764 MAGNESIUM (BY SIMILARITY).  
 FT METAL 1764 1764 MAGNESIUM (BY SIMILARITY).  
 FT DOMAIN 246 251 POLY-ASN.  
 FT DOMAIN 252 256 POLY-LYS.  
 FT DOMAIN 937 941 POLY-ASN.  
 FT DOMAIN 1344 1347 POLY-LYS.  
 FT DOMAIN 1363 1372 POLY-ASN.  
 FT DOMAIN 1680 1684 POLY-ASN.  
 SQ SEQUENCE 1956 AA; 230285 MW; AE708AAE99009335 CRC64;

Query Match 2.88; Score 159; DB 1; Length 1956;  
 Best Local Similarity 17.18; Pred. No. 0.21; Indels 366; Gaps 45;  
 Matches 179; Conservative 144; Mismatches 359;  
 QY 58 VDIEYKQDLYTVEPNARQLVEIAARDIEKLLSNR-----SKALVSLALPAEK 106  
 DB 100 INVY-RYNTSYIIS-----ELVPGDIYEIKNNMTIPCDTILSGSVTSEHMTGES 152  
 QY 107 VOAHQWREDFASNEVYVYNAKDDLDPEKND-----SEPGSQRKPKVFIEDANFGQIS 160  
 DB 153 V-PIHKERLPFEGNAIINKNKYDSNDEKDDYLRINYNNHASINMIKRNHLEETLGKKDR 211  
 QY 161 YQAAVHIPTDIYEGSTIVLNLNW-TSALDEVFKKNEEDPSLIWQVFGSATGLARYP 219  
 DB 212 EYKSNH-----DLCMKKLCVINTYDDVHMKMKMD-----244  
 QY 220 ASPWYDNRTPNKIDLYDVRPRPWYIOGA-ASPDKMLILVDVSGSVGLTKLINTSVSE 278  
 DB 245 ---YNNNNNNKKKINNLLN---FVKGTIYNSNDLLY-----275  
 QY 279 MLETLSDDDFVNVASFNSNAQDVCFOHLVQANVENKKVLDAVNNITAKGITDYKKGFS 338  
 DB 276 -----DDKIGVNIFE---DVNNKKH--KFNQRNINYNKDTNNL-----EINNKHR 317  
 QY 339 FAFEOQLNYSRANCKIIMLFTDGBEERAQIEFNKYKDKKVRVFRFSVGQHNRYERG 398  
 DB 318 YIYDCLLKVEAISQNKIY-----SNEDINKY-----346  
 QY 399 IOMACENKGYEIPSGAINTQBYLDVGLRPMVLGAG-----DKAKQV 444  
 DB 347 ---MLYGGTYVLSLYNINIKYNNKEENRILGL-VIKTGFITTKGKIVNNILYHKKEL 401  
 QY 445 QWNTVYLDALGLVITGLPVFNITQGFENKTNLKNOLILG-----V 487  
 DB 402 NLINOSYKFLII-LIYALFVSFVILLYITLSNNETNHIILKCLDIIDAIPALPTILT 460  
 QY 488 MGVDVSLIEDIKRLTPRTLCPCNGYFA-----IDPBGVYLLHPNLQ-----PKNPKSQ 535  
 DB 461 VGISAISRLKKKFSISCLCPHKINIAGIINTWVFDKGT-TLTENNLOFIGITQNNKNK 519  
 QY 536 EPVTLDFLDAELENDIKVEIRNMIDGEGEKTFRTLVKSQDERYIDKGNRTYTWTPVNG 595  
 DB 520 NMLS-DFIHIK-----EMNTSEYIHSKDDNNIHNKN-----549  
 QY 596 TDYSIALVLPYTSFYVYKAKLEETITQARSKGKKMKD-----SETLKPDPNFESG 645  
 DB 550 -----SIISEYIKDNMKNLHTSSK-KASITKERSNFIQVOTIKSCLLKDHVYKEKK 599  
 QY 646 YTFIAPRDYCNLDKISDNN-TEFLN-----FNFEF--IDRKTNNPNSCNADLINRVLLD 696



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CC EMBL: D89287; BAA13940.1; -
DR InterPro: IPR002035; WWFA.
DR Pfam: PF00052; WVA; 1.
DR SMART; SM00327; WVA; 1.
DR PROSITE; PS0234; WWFA; 1.
KW Serine protease inhibitor; Repeat; Signal; Multigene family;
FT SIGNAL 1 18
FT PROPEP 19 30
FT CHAIN 31 646
FT INTER-ALPHA-TRYP SIN INHIBITOR HEAVY CHAIN
FT H3.
FT PROPEP 647 886
FT DOMAIN 279 439
FT CARBOHYD 88 88
FT CARBOHYD 577 577
FT BINDING 646 646
FT SEQUENCE 886 AA; 99018 MW; AC0594C6852576B8 CRC64;

Query Match 2.9%; Score 164.5; DB 1; Length 886;
Best Local Similarity 23.2%; Pred. No. 0.031;
Matches 66; Conservative 56; Mismatches 112; Indels 51; Gaps 11;

QY 202 SLLMQVFGSATGLARYYPASPWVDSRT--PNKID-----LYDVR--PWYIQA-- 248
Db 208 SALTSGFSGCKGHVSFKPS---LDQRSCTPTDLSLLNGDFTIVDVNRESFGNVQVYNG 264
QY 249 -----ASPKMLILVDVSGVSGLTGLKIRTSVSEMLETSLDSDDFVNVASFNS 296
Db 265 YFVHFAPQGLPVPVKNIVFVIDISGSMAGRKIQTRVALLKILDDMKQDDYLFILFST 324
QY 297 NAQDVSCFOHLVQANVRKKVLLKAVNITAKGIDYKGFSAPEQLLN-----YNVSRA 352
Db 325 GV--TWKDSLVQAPALNEARTVRSISDQGMTINDGLRIGRLMTDAREQHTVPER 382
QY 353 NCKNIIMLFTDG----GEERAQEIFNKYKDKKVRVFRFSVG--OHNYERGPIONMACBNK 407
Db 383 STSIIML--TDGDANTGESRPEKIQENVRKAIEGRFLYNGFGNNLNYNLETMALENH 441
QY 408 GYVEIPSGAIRINTQYLDVGLRPVWVLAGDKAKQVQWTVNYLD 452
Db 442 GVARIYEDSDANUQLQGYEEVANPLI-----TNVEVE 475

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RESULT 10
ID DPOL_THEST STANDARD; PRT; 1829 AA.
AC O33845;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE DNA polymerase (EC 2.7.7.7).
GN POL.
OS Thermococcus sp. (strain TY).
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Thermococcus.
OX NCBI_TaxID=110163;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98094267; PubMed=9434178;
RA Niehaus F., Frey B., Antranikian G.;
RT "Cloning and characterisation of a thermostable alpha-DNA polymerase
from the hyperthermophilic archaeon Thermococcus sp. TY.";
RL Gene 204:153-158(1997).
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
+ [DNA]N.
CC -1- PTM: THIS PROTEIN UNDERGOES A PROTEIN SELF SPLICING THAT INVOLVES
A POST-TRANSCRIPTIONAL EXCISION OF THE THREE INTERVENING REGION
(INTEINS) FOLLOWED BY PEPTIDE LIGATION.
CC -1- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.
CC -----
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```

CC EMBL: Y13030; CAA73475.1; -
DR HSSP; P56689; 1TGO.
DR InterPro: IPR002064; DNA_pol_B.
DR InterPro: IPR003586; Hedgehog_hintC.
DR InterPro: IPR003587; Hedgehog_hintN.
DR InterPro: IPR002203; Intein.
DR InterPro: IPR004042; Intein_endonuc.
DR Pfam; PF00136; DNA_pol_B; 4.
DR Pfam; PF003104; DNA_pol_B_exo; 1.
DR PRINTS; PR00379; INTEIN.
DR SMART; SM00305; HintC; 3.
DR SMART; SM00306; HintN; 3.
DR SMART; SM00486; POLBC; 1.
DR TIGRFAMs; TIGR00592; pol2; 2.
DR PROSITE; PS00116; DNA_POLYMERASE_B; FALSE_NEG.
DR PROSITE; PS00818; INTEIN_CTER; 3.
DR PROSITE; PS00819; INTEIN_ENDONUCLEASE; 2.
DR PROSITE; PS0817; INTEIN_NTER; 3.
KW Transferase; DNA-directed DNA polymerase; DNA replication;
KW DNA-binding; Hydrolase; Endonuclease; Autocatalytic cleavage;
KW Protein splicing.
FT CHAIN 1 409
FT CHAIN 410 769
FT CHAIN 770 855
FT CHAIN 856 1392
FT CHAIN 1393 1441
FT CHAIN 1442 1598
FT CHAIN 1599 1829
FT CHAIN 1829 AA; 211875 MW; A113ABHC57EB9CB3 CRC64;
SQ SEQUENCE 1829 AA; 211875 MW; 2.9%; Score 161; DB 1; Length 1829;
Query Match 2.9%; Score 161; DB 1; Length 1829;
Best Local Similarity 20.1%; Pred. No. 0.14;
Matches 172; Conservative 101; Mismatches 301; Indels 282; Gaps 39;

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QY 16 SLLIGSSSEPPFS-----AVTKSV-----DKMQEDLVTLA 48
Db 229 TLLGRDKEHPKPIHMGDSFAVEIKGRIFDLFPVVRRTINLPTTYTLEAVEAVLGT 288
QY 49 KTASGVNOLVDIYEKYQDL-----YVPEPNARQLVEIAARDIEKLLSNRSALVSLAE 103
Db 289 KSLGAEIEIAIWETESMKKLAQYSWE--DARATYEL-----GKEFFPMEAE 334
QY 104 AEKQAAHWRDFAS--NEWVY-----NAKDDLPKNDSEPGSQRIKPVFI----- 150
Db 335 LAKLIGQSVMDVSRSTGNLVEWYLLRVAVERNELAPNKPDEEYRRLRTYTLGGYVKE 394
QY 151 EDANFGQISYQAAVHIPTD---IYEGSTIV---LNEINWTSALDEVFKNKREDPSL 203
Db 395 PERGLWENTAYLDFRCH--PADTKVIYKGVINISDKEGDYILGIDG----- 441
QY 204 LMQVFGSATGLARYYPASPWVDSNR---TPN-KIDLYDVRVRPWYIQAASPKDMLILVD 259
Db 442 -WQ---RVKKVMKYHYEGKLNINGLKCPNKHVPVVTENDRQTRI-----RSLAKSF 491
QY 260 VSGSVSGLTLKIRTSVSEMLETSLDSDDFVNVASFNSN----- 297
Db 492 LSGKVGK---KIITKL-----PEKIAEFKNKPSEEEILKGLSGILLAEGLT 537
QY 298 -AQDVSCF-----OHLVQANV-RNKKVLKDAV-----NNITAGK---- 329
Db 538 LKADIYFSSSGKKRISHQYRVEITIGENEKELLERILYIFDKLFGIRPSVKKKGDTNA 597
QY 330 --ITDYKGFSAFQELLNLYNVRANCKIIMLTDDGGERAQEIFNKYKDKVYRFRF 387
Db 598 LKITTAKKAVYLQIEELK-NIESLYAPAVLRGF-----FERDATVKNKIRS 642

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CC -----
DR EMBL: X83231; CAA58233.1; .
DR InterPro: IPR002035; VWFA_A.
DR Pfam: PF00092; vwa: 1.
DR SMART: SM00327; VWA; 1.
DR PROSITE: PS0234; VWFA; 1.
KW Serine protease inhibitor; Repeat; Signal; Multigene family;
KW Glycoprotein.
FT SIGNAL 1 21
FT PROPEP 22 33
FT CHAIN 34 647
FT
FT PROPEP 648 887
FT DOMAIN 282 442
FT CARBOHYD 91 91
FT CARBOHYD 580 580
FT BINDING 647 647
FT
FT SEQUENCE 887 AA; 99097 MW; 3B9F0FF96D514096 CRC64;
SQ
Query Match 3.2%; Score 180.5; DB 1; Length 887;
Best Local Similarity 18.5%; Pred. No. 0.0034;
Matches 173; Conservative 139; Mismatches 350; Indels 275; Gaps 39;
QY 27 FPSAVTIKSWDMQEDLVLTAKTAGSVNQLVDIEKYQDLTYVEPNNAQLVEIARDI 86
Db 101 YPGSVKEVAQKQYKAVSQGTAG----LVKASGRKLEKFTVSVNVAAGSKVIFELTY 156
QY 87 EKLNSRSKALVSLAEAEKVAQAAHWRD---FASNEVVYNAKDDLDPEKNDSEPGSQ 143
Db 157 EELL-KRKKGYEMLYKQVQLVRHFEIDAHIFEQGISMLDA----- 199
QY 144 RIKPVFTIEDANFRQISQYQAAHVIPDIYEGSTIVLNLNWTSLDEVEFKKNEEDPSL 203
Db 200 -----DASF-----ITNDL-LGSALTQSP----- 217
QY 204 LMWFGSATGLARYPASPWNDSRT-PNKID-----LVDVRRP-----WY 244
Db 218 -----SGKKGHVSPKIDQQRSCPTCTDSLLNGDFTIVYDVNRSNGVQIVNGYF 269
QY 245 I-----QG-AASPKDMLILVDVSGSVGLTLKLRISVSEMLETSLDDDFNVNVAFSNSA 298
Db 270 VHFAPQGLPVVPKIAFVIVDVGSMGRKIQTQREALLIKLDKREEDVNLILSTGV 329
QY 299 QDVSCFQHLQVANNRKKVLKADVNNITAKITDYKKGFSFAFQLLNNVNSRAN----- 353
Db 330 -TTWKDLVKTATPANLEEARAFVKNIKDRSMNINDGLRGTEML---NKAREDHLPVE 384
QY 354 -CNKIIMLFTDG---GEERAQEIFNKYKDKKVRVFRFSVG-QHNVYRGPQIWMACENK 407
Db 385 RSTSLVMLTDGDANTGESRPEIQENVNAIRKGFPLYNLGFNNLNNYLFESLALNH 444
QY 408 GYVEIPIPSGAIRINTQBYLDVLRPMVLADGAKAQVQWNTNVYLDALDELGI--VITGLP 465
Db 445 GFARIVYDSASLOLOGFYEEVANPLL-----INVELEYENAILDLTRNSYP 493
QY 466 VFNTTGOFENTNKLKOLLIGVMGVDSLEDIKRLTPRFTLCPNGYFYADPNQYVILLHP 525
Db 494 HF-----YDG-----SEIVAGRLVDRVDN-----FKADVKGHGHALN- 526
QY 526 NLPKNPKSQEPVTLDFDALENDIKVEIRNKMIDGESGKTF-----RTLVKSODER 579
Db 527 -----DLTFTEEDVMKEMDAALK-----EGYIFDGYIERLWAYLTITQLEKKNR 574
QY 580 YIDKGNRTYTPVNGTDYSILA--LVLPITYSFYIKAKLEETITQARSKGKKMDSFT-- 635
Db 575 GDEXENIT-----AEALESLKYHFVYPLTSMVVYTKPEDNDQTAIADKPGEEAISASTA 629
QY 636 -LKPDNFEESGYTFIAPRDYCNLKIISNNTFELNFE----NEFTDRTPNPNPSCNADLIN 691
Db 630 YLTQSQSSHSPPYYV-----DGDPHFTIQVPGKNDTICFNIDKPKGVFLSLIQ 677
QY 692 RVLLDAGFTNELVQNVSKQKNKGVKARFVVTDGGITRVYYPKEAGENQWENPETYEDSF 751
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Db 678 DPVTGIATVQGI-----GKGNNASSRTGKT----- 704
QY 752 YKRSILDNDYVFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGIKIDVNSWIE 811
Db 705 -----YFGKLGIANAWMDFRIVTEKILGN-----GALSTFSWLD 742
QY 812 NFKTTSIRDPCAGPYCDCKRNSDMVCDVILDDG-GFLMAN-----HDDYTNQIGRF 862
Db 743 TVTVTQ-----TGLSVTLNRKKNMV--VSFEDGISFVILHGVVKKHVDVHDFLG----- 790
QY 863 FGEIDPSLMRLHVLNLSVAFNKSIDYQSV-CEPGNAP 898
Db 791 FYVVDSHRMSAQTHGLLGQFTQFPDFKVDVVRPGSDP 827
RESULT 9
ITH3_MESAU STANDARD; PRT; 886 AA.
AC P97280;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inter-alpha-trypsin inhibitor heavy chain H3 precursor (ITI heavy
DE chain H3) (HC3).
GN ITH3.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=97420688; PubMed=9276673;
RA Nakatani T., Suzuki Y., Yamamoto T., Sinohara H.;
RT "Molecular cloning and sequencing of cDNAs encoding three heavy-chain
RT precursors of the inter-alpha-trypsin inhibitor in Syrian hamster:
RT implications for the evolution of the inter-alpha-trypsin inhibitor
RT heavy chain family.";
RL J. Biochem. 122:71-82(1997).
RN [2]
RP SEQUENCE OF 31-50; 446-472 AND 504-523, AND SUBUNITS.
RC TISSUE=Plasma;
RX MEDLINE=97018241; PubMed=8864857;
RA Yamamoto T., Yamamoto K., Sinohara H.;
RT "Inter-alpha-trypsin inhibitor and its related proteins in Syrian
RT hamster urine and plasma.";
RL J. Biochem. 120:145-152(1996).
CC -!- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
CC SIMILARITY).
CC -!- SUBUNIT: I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
CC BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2
CC AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.
CC -!- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
CC 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE ITH FAMILY.
CC -!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
CC
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CC AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND  
 CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.  
 CC TISSUE SPECIFICITY: EXPRESSED IN BOTH LIVER AND BRAIN.  
 CC -I- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN  
 CC 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY  
 CC SIMILARITY).  
 CC -I- SIMILARITY: BELONGS TO THE ITH3 FAMILY.  
 CC -I- SIMILARITY: CONTAINS 1 VWFA DOMAIN.  
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 CC  
 CC EMBL: X70393; CAA49843.1; -  
 CC MGD; MG1:96620; Ith3.  
 CC InterPro: IPR02035; VWFA\_A.  
 CC Pfam: PF00092; vwa; 1.  
 CC SMART: SM00327; VWFA; 1.  
 CC PROSITE: PS0234; VWFA; 1.  
 CC Serine protease inhibitor; Repeat; Signal; Multigene family;  
 CC Glycoprotein. 1 18 POTENTIAL.  
 CC SIGNAL 19 30 BY SIMILARITY.  
 CC PROPEP 31 646 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN  
 CC CHAIN H3.  
 CC  
 CC FT PROPEP 647 886 BY SIMILARITY.  
 CC FT DOMAIN 279 439 VWFA.  
 CC FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 577 577 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT BINDING 646 646 CHONDROITIN 4-SULFATE, CROSS-LINK SITE  
 CC (BY SIMILARITY).  
 CC SQ SEQUENCE 886 AA; 98977 MW; 15955308C7F5030A CRC64;  
 CC  
 CC Query Match 3.5%; Score 194.5; DB 1; Length 886;  
 CC Best Local Similarity 19.9%; Pred. No. 0.0005;  
 CC Matches 185; Conservative 138; Mismatches 347; Indels 261; Gaps 44;  
 CC  
 CC YQ 27 FPSAVTIKSWVDKQEDLVLTAKTASGVNLVDYKDYODLYTVEPNARQLVEITAARDI 86  
 CC Db 98 YPGNVEKEVAQKQEKAVSQGTAG---LVKASGRKLEKFTSVNVVAGSKVFTLY 153  
 CC YQ 87 EKLSSNRKALVSLALEAEKQAAHQRDEDFASNEVYVYNAKDDLDPEKNDSPGSRQIK 146  
 CC Db 154 EELL-KRNKGKYMVLKQPKLVRFHEID-----AHIFEP-----Q 189  
 CC YQ 147 PVFIEDANFQRIQSYQHAHVHIPTDIYEGSTIVLNLNWTSLALDEVFKNREEDPSLLWQ 206  
 CC Db 190 GISMLDAE-----ASFITNDL-LGSALTGSF----- 214  
 CC YQ 207 VFGSATGLARYPASPWVDSNRT-PNKID-----LYDVRRRP-----WYI-- 245  
 CC Db 215 -----SGKKHVSFKSLQQRSCPTCTSLSLNGDTIVDVNRESGPNQVINGVFVHF 269  
 CC YQ 246 ---QG-AASPKDMLILVDVSGVSGLTALKIRTSVSEMLETISDDDFVNVASFNSNAQDV 301  
 CC Db 270 FAPQGLPVVPKNIIVFVDSGMSGRKIQTREALLKILDDVKEDDYLNLFST---DV 326  
 CC YQ 302 SCFQ-HLVQANVKNKLVKDVANNITAKGIDYKKGFSFAFQOLLNINYSRAN-----C 354  
 CC Db 327 TTKWDLHLVQATPANLEAKTFFVKNIHQDSMTNINDLLKGIEML---NKAREDHVTPERS 383  
 CC YQ 355 NKIIMLFTDG---GEERAQEIENKYNK--DKKVRFRFSVGOHNYERGPIONWACENKG 408  
 CC Db 384 TSIIMLTGDGANTGESRPEKIQENYRNAIGGKFFLYNLGFG--NNUNYVFLTALENGH 442  
 CC YQ 409 YYYEIPSGAIRINTQYLDVLRPMVLGADKAKQVQWNTNVIDALELGL--VITGTLFV 466  
 CC Db 443 LARRIEDSDANLQGFVEEVANPLL-----INVEYVEPNAILDLTRNSYPH 491

QY 467 FNITQFENKMLKNQLILGVWGVDSLEDIKRLTPRETLCPNGYFYFAIDPNGYVLLHPN 526  
 Db 492 F-----YDG-----SEIVVAGRLVDRNDN-----FKADYKGGHGCALN-- 523  
 QY 527 LQPKNPKSQEPVTLDFDLDAELENDIKVEIRNKMIDGESGEK--TFRTLVKSODERYIDKG 584  
 Db 524 ----DLTTEEVDEMEADALK-----EOGYIFGDYIERLWAYLTTEQLLEKRNKAG 572  
 QY 585 NRTYTWTPVNGDYSLA--LVLPYTSFYIYIKAKLEETITQARSKKMKDSEF-----LK 637  
 Db 573 DEKENIT-AEALDSLKLVHFVPTLTSVMVTKPEDNQDQTSADNAGEBAFAETTTMSFLT 631  
 QY 638 PNFESGYTFIAPRDYCNLDKISDNTEFLNNEFTDRKTPNNPNSCNADLNRLVLD 697  
 Db 632 TQOQSQSPYVY-----DGDPHFIQI-----PGKNDSCIFENIDKPK 668  
 QY 698 GFTNELVNYNSKOKNIKGVKARFVVTDDGTRVYPKREAGNWOENPETYEDSYKSLD 757  
 Db 669 GTVLRLIQD-----PVT--GIT-VTGOIIGD-----KRS-- 694  
 QY 758 NDNYVFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTS 817  
 Db 695 NASSRTGKTYFKLGITNAWMDRVEVTEKILG-----TGAEISTFSLDVTVTQ 747  
 QY 818 IRDCAGPVCCKRNSVMDVILDDG--GFLLMAN-----HDDYTNQIGRFFGEIDP 868  
 Db 748 ----TGLSVTINRKNMV--VSFGDGISFVILLHQVWKHPVHQDFLG-----FYVDS 795  
 QY 869 SILMRHLVNIYVAFNKSVDYQSV-CEPCAAP 898  
 Db 796 HRMSAQTHGLLGQFPQFPDFKVFGRPGSDP 826  
 RESULT 7  
 ITH3\_HUMAN  
 ID ITH3\_HUMAN STANDARD; PRT; 885 AA.  
 AC Q06033; Q99085;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Inter-alpha-trypsin inhibitor heavy chain H3 precursor (ITI heavy  
 DE chain H3) (Serum-derived hyaluronan-associated protein) (SHAP).  
 GN ITH3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=93215656; PubMed=7681778;  
 RA Bourguignon J., Diarra-Mehrpour M., Thiberville L., Bost F.,  
 RA Sesboue R., Martin J.P.;  
 RT "Human pre-alpha-trypsin inhibitor-precursor heavy chain. cDNA and  
 RT deduced amino-acid sequence.";  
 RL Eur. J. Biochem. 212:771-776(1993).  
 RN [2]  
 RP SEQUENCE OF 341-885 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=89137072; PubMed=2465147;  
 RA Diarra-Mehrpour M., Bourguignon J., Sesboue R., Mattei M.-G.,  
 RA Passage E., Sailer J.P., Martin J.P.;  
 RT "Human plasma inter-alpha-trypsin inhibitor is encoded by four genes  
 RT on three chromosomes.";  
 RL Eur. J. Biochem. 179:147-154(1989).  
 RN [3]  
 RP SEQUENCE OF 30-49; 463-477 AND 497-515.  
 RX MEDLINE=89380192; PubMed=2476436;  
 RA Enghild J.J., Thøgersen I.B., Pizzo S.V., Salvesen G.;  
 RT "Analysis of inter-alpha-trypsin inhibitor and a novel trypsin  
 RT inhibitor, pre-alpha-trypsin inhibitor, from human plasma.";  
 RL J. Biol. Chem. 264:15975-15981(1989).  
 RN [4]

```

UN36_CAEEL STANDARD; PRT; 734 AA.
ID UN36_CAEEL AC P34374;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE Protein unc-36
DE UNC-36 OR UNC-72 OR C50C3.11.
GN Caenorhabditis elegans.
OS Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditoidea;
OC Rhabditiidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol NZ;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Alnsough R., Anderson K., Baynes C., Becks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Sims M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
CC -1- SIMILARITY: TO CALCIUM CHANNEL ALPHA-2B SUBUNIT.
CC -1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
CC
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CC -----
DR EMBL; LI4433; AAA27969.1; -.
DR PIR; S44617; S44617.
DR WormPep; C50C3.11; CE00117.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; WVF_A.
DR Pfam; PF00092; vwa; 1.
DR Pfam; PF02743; Cache; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS05234; VWFA; 1.
DR Ionic channel; Ion transport; Voltage-gated channel; Calcium channel;
KW Glycoprotein
KW DOMAIN 250 435 VWFA.
FT CARBOHYD 100 100 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 302 302 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 476 476 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 514 514 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 734 AA; 85034 MW; CCFF78CDDEF4B71F CRG64;

Query Match 10.8%; Score 607; DB 1; Length 734;
Best Local Similarity 26.6%; Pred. No. 8 6e-29;
Matches 180; Conservative 127; Mismatches 258; Indels 112; Gaps 20;

QY 47 LAKTAGSVNQLVDIYEKYODLYTPVPNNARQLVFAARDIEKLNSRS-----KALVSAL 102
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 36 MKETFSKISHETILKQYKLVREEQFDPAELKKSKHRIEDYLKVRSFAYKAKIS--L 93
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 103 EAEKYQAQHQRDFASNEVWYNNAKDLDPEK-NDSEFGSRIKP-----VFIEDANF 155
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 94 EAARSVNDSVTDPQSKEIRFMASKQGNDGTITYESHLGKRLKYNETKSFLNTQANF 153
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 4					
ID	YLJ9_CAEEL	STANDARD;	PRT;	1205 AA.	
AC	P34372;				
DT	01-FEB-1994	(Rel. 28, Created)			
DT	15-JUN-2002	(Rel. 41, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Hypothetical protein C50C3.9 in chromosome III precursor.				
CN	C50C3.9.				
GN	Caenorhabditis elegans.				
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditoidea;				
OC	Rhabditidae; Peloderinae; Caenorhabditis.				
OX	NCBI_TaxID=6239;				
[1]					
SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;				
RC	MEDLINE=94150718; PubMed=7906398;				
RA	Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,				
RA	Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,				
RA	Cruxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,				
RA	Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,				
RA	Johnston L., Jones M., Kershaw J., Kirsten T., Laister N.,				
RA	Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,				
RA	Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,				
RA	Sims K., Smaldon J., Smith A., Smith M., Sonhammer E., Staden R.,				
RA	Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,				
RA	Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,				
RA	Wohlman P.;				
RT	"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.				
RT	elegans.";				
RL	Nature 368:32-38(1994).				
RP	[2]				
REVISIONS.					
RA	Waterston R.;				
RL	Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.				
CC	-I- SIMILARITY: CONTAINS 1 VWFA DOMAIN.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
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CC	-----				
DR	EMBL; LI4433; AAA27971.2; "				
DR	PIR; S44619; S44619.				
DR	WormPep; C50C3.9; CE24860.				
DR	InterPro; IPR002035; VWFA.				
DR	InterPro; IPR004010; Cache.				
DR	Pfam; PF00092; vwa; 1.				
DR	Pfam; PF02743; Cache; 1.				
DR	SMART; SM00327; VWA; 1.				
KW	Hypothetical protein; Signal.				
FT	SIGNAL 1 19	POTENTIAL,			
FT	CHAIN 20 1205	HYPOTHETICAL PROTEIN C50C3.9 IN			
FT		CHROMOSOME III.			
FT	DOMAIN 250 435	VWFA.			
SQ	SEQUENCE 1205 AA; 139339 MW; 79A2F96C052BF91C CRC64;				
Query Match	13.4%; Score 752.5; DB 1; Length 1205;				
Best Local Similarity	24.0%; Pred. No. 3.6e-37;				
Matches 284; Conservative 202; Mismatches 466; Indels 231; Gaps 42;					
QY	47 LAKTASGVNLVDIVYEKYQDLYTVPEPNARQLVEIAARAIDEKLSNRS----	KALVSLAL 102			
:	: : : : :   :   :   :   :   :   :   :   :   :   :   :				
DG	36 MKETFYSKHSHETILKNQYKLVEEQQDPRAELKKSKHRIEDYLUKVSQAAYKAKIS--L 93				
QY	103 EAERQVAHQWRDEFASNEVVYYNAKDLDPEK-NDSEPGSORIKP-----VFIEDANF 155				
:	: : : : : : : : : : :   :   :   :   :   :   :   :   :   :   :				
DG	94 EARVRNDSTVNDPSQSFKIFMSKAOGNGDCTTYIESHLGLKRVNETKSFNLTQNANF 153				
QY	156 -GROISYQHAHVHIPTDIYEGSTTVLVNELNWTSALDEVFKNNREDPSPSLMQVFGSATGL 214				

SEQUENCE OF 961-975; 992-1000 AND 1033-1050.  
 MEDLINE=90368635; PubMed=2168391;  
 de Jongh K.S., Warner C., Catterall W.A.;  
 "Subunits of purified calcium channels. Alpha 2 and delta are encoded  
 by the same gene.";  
 J. Biol. Chem. 265:14738-14741(1990).  
 CC -1- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN  
 CC EXCITATION-CONTRACTION COUPLING.  
 CC -1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:  
 CC ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS  
 CC HETERODIMERS THAT ARE DISULFIDE-LINKED.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE  
 CC SPLICING.  
 CC -1- TISSUE SPECIFICITY: SKELETAL MUSCLE.  
 CC -1- PPM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM  
 CC A PRECURSOR FORM.  
 CC -1- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.  
 CC -1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.  
 -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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 EMBL; M21948; AAA81562.1; -;  
 PIR: S10579; CHRB2;  
 InterPro: IPR004010; Cache.  
 InterPro: IPR002035; VWFA.  
 Pfam: PF00092; vwa; 1.  
 Pfam: PF02743; Cache; 1.  
 SMART: SM00327; VWFA; 1.  
 PROSITE: PS0234; VWFA; 1.  
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;  
 KW Calcium channel; Glycoprotein; Phosphorylation; Signal;  
 KW Alternative splicing.  
 FT SIGNAL 1 26  
 FT CHAIN 27 960  
 FT CHAIN 961 1106  
 FT TRANSEM 448 471  
 FT TRANSEM 921 945  
 FT TRANSEM 1082 1101  
 FT DOMAIN 255 432  
 FT CARBOHYD 94 94  
 FT CARBOHYD 138 138  
 FT CARBOHYD 186 186  
 FT CARBOHYD 326 326  
 FT CARBOHYD 350 350  
 FT CARBOHYD 477 477  
 FT CARBOHYD 606 606  
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 FT CARBOHYD 784 784  
 FT CARBOHYD 827 827  
 FT CARBOHYD 891 891  
 FT CARBOHYD 898 898  
 FT CARBOHYD 988 988  
 FT CARBOHYD 1001 1001  
 FT MOD\_RES 503 503  
 FT MOD\_RES 848 848  
 SQ SEQUENCE 1106 AA; 125042 MW; BOODE7F3C877B618 CRC64;  
 Query Match 96.1%; Score 5380.5; DB 1; Length 1106;  
 Best Local Similarity 94.8%; Pred. No. 1e-313;  
 Matches 1029; Conservative 15; Mismatches 12; Indels 29; Gaps 4;  
 QY 1 MAAGCLIALTLTLPQS--LLIGPSSSEPPFSAVTKSWDKMQEDLVTLAKTAGSGVNLV 58  
 Db 1 MAAGRPLAWTLTLQAWLLIGPSSSEPPFSAVTKSWDKMQEDLVTLAKTAGSGVNLV 60

QY 59 DIYEKYQDLYTVEPNARQLVEIAAARDIEKLLSNRSKALVSALAEAEKVOAAHOREDEFA 118  
 Db 61 DIYEKYQDLYTVEPNARQLVEIAAARDIEKLLSNRSKALVSALAEAEKVOAAHOREDEFA 120  
 QY 119 SNEVYVYNAKDDLDPEKNDSEPGSQRIKPVFTEDANFGRQISYQAAAHVHPDIEGSTI 178  
 Db 121 SNEVYVYNAKDDLDPEKNDSEPGSQRIKPVFTEDANFGRQISYQAAAHVHPDIEGSTI 180  
 QY 179 VLNELNWTLSALDEVKPKNEEDPSLLWQVFGSATGLIARTSPASVWVDSRTPNKIDLYDV 238  
 Db 181 VLNELNWTLSALDEVKPKNEEDPSLLWQVFGSATGLIARTSPASVWVDSRTPNKIDLYDV 240  
 QY 239 RRRPWTIQGAASPDKMLILVDVSGVSGVLTGLIARTSPVSEMLETISDDDFVNVAFNSNA 298  
 Db 241 RRRPWTIQGAASPDKMLILVDVSGVSGVLTGLIARTSPVSEMLETISDDDFVNVAFNSNA 300  
 QY 299 QVDSCFQHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSFAFEQLLNINVRANCNKII 358  
 Db 301 QVDSCFQHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSFAFEQLLNINVRANCNKII 360  
 QY 359 MLFTDGGEEAQRGAEIFNKNKDKKRVRFVSQOHNYERGPQIOWMACENKGGYIYEPSICA 418  
 Db 361 MLFTDGGEEAQRGAEIFNKNKDKKRVRFVSQOHNYERGPQIOWMACENKGGYIYEPSICA 420  
 QY 419 IRTNQEYLDVLGRPMVLGADRAKQVQWNTNVLDALEGLVITGLTPVFNITGQENKTN 478  
 Db 421 IRTNQEYLDVLGRPMVLGADRAKQVQWNTNVLDALEGLVITGLTPVFNITGQENKTN 480  
 QY 479 LKNQLLIGVNGVDVSLIEDIKRLTPRTFLCPNGYVYFAIDPNGVYLLHPNLQPK- 530  
 Db 481 LKNQLLIGVNGVDVSLIEDIKRLTPRTFLCPNGYVYFAIDPNGVYLLHPNLQPKIGVGPT 540  
 QY 531 -----NPKSQEPVTLDFDALENDIKVEIRNKMIDGESGEKTFRTLVSQDER 579  
 Db 541 INLRKRRPNVQNPQSQEPVTLDFDALENDIKVEIRNKMIDGESGEKTFRTLVSQDER 600  
 QY 580 YIDKGNRTYTWTVPNGTDY-LSALVLPYTSFYIYAKLEETITQARSKGKMKDSETLKP 638  
 Db 601 YIDKGNRTYTWTVPNGTDYSSIALVLPYTSFYIYAKLEETITQARSKGKMKDSETLKP 653  
 QY 639 DNFEEGYFTIAPRDYCNDLKISDNNTEFLNNEFIDRKTNPNNPSCNADLNINRVLLDAG 698  
 Db 654 DNFEEGYFTIAPRDYCNDLKISDNNTEFLNNEFIDRKTNPNNPSCNADLNINRVLLDAG 713  
 QY 699 FTNELVQNTYWSKOKNIKGVKARFVVDGGITRVYPKEAGENQOENPETVEDSFYKRSLDN 758  
 Db 714 FTNELVQNTYWSKOKNIKGVKARFVVDGGITRVYPKEAGENQOENPETVEDSFYKRSLDN 773  
 QY 759 DNVYFTAPYFNKSGPGAYESGIMVSKAVEIYOGKLLKPAVVGIGIKIDVNSWIENFTKTSI 818  
 Db 774 DNVYFTAPYFNKSGPGAYESGIMVSKAVEIYOGKLLKPAVVGIGIKIDVNSWIENFTKTSI 833  
 QY 819 RDPGAGPVCDCRKNSDVMDCVTLDDGGFLLMANHDDYTNOIGRFFGEIDPILMRHLVNIS 878  
 Db 834 RDPGAGPVCDCRKNSDVMDCVTLDDGGFLLMANHDDYTNOIGRFFGEIDPILMRHLVNIS 893  
 QY 879 VYAFNKSVDYQSVCEPGAAPKOGAGHRSAYVPSVADILQIGWATAAAWSILQOFLLSIT 938  
 Db 894 VYAFNKSVDYQSVCEPGAAPKOGAGHRSAYVPSVADILQIGWATAAAWSILQOFLLSIT 953  
 QY 939 FPLLEAVEMEDDDFTASLSKOSCIETQOYFDFDNDKSFSGVLDGCGNCSRIHFHEKLMN 998  
 Db 954 FPLLEAVEMEDDDFTASLSKOSCIETQOYFDFDNDKSFSGVLDGCGNCSRIHFHEKLMN 1013  
 QY 999 TNLIFTMWSKGTCTPCDTRLLIIQAEQTSQDPDPCDMVKQPRYKRGDVCFDNNVLEDYTD 1058  
 Db 1014 TNLIFTMWSKGTCTPCDTRLLIIQAEQTSQDPDPCDMVKQPRYKRGDVCFDNNVLEDYTD 1073  
 QY 1059 CGGVS 1063  
 Db 1074 CGGVS 1078









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OM protein - protein search, using sw model

Run on: February 10, 2003, 14:13:50 ; Search time 9.75229 Seconds  
(without alignments)  
4520.920 Million cell updates/sec

Title: US-10-090-827-15

Perfect score: 5599

Sequence: 1 MAAGCLLALTLFLFQSLIG.....PDVCFDNNVLEDTDCGGVS 1063

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5599	100.0	1091	1	CIC2_HUMAN
2	5390	96.3	1091	1	CIC2_RAT
3	5380.5	96.1	1106	1	CIC2_RABIT
4	752.5	13.4	1205	1	YLJ9_CAEEL
5	607	10.8	734	1	UN36_CAEEL
6	194.5	3.5	886	1	ITB3_MOUSE
7	182	3.3	885	1	ITB3_HUMAN
8	180.5	3.2	887	1	ITB3_RAT
9	164.5	2.9	886	1	ITB3_MESAU
10	161	2.9	886	1	DPOL_THEST
11	159	2.8	1956	1	ATX1_PLAFA
12	157.5	2.8	575	1	YFBK_ECOLI
13	154.5	2.8	946	1	ITB2_HUMAN
14	152	2.7	1290	1	BXC1_CLOBO
15	151.5	2.7	420	1	Y103_SYNY3
16	150.5	2.7	921	1	ITB4_PIG
17	150	2.7	654	1	MCPC_BACSU
18	149	2.7	930	1	ITB4_HUMAN
19	148	2.6	964	1	DPOL_CHEPV
20	144	2.6	1087	1	YXNX_CLOTH
21	143	2.6	946	1	ITB2_MESAU
22	142.5	2.5	382	1	YLJ0_CAEEL
23	142	2.5	1169	1	SMC_METJA
24	141	2.5	1251	1	RB22_PLAVB
25	140.5	2.5	935	1	ITB2_PIG
26	140	2.5	2710	1	TOXA_CLODI
27	140	2.5	3305	1	APLP_WANSE
28	139.5	2.5	764	1	PAC_BACAN
29	139	2.5	1513	1	STU1_YEAST
30	138	2.5	1180	1	C4AA_BACTI
31	137	2.4	984	1	HVSA_STRAG
32	136.5	2.4	3063	1	CAIC_HUMAN
33	135.5	2.4	946	1	ITB2_MOUSE

## RESULT 1

ID	CIC2_HUMAN	STANDARD	PRT	1091 AA
AC	P54289;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta subunits precursor.			
DE	subunits precursor.			
GN	CACNA2D1 OR CACNL2A OR CCHL2A.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCHI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92110010; PubMed=1309651;			
RA	Williams M.E., Feldman D.H., McCue A.F., Brenner R.,			
RA	Velicelebi G., Ellis S.B., Harpold M.M.;			
RT	*Structure and functional expression of alpha 1, alpha 2, and beta subunits of a novel human neuronal calcium channel subtype.*;			
RT	Neuron 8:71-84(1992).			
RL	Neuron 8:71-84(1992).			
CC	- - FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN EXCITATION-CONTRACTION COUPLING.			
CC	- - SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS: ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).			
CC	- - SUBCELLULAR LOCATION: Integral membrane protein.			
CC	- - TISSUE SPECIFICITY: CENTRAL NERVOUS SYSTEM, SKELETAL MUSCLE AND AORTA TISSUES.			
CC	- - PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM A PRECURSOR FORM (BY SIMILARITY).			
CC	- - SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.			
CC	- - SIMILARITY: CONTAINS 1 VMFA DOMAIN.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL: M76559; AAA51903.1; -			
DR	Genew: HGNC:1399; CACNA2D1.			
DR	MIM: 114204;			
DR	InterPro: IPR004010; Cache.			
DR	InterPro: IPR002035; VWF_A.			
DR	Pfam: PF00092; vwa; 1.			
DR	Pfam: PF02743; Cache; 1.			
DR	SMART: SM00327; vwa; 1.			
DR	PROSITE: PS0234; VWF_A. 1.			
KW	Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;			
KW	Calcium channel; Glycoprotein; Signal.			
FT	SIGNAL 1 24			
FT	CHAIN 25 944			
FT	L-TYPE CALCIUM CHANNEL ALPHA-2 SUBUNIT			

P52340 human herpe  
O51737 borrelia bu  
P07248 saccharomyc  
P57210 buchnera ap  
Q91145 notophthalm  
P40457 saccharomyc  
O13773 schizosacch  
Q58611 methanococc  
Q58295 methanococc  
Q03661 saccharomyc  
Q58789 methanococc  
P5342 mycoplasma

## ALIGNMENTS

34	134.5	2.4	2077	1	TEGU_HSV6U
35	133	2.4	862	1	MUTS_BORBU
36	133	2.4	1323	1	ADRL_YEAST
37	132.5	2.4	547	1	SYM_BUCAL
38	132.5	2.4	929	1	CALC_NOTVI
39	132.5	2.4	1679	1	Y109_YEAST
40	132	2.4	697	1	YE9C_SCHPO
41	131.5	2.3	1018	1	YC14_METJA
42	131	2.3	1634	1	DPOL_METJA
43	131	2.3	1658	1	YM67_YEAST
44	130.5	2.3	987	1	YD94_METJA
45	129	2.3	1244	1	Y307_MYCPN



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QY 638 --PDNFEESGYTFTAPRDYCNLDKISDNNTFELLNENEF-IDRKTNNPSCNADLINRVL 694
Db 394 SLPSLVENKEI-----ENWONEIELDSSKAKINVKNFQVSVSTANPEYN-----L 442
QY 695 LDAGFTNE-----LVONYWSKOKNIKGVKARF--VVTDDGGITRVYP---KEAGENWQE 742
Db 443 IDGSLNVEVRISRDIQVKTRLSGLTKLDANLFDVAKANYSNOLPGNLKAKDTNFKF 502
QY 743 NPETYE-DSP-----YKRSILDN---DNYVFTAPY---FNKSGPGAYESG 779
Db 503 GERTFTDSEFELFKNAKENNSILNLYKLSLENVYKLNFSQVSEFVKFTKGTGKEKEN 562
QY 780 IMVSKAVEIYIOGKLL-----KPAVVGKIDVNSWIENFTKTSIRDPCAG 824
Db 563 VVSKKITNFKKDVLFDQYRYFDENDHFHKAIALTTKMTNREFIKK----- 610
QY 825 PVCDCKRNSDV 835
Db 611 -IVDARENDL 620

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Search completed: February 10, 2003, 14:22:31  
Job time : 27.2324 secs



variant-specific surface protein 1 - malaria parasite (Plasmodium falciparum) (fragments)  
N;Alternate names: erythrocyte membrane binding protein 1 (EMPI)  
C;Species: Plasmodium falciparum  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 20-Jun-2000  
C;Accession: T28155  
R;Rower, J.A.; Moulds, J.M.; Newbold, C.I.; Miller, L.H.  
Nature 385, 292-295, 1997  
A;Title: Plasmodium falciparum rosetting is mediated by PfEMP1 and requires complement 1  
A;Reference number: Z20477; MUID:97373957; PMID:9230440  
A;Accession: T28155  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-2706 <ROW>  
A;Cross-references: EMBL:Y13402; PIDN:CAA73831.1  
A;Experimental source: strain IT 4/25/5  
C;Genetics:  
A;Intons: 2493/3  
A;Note: R29R+var1

Query Match 2.9%; Score 161; DB 2; Length 2706;  
Best Local Similarity 18.2%; Pred. No. 0.77;  
Matches 183; Conservative 137; Mismatches 345; Indels 338; Gaps 46;

QY 36 WVDKMOEDLVTLAKTASGVNQLDVEKYQDLTYVEPNNA-----RQL 78  
DB 308 WFEWAEEFCRIKKI-----KLENVAKKCHD-----EPNNKYCSGDGHDCKRYLKDNTIF 358  
QY 79 VTAARDIEKLLSNKALVSLAEKVAQAHHQWREDFASNEVYVYNAKDDLDPEKND 138  
DB 359 IDLNCPCENACSNYK-----WIEIQKQFDKQKQK--YMNEI--KIKTNISNNENDK 408  
QY 139 E-----PGSQRIKPVFIEDANFGROIYSOHAHVHTDIYEGSTIVLNELNMTSALDE 191  
DB 409 EYENLDKKGYSTIN-TFLESNHGKQC-----DN 438  
QY 192 VFKNREDSLLWQVPGSATGLARYYPASP-----WVDNSRTPNKI 233  
DB 439 IDKKNKTFNNL-ETFGP-----SGYCEACPIYGVKCSKEKCPVTVENMNSNNRUPTOT 493  
QY 234 DLVDVRRRPWYIOGAASPKDMLLDVDSVSGLTILKLTISVSEMLETLSDDDFVNVAS 293  
DB 494 STKNLN-----ATNIDMLNDGIGNAI----- 515  
QY 294 FNSNAQVSCFQHLVQANVRNK-----VLKDAVNNTAKGIDYKGFSAFEQLL 345  
DB 516 --DNELEKNTKYGIKQKQWQCYLNNIDQCCKINNYMNSGYFDNKIAFNVLFQRL 573  
QY 346 NYNVSANCKIIMLFTDGGEEAAQEIFKNYKDKKVRVFRFSVQGHNYERGPIQWACR 405  
DB 574 RYFVRDNRLLK-----EKIDVCIKENINENICIKRCKTN-----CE 610  
QY 406 NKGYIYIPIPSIGAIRI-----NTQYLDVLGRPMVLADKAKQVQWNTVYLDALGLVIT 461  
DB 611 CVGKWLKKEAEWDKINHYNQKNHIMFILPYWITGFYEK-ITPNDFFKALE-----DV 665  
QY 462 GTLPVFNITQFENKMLKQILGVGVDSVLEDTKRLTPRTLCPNGYFFAIDPNGYV 521  
DB 666 DTINVLDTLRECOD-THCKIEKIRSI-DVDLIEIKIISLWQNKLEVECKS--HHDEDKHEYC 721  
QY 522 LLHPNLOPKPKSQEPVTLDFDAELNDIKVEIRKMKIDGESSEKT-----FRT 571  
DB 722 C-----DILPKSVDDDEUD-REVDEEKESSQTTKRN--ISQKGTGSASCVKGCACAIKVG 775  
QY 572 LKQSQDERYID-----KGNRTYTW-----TPVNGTD-----YSLALVLTYSF 609  
DB 776 VLOQKSGSIDNCNAKRNKNEQCKNTFVDGNEGVCMPPRRKSIQHNLTLLEQTKNK 835  
QY 610 Y-----YIKAKLETT-ITQARSKGKMKDSETLK-----PDNFEI-SGYFIAPRDYC--N 656  
DB 836 YQLREAFIKCAAKETNLWPKYKNDKNEABELLKKGKIPEDFRIMFYTFDFRDFCLEN 895  
QY 657 DL-----KISDNTEFLNFEIDRK-----TPNPNPC-NADLINRVLLDAGFTNEL 703

DB 896 DMGKDVVKVKNINKNFVNNSSKRGFKKIDPENWNNENGQIWNGLCALIHADTKDSIKN 955  
QY 704 VQNY-----W-----SKQNKIKGYKARFVW 723  
DB 956 KDNKYKVKVITILAKRDSNGMTLSEFAKKPFLRFWEVWDYCKERQKYLTEVASTCKS 1015  
QY 724 TDGGITRV-----YPEAGENQWENPETTDFYKSLDN-----DNVY- 762  
DB 1016 IDGQLKCDRCNCKCDEYKRYMKRKKKEENLQDKYKDKRENKGIDKPGIIGIIVKYVL 1075  
QY 763 -----FTAPYFNKSGPGAYESGIMVSKAVEIYIOGLLKPAPVVGIKIDVNSWI-- 810  
DB 1076 ANAKYLLAKKFTASCVTSSGKAQNSATPEVKKNIELLSEBY-----YDADQVCGC 1126  
QY 811 -----ENFTKTSIRDPCAGVCDCK-----RNSVMDVCVIL 841  
DB 1127 TKFIHDDKYSKISGRSNCGLNSDAKKNKIKWRNSDEKDYAFL 1169

RESULT 13  
A44396  
P-type cation translocating ATPase - malaria parasite (Plasmodium falciparum)  
C;Species: Plasmodium falciparum  
C;Date: 10-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jun-2000  
C;Accession: A44396  
R;Krishna, S.; Cowan, G.; Meade, J.C.; Wells, R.A.; Stringer, J.R.; Robson, K.J.  
J. Cell Biol. 120, 385-398, 1993  
A;Title: A family of cation ATPase-like molecules from Plasmodium falciparum.  
A;Reference number: A44396; MUID:93132070; PMID:8421054  
A;Accession: A44396  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: nucleic acid  
A;Residues: 1-1984 <KRI>  
A;Note: sequence extracted from NCBI backbone (NCBIP:122678)

Query Match 2.8%; Score 159; DB 2; Length 1984;  
Best Local Similarity 17.1%; Pred. No. 0.62; Indels 366; Gaps 45;  
Matches 179; Conservative 144; Mismatches 359;

QY 58 VDIEKYQDLTYVEPNNAQVLAARDIEKLLSNR-----SKALVSLALEAK 106  
DB 128 INVY-RYNTSYIASS-----ELVPGDIYEIKNNWTPTCDTIILSGVTSWHMLTGES 180  
QY 107 VQAHHQWREDFASNEVYVYNAKDDLDPEKND-----SEPGSQRIKPVFIEDANFGROI 160  
DB 181 V-PIHKEKLPFEGNAIINKNKYSDNDEKDDYLRINNHASINMKRNHLEETLGKKDR 239  
QY 161 YQHAHVHTDIYEGSTIVLNELNM-TSALDEVFKKNEEDPSSLWQVFGSATGLARYP 219  
DB 240 EYKSNH-----DLCSMKKLCYINNTYDDVHKNKMD----- 272  
QY 220 ASPWVDNSRTPNKIDLYDVRRRPWYIOGA-ASPKDMLLDVDSVSGLTILKLTISVSE 278  
DB 273 ---YNNNNNNKKKKKNNLN---PVKGTYSNNDLLY----- 303  
QY 279 MLETLSDDDFVNVASFNSNAQVSCFQHLVQANVRNKVKLVDAVNNTAKGIDYKGFSA 338  
DB 304 -----DDKIGVNIFE--DDVNNMKH--KFNQNRINNYKNDTNL-----EYNNKHR 345  
QY 339 FAFEOALLNVNVRANCKIIMLFTDGGEEAAQEIFKNYKDKKVRVFRFSVQGHNYERG 398  
DB 346 YIYDCLLKKVEAISOKNLIY-----SNEDINKY----- 374  
QY 399 IQWACENKGYIYEIPISGAIRINTQYLDVLGRPMVLAD-----DKAKQV 444  
DB 375 ---MLYGGTYVLSLYNINKYNNKKEENRILGL-VIKTGFITTKGKIVNNILYHKKREL 429  
QY 445 QWNTVYLDALGLVITGTLPVFNITQFENKTNLKNQLILG-----V 487  
DB 430 NLINDSYKFLIT-LIYALFSVFIILYITLSNNEYTHIIKCLDIITDAIPALPTILT 488  
QY 488 MGVDSVLEDKRLTPFTLCPNGYVFA-----IDPNGYVLLHPNLO-----PKNPKSQ 535

RESULT 12  
T28155

QY 758 NDNYVETAPYENKSGAYESGIMYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTS 817  
Db 695 NASSRTGTYYGKLGITANWDMDFVEVTEKILIG-----TGAELSTFSLWLDFTVTQ 747  
QY 818 INDCAGPVCDCRNSDMCVILDDG-GFLLMAN-----HDDYTNQIGRFFGEIDP 868  
Db 748 -----TGLSVTINRKNKNV--VSFGDGSFVILHQQWKKHPVHQDFLG-----FYVVD 795  
QY 869 SLMRHLNINISYAFNKSYDYSV-CEPGAAP 898  
Db 796 HRMSAQTHGLLGQFFPDPFKVFGIRGSDP 826

RESULT 9  
S30350  
Inter-alpha-trypsin inhibitor heavy chain 3 precursor - human  
N:Alternate names: HC3; inter-alpha-trypsin inhibitor chain H3; pre-alpha-inhibitor heavy chain H3  
C:Species: Homo sapiens (man)  
C:Date: 03-May-1994 #sequence.revision 20-Feb-1995 #text.change 04-Feb-2000  
C:Accession: S30350; S34123; S02141; D34245; A39079; S50133; B53642; A59167  
R:Bourguignon, J.; Diarra-Mehrpour, M.; Thiberville, L.; Bost, F.; Sesbouee, R.; Martin, Eur. J. Biochem. 212, 771-776, 1993  
A:Title: Human pre-alpha-trypsin inhibitor-precursor heavy chain cDNA and deduced amino-acid sequence  
A:Reference number: S30350; MUID:93215656; PMID:7681778  
A:Accession: S30350  
A:Molecule type: mRNA  
A:Residues: 1-885 <BOU1>  
A:Cross-references: EMBL:X67055; NID:g288562  
R:Bourguignon, J.  
A:Submitted to the EMBL Data Library, June 1992  
A:Reference number: S34123  
A:Accession: S34123  
A:Molecule type: mRNA  
A:Residues: 1-310, 'K', 312-343, 'R', 345-885 <BOU2>  
A:Cross-references: EMBL:X67055; NID:g288562; PIDN:CAA47439.1; PID:g288563  
R:Diarra-Mehrpour, M.; Bourguignon, J.; Sesbouee, R.; Mattel, M.G.; Passage, E.; Salier, Eur. J. Biochem. 179, 147-154, 1989  
A:Title: Human plasma inter-alpha-trypsin inhibitor is encoded by four genes on three chromosomes  
A:Reference number: S02141; MUID:89137072; PMID:2465147  
A:Accession: S02141  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 341-356, 'G', 358-845, 'H', 847-885 <DIA1>  
A:Cross-references: EMBL:X14690; NID:g35464; PIDN:CAA32821.1; PID:g35465  
R:Englund, J.J.; Thogersen, I.B.; Pizzo, S.V.; Salvesen, G.  
J. Biol. Chem. 264, 15975-15981, 1989  
A:Title: Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-alpha-trypsin inhibitor  
A:Reference number: A92736; MUID:89380192; PMID:2476436  
A:Accession: D34245  
A:Molecule type: protein  
R:Englund, J.J.; Salvesen, G.; Hefta, S.A.; Thogersen, I.B.; Rutherford, S.; Pizzo, S.V.  
J. Biol. Chem. 266, 747-751, 1991  
A:Title: Chondroitin 4-sulfate covalently cross-links the chains of the human blood protein inter-alpha-trypsin inhibitor  
A:Reference number: A39079; MUID:91093267; PMID:1898736  
A:Accession: A39079  
A:Molecule type: protein  
A:Residues: 631-647 <ENG2>  
R:Diarra-Mehrpour, M.; Bourguignon, J.; Sarafan, N.; Bost, F.; Sesbouee, R.; Muschio-Boncompagni-Ludovisi, F.  
Biochim. Biophys. Acta 1219, 551-554, 1994  
A:Title: Tandem orientation of the inter-alpha-trypsin inhibitor heavy chain H1 and H3 genes  
A:Reference number: S50132; MUID:95002176; PMID:752274  
A:Accession: S50132  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-27 <DIA2>  
A:Cross-references: EMBL:X75318  
R:Wisniewski, H.G.; Burgess, W.H.; Oppenheim, J.D.; Vilcek, J.  
Biochemistry 33, 7423-7429, 1994  
A:Title: TSG-6, an arthritis-associated hyaluronan binding protein, forms a stable complex with inter-alpha-trypsin inhibitor  
A:Reference number: A53642; MUID:9427199; PMID:7516184  
A:Accession: B53642  
A:Molecule type: protein

A:Residues: 30-34, 'X' <WIS>  
R:Jessen, T.E.; Faarvang, K.L.; Ploug, M.  
FEBS Lett. 230, 195-200, 1988  
A:Title: Carbohydrate as covalent crosslink in human inter-alpha-trypsin inhibitor: a new type of crosslink  
A:Reference number: S02431; MUID:88167187; PMID:2450785  
A:Accession: A59167  
A:Molecule type: protein  
A:Residues: 30-32, 'GEKEQAVDT' <JES>  
C:Comment: As pre-alpha-inhibitor, this protein is covalently cross-linked by chondroitin sulfate  
C:Genetics:  
A:Gene: GDB:ITIH3  
A:Cross-references: GDB:120109; OMIM:146650  
A:Map position: 3p13-3p12  
C:Superfamily: inter-alpha-trypsin inhibitor complex component II  
C:Keywords: chondroitin sulfate proteoglycan; glycoprotein; heterodimer; proteinase 1  
F:1-19/Domain: signal sequence status predicted <SIG>  
F:20-29/Domain: propeptide #status predicted <PRO>  
F:30-647/Product: inter-alpha-trypsin inhibitor heavy chain 3 #status experimental <M>  
F:648-885/Domain: carboxyl-terminal propeptide #status predicted <CTP>  
F:87,576/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:647/Modified site: chondroitin sulfate ester carboxyl end (Asp) (in mature form) #s

Query Match 3.3%; Score 185; DB 2; Length 885;  
Best Local Similarity 20.4%; Pred. No. 0.0048;  
Matches 133; Conservative 106; Mismatches 243; Indels 170; Gaps 33;

QY 27 FPSAVTIKSWVDKMQEDLVLTAKTASGVNQLVDIYKQDLYTVPNNARQLVEIAARDI 86  
Db 97 YPGNVKKEVAKKQYKAVSOGKTAG-----LVKASGRKL 131  
QY 87 EKLLSNRSKAL---VSLALEAKVQNAHQWRDEFASNEVVYVYNAKDDLDPEKNDSEPSGS 143  
Db 132 EKFTSVNVAAGSKVTFELTYELLKRHRGK-----YEMYLKVQPK-----Q 173  
QY 144 RIKPVFIEDANFGQISYQHAHVPIIDIEGSTIVLNLNWTLSALDEVKKNREDSLSL 203  
Db 174 LVKHEFIE-----VDIFEQGISMDAEASFITNDLL-----GSA 208  
QY 204 LMQVFGSATGLARYYPASPWVDNSRT-PNKID-----LYDVRRRP-----WY 244  
Db 209 LTKSFGKKGHVSKFPS---LDQSCPTCTDLSLLNGDFTITYDVNRESPGNVQVNGYF 265  
QY 245 I-----QG-AASPCKMLIIVDVGSGVGLTKLRTSSEMLETSSDDDFVNVASFNSNA 298  
Db 266 VHFAPQGLPVVPKNNVAFVIDISGSMAGRKLEQTKLEALLRILEDQEEEDYLFILFSG-- 323  
QY 299 QDVSCF-QHLVQANVRNKKVLKDVANNITAKGITDYKKGFSFAFQLLNYNVSR----- 351  
Db 324 -DYSIWKEHLVQATPENLOEATFKVSKMEDKGTNINDGLLRGISM---NKAEREHRIP 379  
QY 352 ANCNKIIMLFTDG---GEERAQEIFNKYNK--DKKVRVRFVSQGHNYERGPQIWMACE 405  
Db 380 ERSTSIIMLTGCDANVGESRPEKIQENVRNAIGCKFPLNGLFG--NNLNYNFLENMALE 438  
QY 406 NKGYEYIPEISGAIRINTEYLDVLRPMVLGADKAKQVQWNTVYLDALD-----L 456  
Db 439 NHGFARRYEDSDADQLQGGFYEEVANPL-LTGVEMEYPE--NAILDLTQNTYQHFYDGS 495  
QY 457 GLVITGTLTPVFNITQGFENKTNLK-----NOLILGMGVVDVSLDILKLTTPRFTLCPNGY 511  
Db 496 EIVVAGRL-VDEDMNSF--KADVKGHGATNDL---TTFEEVDKMEKEK-----ALQERYD 544  
QY 512 YFAIDPN-----GVVLHPNLOPK---NPKSQEPVTLDFDAELENDEKVEIRNKMIDG 562  
Db 545 IFG---NVIERLWAYLTIEQLLEKRNKHAKEKNTARALDLSLKHVFTPLTSMVVTK 601  
QY 563 ESEGTERTLVKSQDERYI-DKGNITYTWTVPV--GTDYSLALVLTPTSYFYI 612  
Db 602 PE-----DNEDERATADKGEAEATPVSPAMSVLTSTYQPPQNPYYV 644

RESULT 10  
D97033



QY 128 KDDLPKNDSEPGSRIKP-----VFIEDANFGQISYQHAHVH----- 167  
Db 181 EEVLNNSSQEEVTSQKDKSOLAFSPNSFGIKASFNDAQNYENISPEYRQDETGISP 240  
QY 168 -----IPTDIYEGSTIVLNLNMTSALDVEFKNREEDPSLLMQVGSATGLARYYPASPW 223  
Db 241 NBSWIFT-----GNTTVVNHQGNF-----SSQMDGVNSWN--GEATNLSNIEYAG 287  
QY 224 VDN-----SRTPNKIDLY--DVRREPWIYQGAAPKMDLILVDVSGVSGLTG 270  
Db 288 VNNPVDFAKRYAKETETGLDVLNVRGN---VQNPPIKPDIVLIVDMSGMOGAKET 344  
QY 271 LIRTSVMELETSSD---DFVNV--ASPNNAQDVSCFQHLVQANVRNKKVLKD---A 321  
Db 345 AVRQGVDSFSLTQNTAYADYVNVGVIGVSPGNVTGASGYITVPI--DKVSSSHSVKS 402  
QY 322 VNNITA---KGITDKKGSFAFEOLLNLYNVRANCKIIMLFTDGGEEAQAQEIFKNYK 378  
Db 403 INOALAPOFSGCTFTQLGLRKGTML---EODSSDNQKMMILMTDG---VPTFSYKVS 455  
QY 379 DKVR--VFRFSVGHQNYERG---PIQ---WMAKENKGYEIEI-----PSIGAIRINTQE 425  
Db 456 ASKVDNVIYQGSFAESROEPGNTSIQSPYVKDINGSGNIEIRDTWAATLGEAEISKQE 515  
QY 426 YLDVLCRPMVLADG-----KAKQVQNTVYLDLLEGLVITGLTLPVFNITGQFE 474  
Db 516 ISEIHTLQIGLNDGYSIQEVEKSRSTSLIATGTGLYQDANSAN-----DITDYLK 565  
QY 475 NKTN-----LKNQILGVMGVDVSLIEDIKRLTPRTCLPNGYFAIDPNGVYLLHPN 526  
Db 566 NQANVLSRFNTITNGLILPLGAQFEYKDK-----FEITSVG----- 604  
QY 527 LQPKNPKSQEPVTLDFLDAELNDIKVIRNKMIDGESGKTFRTLYKSQDERYIDKGNR 586  
Db 605 -----EDSIDNLPKTKINEKLEISNLNI--GKNOEQVQIHYQVRLNLTETDDEFTNY 653  
QY 587 TY-----TWTPVNGT--DYSIALVLPTYSPFYIKAKLE-----ETIQASKK 627  
Db 654 WYQMGNETLTP--NGSNDPNKVNCPVSAKSSGNLTKLQWLANSENIPIVENVELLIGRR 712  
QY 628 GKMKDSE-----TLKPDNFESSGYTTIAPRYCNDLAKISDNNTFLLNFEFIDRKTPNN 682  
Db 713 SAQISSDWTKTWTKEDDEWRSQLENLPKYSILGEEFYIEIKDEIVLN--SEIYDMITIGE 771  
QY 683 PSCNADLNRYLLD---AGFTNELVQWYKQKNIKVKARFVVTGGITRVYPKAGE 738  
Db 772 DKTIANIEKRLQIKTNSHDNEPLSEVEFVLKNSQGEIEIDKAVTN-----EKGE 822  
QY 739 --NWOENPTYEDSFYKRSNDNDNTVFTAPYFNKSGPGAYESGIMVSK-----AVEYIQ 791  
Db 823 ILFDKTRLNYYGEEYQHEIKSPGHSLEGPKIKT---EFENGQPIIKVDGEQIALDEHYN 879  
QY 792 GKLLKPAVVGKIDVNSWIEFTKTSIRDPACBPVCDCKNSVMDCVILD-----DG-- 844  
Db 880 KFMIS---LNTINDIN--VEEF-----RNSVTIDKRAVDSEKLDGAV 917  
QY 845 --GFLLMANHDYTNQIGRFFGEIDPSLMRHLVNIISVAFNKSVDYQSVCEPQAPKQAG 903  
Db 918 FNLQIESVDDELQQLPL--EITNNLPLG-----YALQSVSPNGYRDEY 964  
QY 904 H--RSAYVPSVADILQIGWATAAASILQOFL-----IDIPFLDENESGKGLVNLNEENGDLHLILFY 939  
Db 965 HFRVFKNGSIVAIGSEG-----IDIPFLDENESGKGLVNLNEENGDLHLILFY 1015  
QY 940 ---PRLEAVEMEDDDFTASLSKQSC--ITEQYQFYDNDG-----KSFSGVLDCGNCRSI 990  
Db 1016 NQAVPPLQLEVDKIDDDFTPLAGVSEFELTLGRKSTDSVSRKINSFDRILKTFN--NE 1073  
QY 991 FHGEKL--MNTNL 1001  
Db 1074 FTGETIALKSNL 1085

## RESULT 8

S54355

inter-alpha-trypsin inhibitor heavy chain 3 precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 04-Feb-2000

C:Accession: S54355

R:Chan, P.; Risler, J.L.; Raguenez, G.; Sallier, J.P.

Biochem. J. 306, 505-512, 1995

A:Title: The three heavy-chain precursors for the inter-alpha-inhibitor family in mou

A:Reference number: S54353; MUID:95194326; PMID:7534067

A:Accession: S54355

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-886 &lt;CHA&gt;

A:Cross-references: EMBL:X70393; NID:9695635; PIDN:CAA9843.1; PID:9695636

C:Superfamily: inter-alpha-trypsin inhibitor complex component II

## Query Match

Best Local Similarity 3.5%; Score 194.5; DB 2; Length 886;

Matches 185; Conservative 138; Mismatches 347; Indels 261; Gaps 44;

QY 27 FPSAVTIKSWDKQEDLVILAKTAGVGNOLVDIYEKYQDLYTVEPNARQLVEIAARDI 86

Db 98 YPGNVKKEVAQKQYKAVSQGTAG---LVKASGRKLEKFTSVNVAAGSKVTTELTY 153

QY 87 EKLISNRKALVSLALEAEKVAQAAHWRDFASNEVVVYNAKDDLDPEKNDSEPGSORIK 146

Db 154 EELL-KRNGKYMVLKQPKQLVRHFEID-----AHIFEP-----Q 189

QY 147 PVFIEDANFGQISYQHAHVHPTDIYEGSTIVLNLNMTSALDVEFKNREEDPSLLMQ 206

Db 190 GISMLDAE-----ASFITNDL-LGSALTKEF----- 214

QY 207 VFGSATGLARYYPASPWVDSNRTPKID-----LYDVRRRP-----WYI-- 245

Db 215 ---SGKKGHVGFPSLDQQRSCPTCTDLSLLNGDFTIVYDVNRSPGNVQIVNGYFVHF 269

QY 246 ---QG-AASPKMDLILVDVSGVSGLTGLKIRTSVSEMLETSLDSDFFVAVASFNQAQV 301

Db 270 FAPQGLPVVFKNIVFVIDVSGSGRGIQOTREALLKILDDVEDDYILNLFIST---DV 326

QY 302 SCFQ-HLVQANVRNKKVLDVANNITAKGTDYKKGFSFAFEQLLNNYSRAN-----C 354

Db 327 TTWKDHLVQATPANLKEAKTFVKNIHQDSMTNINDLLKGIEML---NKAREDHVTPERS 383

QY 355 NKIIIMLTGQ---GEERAQEIFKNYK--DKKRVFRFSVGHQNYERGPQIOMACENKG 408

Db 384 TSIIMLTGDDANTGESRPEKIQENVRNAIGGKFPYLNIGFG--NNLYNFLETALENHG 442

QY 409 YYEIPISGAIRINTQEYLDVLGRPMVLADGKAKQVQNTNVYLDLLEGL---VITGTLVP 466

Db 443 LARRIYEDSDANLQGFVEEVANPLL-----TNVEVEYPENAILDLTRNSYPH 491

QY 467 ENITGOFENKTNKQILGVGMGVDSLEDIKRLTPRTCLPNGYFYFADPNGYVLLHPN 526

Db 492 F-----YDG-----SEIVVAGRLVDRNMDN-----FKADVKGHCALN-- 523

QY 527 LQPKNPKSQEPVTLDFLDAELNDIKVIRNKMIDGESGK--TFRTLYKSQDERYIDKG 584

Db 524 ---DLTFTTEEDVMEEMDAALK-----EOGYIFGDIYERLWYLTIEQLLEKRNKAG 572

QY 585 NRTYTWTPVNGVYDYSIA--LVLPYTSFYIYKAKLETITQARSKKGMKDSFT-----LK 637

Db 573 DEKENIT-AEALDLSLKYHFVTPLTSMVVTKEPDNEDQTSIADNAGEAFAFTTMSFLT 631

QY 638 PDNFEESGVTFTAPRDYCNLDLKSNDNTEFLNFEIDRTKTPNPNPSCNADLINRVLLDA 697

Db 632 TQOSQSPIYVV-----DGDPHFIQI-----PGKNDSCIFNIDEKP 668

QY 698 GFTNELVQWYKQKNIKVKARFVVTGGITRVYPKAGEANQWQENPETYEDSFYKRSLD 757

Db 669 GIVRLIQD-----PVT--GIT-VTQGIIGD-----KRS-- 694

## RESULT 6

T18770

probable calcium channel protein - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 29-Oct-1999

C;Accession: T18770; T25249

R;Sulston, J.

submitted to the EMBL Data Library, June 1995

A;Reference number: Z19019

A;Accession: T18770

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1148 &lt;W1&gt;

A;Cross-references: EMBL:Z49907; PIDN:CAA90091.1; GSPDB:GN00020; CESP:T24F1.6

A;Experimental source: clone B0491

R;Chui, C.

submitted to the EMBL Data Library, June 1995

A;Reference number: Z20004

A;Accession: T25249

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1148 &lt;W1&gt;

A;Cross-references: EMBL:Z49912; PIDN:CAA90141.1; GSPDB:GN00020; CESP:T24F1.6

A;Experimental source: clone T24F1

C;Genetics:

A;Gene: CESP:T24F1.6

A;Map position: 2

A;Introns: 91/2; 131/3; 170/3; 283/1; 322/2; 410/3; 487/1; 563/1; 602/3; 654/3; 683/3; 7

## Query Match

Best Local Similarity 10.4%; Score 580.5; DB 2; Length 1148;

Matches 244; Conservative 217; Mismatches 437; Indels 251; Gaps 43;

Qy 37 VDKMQEDLVTLA-----KTASGVNQLVDIYKQDLYTVPEPNARQLVEIAARDI 86  
Db 99 VDTIEEPASIAQFSANTILDFOTFSFLVQEEFKLPDIKSKEDAEKLVATEHL 158  
Qy 87 EKLNSRSKALVSLAEAEKQAAHQRDFASNEVYVYNAKDDLPDPEKNDSEPSQR-- 144  
Db 159 DRLVTNRVDALKKLASSAEAAVF-----DEYDQAVAVPQADKRCE 201  
Qy 145 --IKPVFTEDANFGRIQSYQH---AAVHIPDIYEGSTIVLNLNLTSA--LDEVFKNR 197  
Db 202 AYMKMNSDMHFVSNM--VEHNSKSGIHITVESYQCDPRVMRDFDTGTHLEKTMDSNK 260  
Qy 198 BEDPSLLMQVFGSATGLARYYPASPVDNSRTPNKKIDLYDVRPPWYIQAASPKDMLIL 257  
Db 261 EKAPEMGHQYIGTYSGLTRMTPRRH--KVEPTITIDLFDPRFPWFVNAESVPKDIVFL 319  
Qy 258 VDVSQSVGLTKLIRTSVSEMLETSDDDFVNVAFSNSAQD--VSCFOH--LVQANYRNK 315  
Db 320 LDYSGSVKGPMTMLIKITMMYILSTLSPNDYFFGYENNHNENPIISCANRTFMPATTSNK 379  
Qy 316 KVLDAVNNTAKGTDYKKGSTAFEOQ---LNVNVS-----RANCKIIMLTGDGEE 367  
Db 380 KYFFELGMLKEKDAQHATPLKFSLDVLRGNLDSNLSFLADYKSEGHKLLIIFTDGVE 439  
Qy 368 RAQEFN---KYNKDKVFRFVSQGHNYERGPLOMACENKGYVEIPISGAIRNTQ 424  
Db 440 WPHQLDLEFQTRNSELIRIFGFSMGYGTSLPLQOYNACKSHGGYSEIDSMVQKQSR 499  
Qy 425 EYLDVLRPMVLADKAK-----QVQWNTVNYLDALBELGVITGTLPVFNITQFNKNT 477  
Db 500 TIQNVLSQ---VRGDELKGTNAEKREPSWTQLYMETQGTGPIVTLSPILF-----SQR 551  
Qy 478 NLKNQLILGVMGVDYSLIEDIKLPRFTLCPNGYFYAFDPPGYVLLHPNLQ--PKNPX--- 533  
Db 552 IWRDQKLAGVAIDISIKFTKHLB--TSSEOMYGYVDNNMGLIYHPQLQIPKTEVHCV 609  
Qy 534 -----SQBPV-----TLDFLDAELENDIKVEIRN 557  
Db 610 RRSACYDAQVQKQKAGSLRVHYGSDERYVLVGLIDSIPTLMDYLEDGSTAIRDLRR 669

Qy 558 KMIDGESSEKTRTLVKSQDERYIDKGNRTYTWTPVNGCTDYSLALV--LPTYSFYIYKAK 615  
Db 670 -----RITTKCYEEAIAKDSKEYHCSHIKDSPTLVIVNNIOLKTVYDDSV 717  
Qy 616 LEETITQ-----ARSKKGMKDSITLKPDNFEESGYTFIAPRDYC--NDLKISDNT 665  
Db 718 QELGLTDNKLVTFFYPRRDVCQWKILDEYAAHFRV--WSDISEKEICAQDDMRUPRAFT 775  
Qy 666 EFLNFNEFIDRKTNPNSCNADLINRVLLDAGFTNELVQNYWSKQNKIKGVKARFVVTD 725  
Db 776 KGLSWTQSWPKASDIEHTC-----LLAQYPENASVPHVNS-----FVHTR 817  
Qy 726 GQITRYYPKEAGENQENPEYEDSFYKRSLDNDNYVFTAPYFNKSGPGCAYESGLMWSKA 785  
Db 818 SKLTAFYPTCSSHDMKAVNKKFDEEI--KLTDNDFV---QFSMR-----SESLIYRT 866  
Qy 786 VELYIQGKLLKPAVVGIKIDVN---SWIENFTKTSIROPCAGVCDCKRNSD-----VMD 837  
Db 867 IADYDNNRL---AVGTQWKENFFDOYDFNFT-----RQNDPWKICRQOE 908  
Qy 838 CVILDDGGFLLMANHDDYTNOICRFFGEIDPSLMRHLNIVSYAFNKSVDYQSVCEPGAA 897  
Db 909 CSIIITNGHVIASSAHRAPAHAKF---DPQLESYLVKNLVSTNSWTEVQSECK---- 960  
Qy 898 PKQAGHRSAYVPSVADILQIGWNATAA--AWSILQOQLLSLTFFPRLLEAVEMEDDDFTA 955  
Db 961 -----AKRVAPWSAAPGSSSILRYFTST-----FKLAKTSFWR 995  
Qy 956 SLKSQSCITEQYQYFDNDKSFSGVLDGCGN--SRIFHGKELMNTNLIFIMYESGTC-- 1012  
Db 996 NLLESALTLDVDAQPSMTGCTCFQIKPFERCFMFFHYRMTLNTK--QLQITGMSCTSR 1054  
Qy 1013 -----PCDTRLIIQAEQTSQGNP-----CDMVQKQPRYKGPDPVCFD--N 1050  
Db 1055 YAKLYPVPVHTLSLIADRACQYRKRIFSEPRKLEKCDVY--HSHARRRRDALNDWKI 1113  
Qy 1051 NVLEDTDC 1059  
Db 1114 DLQNKHVD 1122

RESULT 7  
C86880  
hypothetical protein yvcC [imported] - Lactococcus lactis subsp. lactis (strain IL140  
C;Species: Lactococcus lactis subsp. lactis  
C;Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001  
C;Accession: C86880  
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Eh  
Genome Res. 11, 731-753, 2001  
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis  
A;Reference number: A86625; MUID:21235186; PMID:11337471  
A;Accession: C86880  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1450 <STO>  
A;Cross-references: GB:AE005176; PID:g12725093; PIDN:AAK06141.1; GSPDB:GN00146  
A;Experimental source: strain IL1403  
C;Genetics:  
A;Gene: yvcC

Query Match 3.5%; Score 198; DB 2; Length 1450;  
Best Local Similarity 21.0%; Pred. No. 0.0017;  
Matches 242; Conservative 149; Mismatches 439; Indels 322; Gaps 56;

Qy 37 VDKMQEDLVTLAKTAGVNQVDIYKQDLYTVPEPNARQLVEIAARDIEK-----L 89  
Db 69 INKTENDKELKLFSEGNQPIEEE--NESWTLKEKNT-----IISDFEKENEKIVL 120  
Qy 90 LSNRSKALVSLAEAEKQAAHQR--EDFA-----SNEVYVNA 127  
Db 121 RANNSISLLNLEIQADAKLIENDQEVISEDILAKESTIFSLYIPENNKADSKDKNT 180

Db 14 ASALLA-TALLYAALGDVVRSQQIPLSV-VKLWASATGGEIKSTAAYKSGSLLQKKYK 71  
QY 63 KYODLYTVPNNAROLVETAEADIEKLLSNRSKALVSLALEAEKVOAAHQWREDFASNEV 122  
Db 72 EYKDVAIETDGLQVLKLAIMEFHKSEAVRRVLEAAEAAHLKHEFDADL---QY 128  
QY 123 VYNAK---DDLPEKNDSPGSRQIKPVFIEDANFR-QIYSQHAHVHPTDIDYEGSTIV 179  
Db 129 EYFNVLINERDKGNFLEKGEFI---LAPNDHFNLPVNLISLDVQVPTNMVKNKDAPI 185  
QY 180 LNELNWTSDALDEVFKKNEEDPSLLWQVFGSATGLIARYYPASPWWDSNRTPKNIDLYDVR 239  
Db 186 VNGVYVSESLNKFVDFNEDRPSLIQVFGSAKGFPGIKWEPDE---NGVIAPDCR 242  
QY 240 RRPWYIOGAASPKMLILVDVSGSLTGLKIRTSVSEMLETSLDSDFFVNVASFNSAQ 299  
Db 243 NRKWTIOAATSPKVVILVDVSGMKGLRLTIAKTQVSSILDTLGDGDDFFNIITYNERLH 302  
QY 300 DYS-CFO-HLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAPEQLLNNVSRAN--CN 355  
Db 303 YVEPCLNGTLVQADRTKEHREHLDKLFAKIGIMLDTALNEAFNLSDFNHTQGGSTCS 362  
QY 356 KIIMLFTDGGERAQEIKNYN-KDKKVRVPFVSQGHYERGPVQWACENKGYEYIEP 414  
Db 363 QAAILITDCAVDYDTIFAKYNWDPKRVIRIYTLIGREAFADNLKMACANKGFFQIIS 422  
QY 415 SIGAIRINTQEVLDVLRPWLADGAKAQVQWTVNYLD-----ALEGLVI--TGT 463  
Db 423 TLADVOENMEYHLVLRPKVI--DOEHVVMTEAYIDSTLPQAQKADDDQGLVMTTVA 480  
QY 464 LPVFNITQFENKTLKQLILGVGVGVDSLEDIKRLTPRETLCPNGYFAIDPNGYVILL 523  
Db 481 MEVFS---KQNETSKG-ILLGVGTDVPVKELKIPKYLGIHGFATNNGVILT 535  
QY 524 HNLQOP---KNPKSQEP---VTLDLDAELENDIKVEIRNKMIDGESGEKTFRTLVKSQDE 578  
Db 536 HPELRPLYEKGKRRKPNYSVDLSEVBEWEDDDV-LRNAMVNRKTKC--FSMEVK---- 588  
QY 579 RYIDKGNRT-----YTWTPVNGTDSLALVLPY-YFYYIYKALEETITQARSKKGMK 631  
Db 589 KTVDDKGRVLMVNTDYYTDYDKGTPFSLGVALSRGHGKYFP-----RGNVT 634  
QY 632 DSETLKPNFESGYTFIAPRDYCN-DLKISDNNTFELNNEFIDRKTNNPNSCADLI 690  
Db 635 IEEGL--HDLEHPDVSADSEYCNLDLHPEHRHLSQLEALKLKGKEP-LLOCDKELI 691  
QY 691 NRVLDAFTNELLVONYWS-----KOKNIKVKAREVVTDDGGITRVYP----- 733  
Db 692 QEVLFDA-VVSAPTEAVYNTSLANKSENSDKGVBAFLGTHTGLSRINLFGARQLTNQD 750  
QY 734 -KEAGENQWENPETYEDSFYKRSIDN-DNYVFTAPY-----FNKSGGAYESGLMWKAV 786  
Db 751 FLKAGDKENIFNADHFFPLWYRRAAEQIAGSFYSIPESTGTGVNKS-----NVYTA 804  
QY 787 EYIQGKLLKPAVYGIKIDVNSWENETKTSIRDPGAPVCDCKRNSDVMDVCDLDDGGF 846  
Db 805 QLLDERKSPVVAAGVIOKMLEFFORKEFTWTSARQCASLDGKSCSDDETVCYLLDNGF 864  
QY 847 LLMANHDDYTNOIGRFFGEIDPSLMRHLNIVSYAFNKSVDYQSVCPGAPKQAGHRS 906  
Db 865 ILVS--EDYT-OTGDFEVEGAVMKNLLTWSGFKRTLLDYQAMCR--ANKESSDAH 918  
QY 907 AYPVSADILQIGWATYAAWISILQOFLSLTPRLLLEAVEMEDDDDTASLK----- 961  
Db 919 GLDDPYKAFL-----SAAKWIMTELVLFLVEF-----NLCSWNHSDMTAKAQLKOTLEP 968  
QY 962 CITQOTQVFFDNDKSFSGVLDGNCISIFHGEKIMNTLIFIMWESKGTCPDCTRLIIO 1021  
Db 969 CDTEYPAFVSERTIKETGNIACEDCSKFSVIOQIPSSNLFMVVVDV--SCLCESVAPIT 1026  
QY 1022 AEQTSDCPN---PCDMVKQPRYKGPVDCFDNNVLEDYTDGCGVS 1063

Db 1027 MAPIEIRYNBSLACERLKAQKIRRRPESCHGFHPENARECGGAS 1071

RESULT 5  
S44617

C50C3.11 protein - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 30-Jun-2001

C:Accession: S44617

R:Favella, A.D.

submitted to the EMBL Data Library, May 1993

A:Description: Sequence of the C. elegans cosmid C50C3.

A:Reference number: S44627

A:Accession: S44617

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-734 <PAV>

A:Cross-references: EMBL:L14433; NID:g289649; PID:g289650

C:Genetics:

A:Introns: 24/2; 87/3; 175/1; 259/1; 290/3; 346/3; 460/3; 538/3

Query Match 10.8%; Score 607; DB 2; Length 734;

Best Local Similarity 26.6%; Pred. No. 1.5e-28;

Matches 180; Conservative 127; Mismatches 258; Indels 112; Gaps 20;

QY 47 LAKTASGVNQLVDIYKYQDLYTVEPNNARQLVEIAARDIEKLLSNRS----KALVSLAL 102

Db 36 MKETFSKISHETILKQNYEKLVEEQDFPRAELKSKHRIEDYLVKRSQFAYKAKIS--L 93

QY 103 EAEKVQAAHQWREDFASNEVYVYNAKDDLDPEK-NDESPGSQRIKP-----VFIEDANP 155

Db 94 EASVRNDSTVNDPQSKSFIRFMSAKQGGDGTIYIENHLGKRLKYNETKSPNLTQANF 153

QY 156 -GRQISYQHAHVHPTDIYEGSTIVLNEINWTSALDEVEFKKNEEDPSLLWQVFGSATGL 214

Db 154 YTLPTSSVSSAVHIPPLYDRNEDLLRKIDW-SDIDAVYRTNEETKDLAFQFCSEAY 212

QY 215 ARYPASPWV-DNSRTPNKILDYVRRRPWYIOGAASPKMDLILVDVSGVSGSLTLKLR 273

Db 213 MRYTPAASFWDNQ--DEHLDLDFCRNTEWYINSATNSKNVLMIDWMSGMLGQRYEVAK 270

QY 274 TSVSEMLETLSDDDFNVVASFNSNA---QDVSCFQHLVQANVRNKKVLKADVANNITAKGI 330

Db 271 OTTEALLETLSHNDYFNIMFTFSKNTFLDGCNGTNGLLQATMRNKKALRRKMDTYQSEK 330

QY 331 TDYKKGFSFAFEOQLLNN-----VSRANCKIIMLFTDGEERAQOEIFNKYNKDKKRVYF 385

Db 331 AEYEKALPLAFSVLLDINNNGGDNNGACENVIMLITDGPANAYKIFDMYNADKKRVYF 390

QY 386 RFSVGQHNTERGPIQWACENKGYEYIEPSIGAIRINTQEYL----DVLGRPMVLADKA 441

Db 391 TELVSGDEAIDFNEVREMACNRRGYMVHVANMADVDEKIHHTIRMSRVVGRVHVESGQLS 450

QY 442 KQVQTNVNYLDALEGL--VITGTLPVFNITGOFENKTN----- 478

Db 451 ---WWTGTVRERYLPRPEIFAEVPDITNOSFAMVMKASRRKIRLOKSEARSMEFTTV 507

QY 479 ---LKNQILGVGMGVDSLEDIKRLTPRETLCPNGYFAIDPNGYVLLHPNLQKNP-- 532

Db 508 SYPVIIVNETFMGVAANIPILTEVAQKSHPANIGSKSYFFMLDQNGFVWTHPOLRIDPPT 567

QY 533 ---KSQEPVTLDFLD-----AELENDIKYEIRNKMID 561

Db 568 KYHKQNNMMDLLELVGQGNVRSQKSAQVSDLVCSGANVACEVDLDRKAVRKMIID 627

QY 562 GESGEKTFRTLVKSQDERY----IDK--GNKTYTWTVPNGTDSLALVLPYISFYKA 614

Db 628 CUNSD-----VOQLDVLVATELLORVYPTNTYAEICINHANFVLGLAVAKGDDYRVVK 681

QY 615 KLEETITQARSKKGMK 631

Db 682 K-----QKKYDFGRVK 692

Db 1020 MQAEQTSDDGPDPCDMVKQPRYKGPVDFDNNVLEDTDCGGVS 1063

RESULT 3  
CHRA2

N:Alternate names: dihydropyridine-binding protein, 140K  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 22-Jun-1999  
C:Accession: S10579; A39518; A33409  
R:Ellis, S.B.; Williams, M.E.; Ways, N.R.; Brenner, R.; Sharp, A.H.; Leung, A.T.; Campbell, S.C. 241, 1661-1664, 1988  
A:Title: Sequence and expression of mRNAs encoding the alpha(1) and alpha(2) subunits of dihydropyridine-sensitive calcium channel  
A:Reference number: S10579; MUID:88336904; PMID:2458626  
A:Accession: S10579  
A:Molecule type: mRNA  
A:Residues: 1-1106 <EL>  
A:Cross-references: EMBL:M21948; NID:g164762; PID:AAA81562.1; PID:g164763  
A:Note: 57-Asn, 106-Lys, and deletion of 620-Ser were also found  
R:Jay, S.D.; Sharp, A.H.; Kahl, S.D.; Vedvick, T.S.; Harpold, M.M.; Campbell, K.P. J. Biol. Chem. 266, 3287-3293, 1991  
A:Title: Structural characterization of the dihydropyridine-sensitive calcium channel alpha(1) subunit  
A:Reference number: A39518; MUID:91131638; PMID:1847144  
A:Accession: A39518  
A:Molecule type: protein  
A:Residues: 961-973 <JAY>  
A:Note: this sequence represents the amino end of a glycosylated peptide that appears at the amino end and identical molecular weights (17K) following deglycosylation  
R:Hamilton, S.L.; Hawkes, M.J.; Brush, K.; Cook, R. Biochemistry 28, 7820-7828, 1989  
A:Title: Subunit composition of the purified dihydropyridine binding protein from skeletal muscle  
A:Reference number: A33409; MUID:90122765; PMID:2558713  
A:Accession: A33409  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 27-44, 'S', 46-47 <HAM>  
C:Superfamily: calcium channel alpha-2 chain  
C:Keywords: calcium; disulfide bond; glycoprotein; ion channel; membrane protein; phosphatase  
F:1-26/Domain: signal sequence #status predicted <SIG>  
F:27-1106/Product: calcium channel alpha-2 chain #status predicted <MAT>  
F:94,138,186,326,350,470,477,606,613,678,697,784,827,891,898,988,1001,1081/Binding site:  
Query Match 96.1%; Score 5380.5; DB 1; Length 1106;  
Best Local Similarity 94.8%; Pred. No. 2,9e-315;  
Matches 1029; Conservative 15; Mismatches 12; Indels 29; Gaps 4;

QY 1 MAAGCLLALTLTQFS--LLIGPSSEPPSPSAVTIKSWDKMQEDLVTLAKTASGVNQLV 58  
Db 1 MAAGRLAWTLTLQAWLILIGPSSEPPSPSAVTIKSWDKMQEDLVTLAKTASGVHQLV 60  
QY 59 DIYEKYODLYTEPNNAQOLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDPFA 118  
Db 61 DIYEKYODLYTEPNNAQOLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDPFA 120  
QY 119 SNEVYVYNAKDDLDPEKNDSEPGSQRIKPVFTEDANFRQISQVAAVHIPTDIYEGSTI 178  
Db 121 SNEVYVYNAKDDLDPEKNDSEPGSQRIKPVFTEDANFRQISQVAAVHIPTDIYEGSTI 180  
QY 179 VLNELNWTGALDVEFKKNEEDPSLLMQVFGSATGLIARYYPASPWWNSRTPNKIDLYDV 238  
Db 181 VLNELNWTGALDVEFKKNEEDPSLLMQVFGSATGLIARYYPASPWWNSRTPNKIDLYDV 240  
QY 239 RRPWPVIOGAASPKDMLILVDVSGVSGLTGLKIRTSVSEMLETISDDDFVNVASFNSA 298  
Db 241 RRPWPVIOGAASPKDMLILVDVSGVSGLTGLKIRTSVSEMLETISDDDFVNVASFNSA 300  
QY 299 QDVSCFQHLVQAVNRKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNYNVSRANCKII 358  
Db 301 QDVSCFQHLVQAVNRKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNYNVSRANCKII 360  
QY 359 MLPTDGEERAQBIKFNKYNKKKVRFRFSVQGHNVYERGIQWACENKGGYIYIPSTGA 418  
Db 361 MLPTDGEERAQBIKFNKYNKKKVRFRFSVQGHNVYERGIQWACENKGGYIYIPSTGA 420

QY 419 IRIINTQEYLDVLRPMPVLGDKAKQVQWNTVYLDALGLVITGTLPVFNTITGQFENKTN 478  
Db 421 IRIINTQEYLDVLRPMPVLGDKAKQVQWNTVYLDALGLVITGTLPVFNTITGQFENKTN 480  
QY 479 LKNOLILGVMGVDSLESDIKRLTPRFTLCPNGYYFAIDPNGYVLLHHPNLQPK----- 530  
Db 481 LKNOLILGVMGVDSLESDIKRLTPRFTLCPNGYYFAIDPNGYVLLHHPNLQPKPGVGIPT 540  
QY 531 -----NPKSQEPVTLDFDALENDIKVEIRNMKIDGESGKTFFTLVKSODER 579  
Db 541 INLRKRRPNVQPKSQEPVTLDFDALENDIKVEIRNMKIDGESGKTFFTLVKSODER 600  
QY 580 YIDKGNRTYTWTPVNGTDY-SLALVLPYSPYYIKAKLEETITQARSKKGMKMOSETLKP 638  
Db 601 YIDKGNRTYTWTPVNGTDYSSALVLPYSPYYIKAKLEETITQARY-----SETLKP 653  
QY 639 DNFEESGYTFAPRDYCNLDKISDNNTFELNFEETDRKTPNPNPCNADLINRVLLDAG 698  
Db 654 DNFEESGYTFAPRDYCNLDKISDNNTFELNFEETDRKTPNPNPCNADLINRVLLDAG 713  
QY 699 FTNELVQNYWSKQKNIKGVKARFVVTDGIIITRVYPKEAGENWQENPETYEDSFYKRSIDN 758  
Db 714 FTNELVQNYWSKQKNIKGVKARFVVTDGIIITRVYPKEAGENWQENPETYEDSFYKRSIDN 773  
QY 759 DNYVETAPYFNKSPGAYESIMVSKAVEIYIOGKLLKPAVVGKIDVNSWNIETFTSI 818  
Db 774 DNYVETAPYFNKSPGAYESIMVSKAVEIYIOGKLLKPAVVGKIDVNSWNIETFTSI 833  
QY 819 RDPACAGPCCDKRNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGETDPSLMRHLVNI 878  
Db 834 RDPACAGPCCDKRNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGETDPSLMRHLVNI 893  
QY 879 VYAFNKSVDYOSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAAWSILOQFLLSLT 938  
Db 894 VYAFNKSVDYOSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAAWSILOQFLLSLT 953  
QY 939 FPRLLAEVEMEDDDFTASLSKQSCITEQTOYFFDNDKSFSGVLDGNCGRIFHGEKLMN 998  
Db 954 FPRLLAEVEMEDDDFTASLSKQSCITEQTOYFFDNDKSFSGVLDGNCGRIFHGEKLMN 1013  
QY 999 TNLIFIMVESKGTCPDTRLLIQAEQTSDDGPDPCDMVKQPRYKGPVDFDNNVLEDT 1058  
Db 1014 TNLIFIMVESKGTCPDTRLLIQAEQTSDDGPDPCDMVKQPRYKGPVDFDNNVLEDT 1073  
QY 1059 CGGVS 1063  
Db 1074 CGGVS 1078

RESULT 4

T30256  
calcium channel alpha-2-delta-C chain - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 20-Jun-2000  
C:Accession: T30256  
R:Klugbauer, N.; Lacinova, L.; Marais, E.; Hobom, M.; Hofmann, F. J. Neurosci. 19, 648-691, 1999  
A:Title: Molecular diversity of the calcium channel alpha2delta subunit.  
A:Reference number: 220794  
A:Accession: T30256  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1091 <KLU>  
A:Cross-references: EMBL:AJ010949; PIDN:CAA09423.1  
A:Experimental source: brain  
C:Superfamily: calcium channel alpha-2 chain

Query Match 20.0%; Score 1119.5; DB 2; Length 1091;  
Best Local Similarity 28.5%; Pred. No. 4.4e-59;  
Matches 321; Conservative 230; Mismatches 443; Indels 131; Gaps 41;

QY 3 AGCLLALTLTQFSSEPPSPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDIYE 62

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Db 301 VSCFHLVQAVNRKVKLVDAVNITAKGIDYKKGFSFAFQLLNYSRANCKIIML 360
QY 361 FTGGGERAQRQIEFNKYNKKVRFVRSVQGHNYERGPQIOWMACENKGYIYETPSIGAIR 420
Db 361 FTGGGERAQRQIEFNKYNKKVRFVRSVQGHNYERGPQIOWMACENKGYIYETPSIGAIR 420
QY 421 INTQVEYLDVLRGPMVLGADKAKOVQNTNYYLDALGLVITGTLVPFNTGTGFENKTNLK 480
Db 421 INTQVEYLDVLRGPMVLGADKAKOVQNTNYYLDALGLVITGTLVPFNTGTGFENKTNLK 480
QY 481 NQILGVMGVDSLEDIKRLTPFTLCPNGYIFAIDPNQYVLLHPNLQPKNKSQEPVTL 540
Db 481 NQILGVMGVDSLEDIKRLTPFTLCPNGYIFAIDPNQYVLLHPNLQPKNKSQEPVTL 540
QY 541 DFLDAELENDIKVEIRNKMIDGESGKTPRTLKVSODERYIDKGNRTYTWTPVNGTDSL 600
Db 541 DFLDAELENDIKVEIRNKMIDGESGKTPRTLKVSODERYIDKGNRTYTWTPVNGTDSL 600
QY 601 ALVLPYSFYIYAKLEETITQARSKKGKMDSETLKPONFEESGYTFIAPRDYCNDLKI 660
Db 601 ALVLPYSFYIYAKLEETITQARSKKGKMDSETLKPONFEESGYTFIAPRDYCNDLKI 660
QY 661 SDNNTFLLNFNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQYWSKQNKIKGVAR 720
Db 661 SDNNTFLLNFNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQYWSKQNKIKGVAR 720
QY 721 FVVTGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
Db 721 FVVTGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDCKRNSVMDCVI 840
Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDCKRNSVMDCVI 840
QY 841 LDGGFLLMANHDDYTNOIGRFFGIDPSLMRHLNIVSYAFNKSIDYQSCYCEGAPKQ 900
Db 841 LDGGFLLMANHDDYTNOIGRFFGIDPSLMRHLNIVSYAFNKSIDYQSCYCEGAPKQ 900
QY 901 GAGHSAYVPSVADILQIGWATAAWSILOQFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960
Db 901 GAGHSAYVPSVADILQIGWATAAWSILOQFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960
QY 961 SCITBQTYFFDNDSKSPGVLDCGNCRIHFGEKLMNTNLIIFWVSKGTCPCDTRLLI 1020
Db 961 SCITBQTYFFDNDSKSPGVLDCGNCRIHFGEKLMNTNLIIFWVSKGTCPCDTRLLI 1020
QY 1021 QAEQTSQDGNPCDMVKOPRYRKGPVDFDNNVLEDYTDGCGVS 1063
Db 1021 QAEQTSQDGNPCDMVKOPRYRKGPVDFDNNVLEDYTDGCGVS 1063

RESULT 2
A44147
N:Alternate names: calcium channel protein alpha-2 chain precursor - rat
N:Contains: calcium channel alpha-2 chain
C:Species: Rattus norvegicus (Norway rat)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 20-Aug-1999
C:Accession: A44147
R:Kim, H.L.; Kim, H.; Lee, P.; King, R.G.; Chin, H.
Proc. Natl. Acad. Sci. U.S.A. 89, 3251-3255, 1992
A:Title: Rat brain expresses an alternatively spliced form of the dihydropyridine-sensitive
A:Reference number: A44147; MUID:92228762; PMID:1314383
A:Accession: A44147
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1091 <KIM>
A:Cross-references: GB:M86621; NID:g203954; PIDN:AAA41088.1; PID:g203955
A:Superfamily: calcium channel alpha-2 chain
C:Keywords: calcium; glycoprotein; ion channel; transmembrane protein

Query Match 96.3%; Score 5390; DB 2; Length 1091;
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Best Local Similarity 95.8%; Pred. No. 7.7e-316;
Matches 1019; Conservative 24; Mismatches 19; Indels 2; Gaps 2;
QY 1 MAAGCLLALTTLFQSLIGPSSEPPFPSPVITKSWDKMQEDLVTAKTASGVNQLVDI 60
Db 1 MAAGCLLALTTLFQSLIGPSSEPPFPSPVITKSWDKMQEDLVTAKTASGVNQLVDI 60
QY 61 YEKYQDLTYVPNNARQIETAARDIEKLLNSRKALYSALAEKQVAAHQWREDFASN 120
Db 61 YEKYQDLTYVPNNARQIETAARDIEKLLNSRKALYSALAEKQVAAHQWREDFASN 120
QY 121 EVVYNNAKDDLDPEKNDSESGSQRIKPVIEDANFGROIYSQHAHVHTPTDIYESSITVL 180
Db 121 EVVYNNAKDDLDPEKNDSESGSQRIKPVIEDANFGROIYSQHAHVHTPTDIYESSITVL 180
QY 181 NELNWTSALEDVFPKKNREEDSLQVFGSATGLARYYPASPWVDNRSRTPNKIDLYDVR 240
Db 181 NELNWTSALEDVFPKKNREEDSLQVFGSATGLARYYPASPWVDNRSRTPNKIDLYDVR 240
QY 241 RPWTIOGAASPQMLILVDVSGSVGLTKLIRTSVSEMLETILSDDDFVNVASFNSNAQD 300
Db 241 RPWTIOGAASPQMLILVDVSGSVGLTKLIRTSVSEMLETILSDDDFVNVASFNSNAQD 300
QY 301 VSCFHLVQAVNRKVKLVDAVNITAKGIDYKKGFSFAFQLLNYSRANCKIIML 360
Db 301 VSCFHLVQAVNRKVKLVDAVNITAKGIDYKKGFSFAFQLLNYSRANCKIIML 360
QY 361 FTGGGERAQRQIEFNKYNKKVRFVRSVQGHNYERGPQIOWMACENKGYIYETPSIGAIR 420
Db 361 FTGGGERAQRQIEFNKYNKKVRFVRSVQGHNYERGPQIOWMACENKGYIYETPSIGAIR 420
QY 421 INTQVEYLDVLRGPMVLGADKAKOVQNTNYYLDALGLVITGTLVPFNTGTGFENKTNLK 480
Db 421 INTQVEYLDVLRGPMVLGADKAKOVQNTNYYLDALGLVITGTLVPFNTGTGFENKTNLK 480
QY 481 NQILGVMGVDSLEDIKRLTPFTLCPNGYIFAIDPNQYVLLHPNLQPKNKSQEPVTL 540
Db 481 NQILGVMGVDSLEDIKRLTPFTLCPNGYIFAIDPNQYVLLHPNLQPKNKSQEPVTL 540
QY 541 DFLDAELENDIKVEIRNKMIDGESGKTPRTLKVSODERYIDKGNRTYTWTPVNGTDSL 599
Db 541 DFLDAELENDIKVEIRNKMIDGESGKTPRTLKVSODERYIDKGNRTYTWTPVNGTDSL 599
QY 600 LALVLPYSFYIYAKLEETITQARSKKGKMDSETLKPONFEESGYTFIAPRDYCNDLK 659
Db 600 LALVLPYSFYIYAKLEETITQARSKKGKMDSETLKPONFEESGYTFIAPRDYCNDLK 659
QY 660 ISDNNTFLLNFNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQYWSKQNKIKGVAR 719
Db 660 ISDNNTFLLNFNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQYWSKQNKIKGVAR 719
QY 720 RFVVTGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESG 779
Db 720 RFVVTGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESG 779
QY 780 IMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDCKRNSVMDCV 839
Db 780 IMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDCKRNSVMDCV 839
QY 840 ILDDGGFLLMANHDDYTNOIGRFFGIDPSLMRHLNIVSYAFNKSIDYQSCYCEGAPK 899
Db 840 ILDDGGFLLMANHDDYTNOIGRFFGIDPSLMRHLNIVSYAFNKSIDYQSCYCEGAPK 899
QY 900 QGAGHSAYVPSITDILQIGWATAAWSILOQFLLSLTFPRLLEAVEMEDDDFTASLSK 959
Db 900 QGAGHSAYVPSITDILQIGWATAAWSILOQFLLSLTFPRLLEAVEMEDDDFTASLSK 959
QY 960 QSCITEQTYFFDNDSKSPGVLDCGNCRIHFGEKLMNTNLIIFWVSKGTCPCDTRLL 1019
Db 960 QSCITEQTYFFDNDSKSPGVLDCGNCRIHFGEKLMNTNLIIFWVSKGTCPCDTRLL 1019
QY 1020 IQAEQTSQDGNPCDMVKOPRYRKGPVDFDNNVLEDYTDGCGVS 1063
Db 1020 IQAEQTSQDGNPCDMVKOPRYRKGPVDFDNNVLEDYTDGCGVS 1063
```

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 10, 2003, 14:13:54 ; Search time 20.2324 Seconds  
(without alignments)  
5050.861 Million cell updates/sec

Title: US-10-090-827-15

Perfect score: 5599

Sequence: 1 MAAGCGLLALTLTFLQSLLIG.....PDVCFDNNVLEDTDCGCVS 1063

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_73: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5599	100.0	1091	2 JH0565	calcium channel al
2	5390	96.3	1091	2 A44147	calcium channel pr
3	5380.5	96.1	1106	1 CHRBA2	calcium channel pr
4	1119.5	20.0	1091	2 T30256	calcium channel al
5	607	10.8	734	2 S44617	C50C3.11 protein -
6	580.5	10.4	1148	2 T18770	probable calcium c
7	198	3.5	1450	2 C86880	hypothetical prote
8	194.5	3.5	886	2 S54355	inter-alpha-trypsi
9	185	3.3	885	2 S30350	inter-alpha-trypsi
10	175.5	3.1	1819	2 D97033	uncharacterized pr
11	164.5	2.9	889	2 JC5576	inter-alpha-trypsi
12	161	2.9	2706	2 T28155	variant-specific s
13	159	2.8	1984	2 A44396	P-type cation tran
14	157.5	2.8	575	2 D64998	hypothetical prote
15	156.5	2.8	918	2 E90542	lipoprotein [impor
16	155.5	2.8	680	2 A97331	membrane associate
17	155	2.8	1516	2 E71619	RAD2 endonuclease
18	155	2.8	2364	2 I40884	cytotoxin L - Clos
19	154.5	2.8	946	1 IYH02	inter-alpha-trypsi
20	154.5	2.8	1315	2 T28679	fibrinogen-binding
21	153	2.7	932	2 JC5953	inter-alpha-inhibi
22	152	2.7	1291	2 S46431	botulinum neurotox
23	152	2.7	1291	2 A49777	botulinum neurotox
24	151.5	2.7	420	2 S76691	hypothetical prote
25	151.5	2.7	1426	2 A99580	hypothetical prote
26	150.5	2.7	921	2 JC4625	inter-alpha-trypsi
27	150.5	2.7	1385	2 D89824	hypothetical prote
28	150	2.7	654	2 A69656	methyl-accepting c
29	150	2.7	1027	2 B90527	atp-binding protei

proteinase (EC 3.4  
inter-alpha-trypsi  
thoptry protein -  
DNA-directed DNA p  
hypothetical prote  
methyl-accepting c  
hypothetical prote  
hypothetical prote  
probable retrolem  
internalin protein  
probable peptidogl  
hypothetical prote  
hypothetical prote  
cellulose 1,4-beta  
fibronectin-binding  
ATP-dependent exon

30 149 2.7 459 2 F64688  
31 149 2.7 930 2 JX0368  
32 148.5 2.7 2401 2 T28676  
33 148 2.6 964 2 S25855  
34 146.5 2.6 1285 2 B72420  
35 146 2.6 688 2 D96930  
36 146 2.6 4688 2 F82885  
37 145.5 2.6 676 2 T47637  
38 145.5 2.6 689 2 F84811  
39 145.5 2.6 1237 2 AC1583  
40 145.5 2.6 2013 2 AD1129  
41 145.5 2.6 3216 2 C90538  
42 145.5 2.6 5005 2 F82884  
43 144 2.6 1087 1 S41797  
44 144 2.6 1091 2 S33850  
45 143.5 2.6 1252 2 H97178

ALIGNMENTS

RESULT 1  
JH0565  
calcium channel alpha-2b chain precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 20-Aug-1999  
C:Accession: JH0565  
R:Williams, M.E.; Feldman, D.H.; McCue, A.F.; Brenner, R.; Velicelebi, G.; Ellis, S.B  
Neuron 8, 71-84, 1992  
A:Title: Structure and functional expression of alphas, alpha2, and beta subunits of  
A:Reference number: JH0564; MUID:92110010; PMID:1309651  
A:Accession: JH0565  
A:Molecule type: mRNA  
A:Residues: 1-1091 <WIL>  
A:Cross-references: GB:M76559; NID:gl79761; PIDN:AAA51903.1; PID:gl79762  
A:Experimental source: basal ganglia  
A:Note: several conflicts are found between Genbank submission, authors' translation  
C:Comment: this protein is a subunit of the voltage dependent calcium channel.  
C:Superfamily: calcium channel alpha-2 chain  
C:Keywords: glycoprotein; phosphoprotein  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-1067/Product: calcium channel alpha-2b chain #status predicted <CAL>  
F:32-268,326,539,635,1087/Binding site: phosphate (Thr) (covalent) (by protein kinase  
F:91-142,250,625,817/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #  
F:92,136,184,324,348,468,475,585,594,663,682,769,812,876,883,973,986/Binding site: ca  
F:501/Binding site: phosphate (Thr) (covalent) #status predicted  
F:833/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status pre

Query Match 100.0%; Score 5599; DB 2; Length 1091;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCGLLALTLTFLQSLLIGSPSEPPPSAVTIKSWDKMQEDLVTLAKTAGVNLVDI 60  
DB 1 MAAGCGLLALTLTFLQSLLIGSPSEPPPSAVTIKSWDKMQEDLVTLAKTAGVNLVDI 60  
QY 61 YEKYQDLYVEPNARQLVEIAARDIEKLLSNRKALVSLAEAEKVAHQHOREFASN 120  
DB 61 YEKYQDLYVEPNARQLVEIAARDIEKLLSNRKALVSLAEAEKVAHQHOREFASN 120  
QY 121 EVVYNAKDDLDPEKNDSEPPGSGRIKPVFIEDANFGRIQISYQHAHVHPTDIEGSTIVL 180  
DB 121 EVVYNAKDDLDPEKNDSEPPGSGRIKPVFIEDANFGRIQISYQHAHVHPTDIEGSTIVL 180  
QY 181 NELNWT SALDEVFKK NREEDPSLLWQVFGSATGLARYYPASVPWDSNRPKNIDLYDVR 240  
DB 181 NELNWT SALDEVFKK NREEDPSLLWQVFGSATGLARYYPASVPWDSNRPKNIDLYDVR 240  
QY 241 RPWYIOGAASPKDMLILVDVSGVSGITLKLRISYSEMLETISDDDDFNVAFSFNSNAO 300  
DB 241 RPWYIOGAASPKDMLILVDVSGVSGITLKLRISYSEMLETISDDDDFNVAFSFNSNAO 300  
QY 301 VSCFQHLVQAVNRNKKVLDAVNNTAKGITDYKKGFSFAFEQLLNYNVSRANCKIIML 360

1. The first part of the document is a list of the names of the persons who were present at the meeting. The names are listed in alphabetical order.

2. The second part of the document is a list of the topics that were discussed at the meeting. The topics are listed in alphabetical order.

3. The third part of the document is a list of the actions that were taken at the meeting. The actions are listed in alphabetical order.

4. The fourth part of the document is a list of the decisions that were made at the meeting. The decisions are listed in alphabetical order.

5. The fifth part of the document is a list of the recommendations that were made at the meeting. The recommendations are listed in alphabetical order.

Tue Feb 11 13:48:04 2003

```
QY 755 SLDN--DNVFTAPYKNSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGIKIDVNSWIEN 812
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
679 AAEQIPGSPFISLPF--STGPNKSNVVTASTSIQLLDERKSPVVAAGVQMKLEFFQPK 736
QY 813 FTWTSIRDFCAGVPCDKRNSVDMDCVILDDGGFLMANHDDYTNOIGRFFGEIDPSLMR 872
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
737 FWTASRQCASLDGKCSISCDDETVCNLYLDNNGFILVS--EDYT-OTGDFGEIEGAVMN 793
QY 873 HLWNISVYAFNKSVDYQSVCEPGAAPKQGA-GHRSAYVPSIADILHIGWATAAASILQ 931
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
794 KLLTMSFKRITLYDQAMCRANKESDGAHGLDPI-----NAFLSAVKWIMTE 843
QY 932 QFLLSLTFPRLLAEVEMEDDDFTASLSK-----QSCITEQTOYFFDNDKSFSGVLDCGN 986
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
844 LVLFLVEF-----NLCSWHSDMTAKAKLKQTLPCDTEYPAFVSERTIKETTGNACED 899
QY 987 CSRIFHVKEKLMNTNLIIFIMVESKGTCPDPT 1016
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
900 CSKSFVIQIIPSSNLFMNVVDS--SCLCES 927
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Search completed: February 10, 2003, 14:28:01  
Job time : 46.7275 secs



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Db 129 EYNAVILNRDRDGNFLELGKEFI--LAPNDHFNNLPVNISILSDVQVFTNMYNKDPAIV 186
QY 181 NELNWTSAIDVEFKKREEDPSLLQVFGSAGCLARYYPASPVWNSRTPNKIDLYDVR 240
Db 187 NGVWSESLNKVDFNDRDPSLWQIFGSAKGFYFGIKWEPDE--NGVIAFDCRN 243
QY 241 RPWYIOGAASPKDMLILVDVSGSVSLTLKLTISYSEMLETLSDDDFVNVASFNSNAQD 300
Db 244 RKWYIOGAASPKDMLILVDVSGSVSLTLKLTISYSEMLETLSDDDFVNVASFNSNAQD 303
QY 301 VS-CFQ-HLVQANVRNKKVLDKAVNNITAKGTDYKGFSAFQELNLYNVRAN--CNK 356
Db 304 VEPCLNGTLVQADRTNKEHREHLKDLFAKIGCMGLDIALNEAFNLSDFNHTGOGSICQ 363
QY 357 IIMLFTDGGEEARAEAFKYN--KDKRVVFTSVGQHNVDYRGPIOMACENKGYEYFIPS 415
Db 364 AIMLITDGAVDYDTIFAKYNNPDRKVRITLYIGREAFADNLKMACANKGFTQIST 423
QY 416 IGAIRINTQYLDVGRPMVLADGAKAQVOMTVNYLD-----ALELGLVI--TGTL 464
Db 424 LADQVENVMEYLHVLRSRPVI--DQEHVWVTEAYIDSTLPQAKLADDQGLVLTVM 481
QY 465 PVFNITGQENKTNLKNQILGVGVDSVLEDIKRLTPFTLCPNGYFPAIDPNGYVLLH 524
Db 482 PVFS-----KONETRSKG--ILLGVGVDPVKELLKTPYKLGTHGYAFATNNGYLLTH 536
QY 525 PNLQP---KNPKSQBP--VTLDLDAELNDIKVIRKMDIGESGEXTERTLVKSQDER 579
Db 537 PELRPLYEBGKRRKPNYSVVDLSEVEWEDDDV--LRNANVRNKTGK--FSMEVK---K 589
QY 580 YIDKGNRT-----YTPVNGTYSALVLT--YSFYIKAK--IEETITQARSKKGKM 630
Db 590 TVDKGRVLMVMTDYYTDIKGTPELSGLVALSRHGKYYFRGNVTIEBGL----- 639
QY 631 KDSETLKPDPNFESGYTFIAPDYCN--DLKISDNNTEFLNFEIDRKTNNPNSCNTDL 689
Db 640 -----HDLHPDVSILADSEWVCNTDLHPEHRLSQAELKYLKAGKEP--LIQCDKEL 690
QY 690 INRVLLDAGFNNELVQNTWS-----KOKNIKGKARFVVTGGITRYP----- 733
Db 691 IOEVLFDA--VVSAPTEAYWTSALNKSNSDKGEVAFGLTRTGLSRNLNLFVGAELTNQ 749
QY 734 --KEAGENQENPETYEDSFYKRSIDN--DNYVTAPY-----FNKSGPAYESGIMVSKA 785
Db 750 DFLKAGKENTFNADHPFLWYRRAEQTAGSFVYSIPFSTGTNKS-----NVVTASTS 803
QY 786 VEIYIQGKLLPAAVGIKIDVNSNIENFTKTSIRDCAGPVDCCKRNSDYNDQVILDGG 845
Db 804 IOLLDERKSPVAAVGIQMLKLEFFQRFWTSARQASIDGKCSODETVNCLYLDNNG 863
QY 846 FLLMANHDDYTNQIGRFFGEIDPSLMRLHVNISYAFNKSYSQVSGEPAAPKQAGAGR 905
Db 864 FILVS--EDYT--QTGDFFEVEGAVMKNLLTMGSFKRITLYDQACR--ANKESDSA 917
QY 906 SAYVPSIADIHLICWATAWSLIQOFLASLTPRLLLEAVEDEDDFTASLSK-----Q 960
Db 918 HGLDLPYKAFI-----SAKWINTELVLFLVEF-----NLCSMWSDMTAKAKLQTL 967
QY 961 SCITEQYTFDNDKSFSGVLDGCGNSRIFHVEKLMNTNLIIFIMVESKGTCPCDT 1016
Db 968 PCDTEYPAFVSERTIKETTGNACEDSKSFVIQQIPSSNLFMVVDS--SCLCES 1021
```

## RESULT 15

```
Q9NT16
ID Q9NY16 PRELIMINARY; PRT; 997 AA.
AC Q9NY16;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
*DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
```

```
DE Calcium channel alpha2-delta3 subunit.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=21142395; PubMed=11245980;
RA Hanke S., Bugert P., Chudek J., Kovacs G.;
RT "Cloning a calcium channel alpha2delta-3 subunit gene from a putative
RT tumor suppressor gene region at chromosome 3p21.1 in conventional
RL renal cell carcinoma.";
RL Gene 264:69-75(2001).
DR EMBL; AJ272268; CAB75962.1; -.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 2.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS0234; VWEA; 1.
SQ SEQUENCE 997 AA; 112996 MW; B56D13133FD67B8D CRC64;
```

## Query Match

Best Local Similarity 19.5%; Score 1045; DB 4; Length 997;

Matches 285; Conservative 206; Mismatches 377; Indels 122; Gaps 36;

```
QY 86 IEKLLNRSKALVRLALAEKQVAAHQWRDEFASNEVVYNAK--DDLDPKNDSEPGSQ 143
Db 1 MEEMFHKKSAVRRLVEAAEEAHLKHEFDADL--QYEFNAVLINERDKDGNFLELGKE 57
QY 144 RIKPVFTDDANFGQISYQHAHVHIPTDIEGSTIVLNELNWTSAIDVEFKKREEDPSL 203
Db 58 FI--LAPNDHFNNLPVNISILSDVQVFTNMYNKDPAIVNGVWSESLNKVDFNDRDPSL 115
QY 204 LQVFGSATGLARYYPASPVWNSRTPNKIDLYDVRNRPWYIOGAASPKDMLILVDVSGS 263
Db 116 IWQYFGSAKGFYFGIKWEPDE--NGVIAFDCRNKRWYIOGAASPKDMLILVDVSGS 172
QY 264 VSGTLTKLITSVSEMLETSLDSDDFVNVASFNSNAQDVS--CFQ-HLVQANVRNKKVLDK 321
Db 173 MKGLRLTIKQTVSSILDTLGDGDDFFNITAYNEELHYVEPCLNGTLVQADRTNKEHREH 232
QY 322 VNNITAGITDYKKGFSFAPEQLNLYNVRAN--CNKIIMLFTDGGEEARAEAFKYN--K 378
Db 233 LDKLFAGKIGMLDIALNEAFNLSDNHTGOGSICQALMLITDGAVIDYDTIFAKYNNP 292
QY 379 DKRVVFTSVGQHNVDYRGPIOMACENKGYEYFIPSGAIRINTQYLDVGRPMVLADG 438
Db 293 DRKVRITLYIGREAFADNLKMACANKGFTQISTLADVQENVMYELHVLRSRPVI-- 350
QY 439 DKAKOVQWTVNYLDAL-----ELG--LVITGTLVPFNITGQENKTNLKNQILGV 487
Db 351 DQEHVWVTEAYIDSTLPQAKLTDGQGVLTMTVAMPVFS-----KONETRSKG--ILLGV 405
QY 488 MGVDSLEDIKRLTPFTLCPNGYFPAIDPNGYVLLHNPQ--PKNPKSQBP--VTLDG 542
Db 406 VCTDVPVKELLKTPYKLGTHGYAFATNNGYVILTHPELRLYEBGKRRKPNYSVVDL 465
QY 543 LDAELNDIKVIRKMDIGESGEXTERTLVKSQDERYIDKGNRT-----YTPVNGT 596
Db 466 SEVEWEDDDV--LRNANVRNKTGK--FSMEVK-----KTVDKGRVLMVMTDYYTDIKGT 518
QY 597 DYSLALVLT--YSFYIKAK--IEETITQARSKKGKMDSETLKPDPNFESGYTFIAPRD 653
Db 519 PFSGLVALSRHGKYYFRGNVTIEBGL-----HDLHPDVSILADSEWS 560
QY 654 YCN-DLKISDNNTEFLNFEIDRKTNNPNSCNTDLINRVLLDAGFNNELVQNTWS--- 709
Db 561 YCNTDLHPEHRLSQAELKYLKAGKEP--LIQCDKELIQEVLFDA--VVSAPTEAYWTS 618
QY 710 ---KOKNIKGKARFVVTGGITRYP-----KEAGENQENPETYEDSFYKRSIDN 754
Db 619 LNKSNSDKGEVAFGLTRTGLSRNLNLFVGAELTNQDNLKAGKENTFNADHPFLWYR 678
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Db 825 LSNONHOMQVGRFFSEVDANLMLALYNNSFYTRKESYDYQAAACAPPPNGLGAAPRGVF 884
QY 909 VPSADILHIGWATAAAGWILQOFLSLTFPRLLAEVEMEDDDFTASLSKQSCITEQQT 968
Db 885 VPTVADFLNLAWMTSAAGWLFQOLLYGLYHSHWFQDPAEAG-SPEIRESSCYMKQTQ 943
QY 969 YFFDNDKSFSGVLDCGNCRIHFHVEKIMNTNLFITMVKSGTCPCD 1015
Db 944 YFGSVNASYNALIDCGNCSRLFHQRLTNTNLLFVVAERPLCSQCE 990

RESULT 13
Q9NSA6 PRELIMINARY; PRT; 975 AA.
ID Q9NSA6 PRELIMINARY; PRT; 975 AA.
AC Q9NSA6 PRELIMINARY; PRT; 975 AA.
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE LUAC11.1 (Calcium channel, voltage-dependent, L type, alpha 2D subunit
DE (K1AA0558)) (Fragment).
CN LUAC11.1
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Barlow K.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; 284492; CAB41767.2; -.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; WWF_A.
DR Pfam; PF02743; Cache; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50234; VVFA; 1.
FT NON_TER 1
SQ SEQUENCE 975 AA; 110192 MW; C7874D46B88242BF CRC64;

Query Match 50.3%; Score 2691; DB 4; Length 975;
Best Local Similarity 57.3%; Pred. No. 1.1e-155;
Matches 519; Conservative 136; Mismatches 212; Indels 38; Gaps 14;

QY 132 DPEKNDSEPGSQ--RIKPVFIDDANFGRIQISYQAAVHIPTDIYEGSTIVLNELNWTLSAL 189
Db 2 DPESEDVERGSKASTLRLEDIEDPNFKNKVSYAAVQIPTDIYKGSTVILNLTNWEAL 61
QY 190 DEVEKKNREEDPSLWQVFGSATGLARYYPASPVYDNRTPNKIDLYDVRPRPWYIOGAA 249
Db 62 ENVPENRRQDPTLLWQVFGSATGTYRYYPATPW----RAPKKIDLYDVRPRWYIOGAS 117
QY 250 SPKMDLILVDVSGVSGLTLLKIRTSVSEMLETLSDDDFVNVASFNSNAQDVSCFQHLVQ 309
Db 118 SPKMDVILVDVSGVSGLTLLKMTKSVCEMLDTSDDDFVNVASFNSNAQDVSCFTHLVQ 177
QY 310 ANVRKKVLKDAVNITAKITDYKKGFSFAFEQLLNVSFRANCKIIMLFTDGGGERA 369
Db 178 ANVRKKVFEKAVQGVAKGTGKYKAGFEYAFDQLQNSITRANCKIMMFTDGGEDRV 237
QY 370 QEIFAKYN-KDKKRVVFVSVGHNYDRGIQWACENKGYEIPSGAIRINTQEYLD 428
Db 238 QDVFEXYNNPNTVRVFFSVGHNYDVTPLQWACANKGYEIPSGAIRINTQEYLD 297
QY 429 VLGRPMVLADGAKQVQNTNVLDALEGLVITGLPVFNIT--QCNENKTNLKNQLILG 486
Db 298 VLGRPMVLADGAKQVQNTNVLDALEGLVITGLPVFNITQDGPGEK----KNQLILG 353
QY 487 VMGVDVSLIEDIKRLTFRFTLCPNGYFAIDPNGYVLLHPNLPKPKSQEPTVTLDFLDAE 546
Db 354 VMGIDVALNDIKRLTFRFTLCPNGYFAIDPNGYVLLHPNLPKPKSQEPTVTLDFLDAE 413
QY 547 LENDIKVEIRNKNMIDGSEKTRFRLVQSODERYIDKGNRTYTWTPVANGTYSALVLP 606
Db 414 LEDENKEEIRRSIDGNKCHKQIRTLVKSIDERYIDVTRNTYTWTPIRSTNYSGLVLPP 473

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QY 607 YSFYVIKAKIETITQASKKGKMKDSETLKPDNPEESGYTFIAPRDYCNDLKISDNTE 666
Db 474 YSTFYLQANLSQILQ-----VRYFFLLPSPSESEGHVFIAPREYCKDNLASDNTE 526
QY 667 FLINNEFIIDRTNPNPCNTDLINRVLLDAGFTNELQVNYWSKOK-NIKGVKARFVVD 725
Db 527 FLKNFIELMEKVTDPDSKOCNELLNLILDTGITQOLVERWVRDQDLNTYSLAVFAATD 586
QY 726 GGITRVYPKEAGENQENPETEYEDSFYKRSLDNDNYVTAPYFNK-SGPGAYES---GIM 781
Db 587 GGITRVFPNKAEDWTENPEPNASFYRRSLDNHGVFKPPHODALLRPLELENDVTGIL 646
QY 782 VSKAVEIYIQGLKLPVAVGVIKIDVNSWIEFN-----TKTSIRDP--CAGP-----VCDC 830
Db 647 VSTAVELSLGRRTLPAVVGKIDLEAWAEKFKVLASNRTHQDQPKC-GPNSHGEMDCE 705
QY 831 RNSDVMDCVILDDGFLMANHDDVTNOIGRFFGETDPSLMRHLVNIISVYAFNKSVDYQS 890
Db 706 VNNEDLLCILLIDGGFLVLSNQHWDQVGRFSEVDANLMLALYNNSFYTRKESYDQQA 765
QY 891 VCEPGAAPKQAGHRSAYVPSIADILHIGWATAAASISLOQLFLLSLTFPRLLAEVEMED 950
Db 766 ACAQPPGNLGAAPRGVFPVTVADFLNLAWMTSAAGWLFQOLLYGLYHSHWFQADPAEA 825
QY 951 DFTASLSKQSCITEQTYFFDNDKSFSGVLDCGNCRIHFHVEKIMNTNLFITMVKSG 1010
Db 826 EG-SPETRESSCYMKQTYIFGVSNAYNALIDCGNCSRLFHQRLTNTNLLFVVAERPL 884
QY 1011 TCPDCD 1015
Db 885 CSQCE 889

RESULT 14
Q92IL5 PRELIMINARY; PRT; 1091 AA.
ID Q92IL5 PRELIMINARY; PRT; 1091 AA.
AC Q92IL5 PRELIMINARY; PRT; 1091 AA.
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Calcium channel alpha-2-delta-C subunit.
GN CACNA2D3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Klugbauer N., Lacinova L., Marais E., Hobom M., Hofmann F.;
RT "Molecular diversity of the calcium channel alpha2delta subunit.";
RL J. Neurosci. 19:648-691(1999).
DR EMBL; AJ010949; CAA09423.1; -.
DR MGD; MGI:1338890; CACNA2D3.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; WWF_A.
DR Pfam; PF02743; Cache; 2.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50234; VVFA; 1.
SQ SEQUENCE 1091 AA; 122777 MW; 7ABE2BD410077A0A CRC64;

Query Match 20.8%; Score 1112; DB 11; Length 1091;
Best Local Similarity 28.9%; Pred. No. 3.1e-59;
Matches 311; Conservative 224; Mismatches 411; Indels 130; Gaps 39;

QY 3 AGCLLALTTLFOSLLIGSPSQEPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDIYE 62
Db 14 ASALLA-TALLIYAALGDVVRSEQQIPLSV-VKLWASAFGEIKSIAAKYSGSOLLQKKYK 71
QY 63 KYQDLYVPEPNARQLVEIARDETEKLLSNPSKALVRLAEAEKVQAAHOREDFASNEV 122
Db 72 EYKDVATEIEDIGLQLVKKLAKIMEEMFHKSEAVRRLVRAAEBAHLKHEFDADL---QY 129

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QY 208 FGSATGLARYYPASPPWVDNSRTNPKIDLYDVRRRPWYIOGAASPKDMLILVDVSGSVGL 267
DB 181 FGSATGVTYYPATPW---RAPKKIDLYDVRRRPWYIOGAASPKDMLIVVDVSGSVGL 236
QY 268 TLKLIKTSVSEMLETSDDDFVWVASFNSNAQDVSCFQHLVQANVRNKKVLDKAVNNITA 327
DB 237 TLKLMKTSVCEMLDTSDDDYVNVASFNEKAQPVSCFTHLVQANVRNKKVFEAOGVMA 296
QY 328 KGTIDYKKGFSFAFEQLLNVNVRNCKITIMLFTDGGGERAQEIPAKYN-KDKKVRVPT 386
DB 297 KGTIDYKKGFSFAFEQLLNVNVRNCKITIMLFTDGGGERAQEIPAKYN-KDKKVRVPT 386
QY 387 FSVGQHNVDYTPLOWMACNKGYYEIPSPISGAIIRNTQYLDVLRPVMVLAGDKAKQVOM 446
DB 357 FSVGQHNVDYTPLOWMACNKGYYEIPSPISGAIIRNTQYLDVLRPVMVLAGDKAKQVOM 446
QY 447 TNYVDALGLGLVVTGLPVFNLTQDGPGEK-----KNQILGVMGIDVALNDIKRLTPNY 472
DB 417 TNYVDALGLGLVVTGLPVFNLTQDGPGEK-----KNQILGVMGIDVALNDIKRLTPNY 472
QY 505 TLCPNGYFAIDPNCYVLLHNPLOPKNSOEPVTLDFDLAELENDIKVEIRNKMIDGES 564
DB 473 TLGANGYVFAIDNGYVLLHNPLOPKNSOEPVTLDFDLAELENDIKVEIRNKMIDGES 564
QY 565 GEKTFRLVKSQDERYIDKGNRTYTWTPVNGTIDYSLALVLTPTSYFYIKAKIETITQAR 624
DB 533 GHKQIRTLVKSQDERYIDVTRNRYTWPIRSTNYSGLVLPYVSTYVLOANLRQILQVK 592
QY 625 SKKGKMKDSETLKPNDFEESGTYFIAPDRYCNLDKISDNNTFEFLNFKVEIRNKMIDGES 564
DB 593 LPISKLDKDFEELPSSPESEGHVFIAPREYCKDLNADSDNTEFLKDFIEMKVTIDPSQ 652
QY 685 CNTDLINRVLLDAGFTNVLQVYVSWKQK-NIKGVKARFVVTGGITRVYKPEAGENWQEN 743
DB 653 CNFLHNLHLLDGTITQQLVERWRQDNLNTYSLAVFAATDGGITRVYKPEAGENWQEN 743
QY 744 PETVEDSFYKRSLDNDNYVFTAFYFNK-SGPGAYES---GIMVSKAVEIYIOCKLLKPAV 799
DB 713 PEPNASFYKRSLDNDNYVFTAFYFNK-SGPGAYES---GIMVSKAVEIYIOCKLLKPAV 799
QY 800 VGKIDVNSWENF-----TKTSIRDP--CAGP-----VCDCKRNSDMDVILDDGGFL 848
DB 773 VGKIDVNSWENF-----TKTSIRDP--CAGP-----VCDCKRNSDMDVILDDGGFL 848
QY 849 MANHDDYTNQIGRFFGEIDPGLMRHLVNTSYAFNKSVDYQSCVCEPAAKOGAGHRSAY 908
DB 832 LSNQNHQWQVGRFFSEVDANLMLYNNSTYTRKESYDQACAPQPPGNLGAAPRGVF 891
QY 909 VPSIADILHGWATAAASWIIQQFLLSLTPRLLAEVEMEDDDFTASLSKOSCITEOTQ 968
DB 892 VPTIADFLNLMWTSAAASWIIQQFLLSLTPRLLAEVEMEDDDFTASLSKOSCITEOTQ 968
QY 969 YFFDNDKSFSGVLDGCGNSRIFHVEKLMNTNLIIFIMVESKGTCPD 1015
DB 951 YFFGWSNAYNALIDCGNSRIFHVEKLMNTNLIIFIMVESKGTCPD 1015

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## RESULT 12

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Q9UEW0 PRELIMINARY; PRT: 1076 AA.
AC Q9UEW0;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Alpha 2 delta calcium channel subunit isoform II.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN NCB1_TaxID=9606;
RP SEQUENCE FROM N.A.
RA Wei M.-H., Latif F., Duh F.-M., Adreazoli-Angeloni D., Kashuba V.,
RA Zabarovsky E., Johnson B., Lerman M.I.

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RT "A new alpha 2 delta subunit of the L-type voltage gated calcium
RT channel resides in the lung cancer critical region on 3p21.3."
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF042793; AAB96914.1;
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS0234; VWA; 1.
SQ SEQUENCE 1076 AA; 122116 MW; EEC474836B7EDA85 CRC64;

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## Query Match

```

Best Local Similarity 53.68; Score 2866.5; DB 4; Length 1076;
Matches 555; Conservative 163; Mismatches 248; Indels 41; Gaps 15;

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QY 33 IKSVDKMQEDLVTLAKTAGVNLQVLDIYKQYQDLYVTEPNARQOLVETIARIEKLLSN 92
DB 1 MOWARLEQEVDCVMRIFGVQQLREIYKDNRLNFVQENEPQKLVKAGDIESLLDR 60
QY 93 RSKALVRLALEAEKQVAAHQWEDFASNEVYVYNAKDDL--DPEKNDSPPGSG--RIKP 147
DB 61 KVQALKRLADAENFQRAHRWQDNKEEDIVYDADAELEDDPESEDVERGSKASTLRL 120
QY 148 VFIDDAFNGRQISYQAAVAHIPTDIYEGSTIVNELNMTSALDEVFKKREEDPSLLQV 207
DB 121 DFIEDPNFKKNVSYAAVQIPDIYKGVIVLNELENVFMEHNRQDPTLLQV 180
QY 208 FGSATGLARYYPASPPWVDNSRTNPKIDLYDVRRRPWYIOGAASPKDMLILVDVSGSVGL 267
DB 181 FGSATGVTYYPATPW---RAPKKIDLYDVRRRPWYIOGAASPKDMLIVVDVSGSVGL 236
QY 268 TLKLIKTSVSEMLETSDDDFVWVASFNEKAQPVSCFTHLVQANVRNKKVFEAOGVMA 296
DB 237 TLKLMKTSVCEMLDTSDDDYVNVASFNEKAQPVSCFTHLVQANVRNKKVFEAOGVMA 296
QY 328 KGTIDYKKGFSFAFEQLLNVNVRNCKITIMLFTDGGGERAQEIPAKYN-KDKKVRVPT 386
DB 297 KGTIDYKKGFSFAFEQLLNVNVRNCKITIMLFTDGGGERAQEIPAKYN-KDKKVRVPT 386
QY 387 FSVGQHNVDYTPLOWMACNKGYYEIPSPISGAIIRNTQYLDVLRPVMVLAGDKAKQVOM 446
DB 357 FSVGQHNVDYTPLOWMACNKGYYEIPSPISGAIIRNTQYLDVLRPVMVLAGDKAKQVOM 446
QY 447 TNYVDALGLGLVVTGLPVFNLTQDGPGEK-----KNQILGVMGIDVALNDIKRLTPNY 472
DB 417 TNYVDALGLGLVVTGLPVFNLTQDGPGEK-----KNQILGVMGIDVALNDIKRLTPNY 472
QY 505 TLCPNGYFAIDPNCYVLLHNPLOPKNSOEPVTLDFDLAELENDIKVEIRNKMIDGES 564
DB 473 TLGANGYVFAIDNGYVLLHNPLOPKNSOEPVTLDFDLAELENDIKVEIRNKMIDGES 564
QY 565 GEKTFRLVKSQDERYIDKGNRTYTWTPVNGTIDYSLALVLTPTSYFYIKAKIETITQAR 624
DB 533 GHKQIRTLVKSQDERYIDVTRNRYTWPIRSTNYSGLVLPYVSTYVLOANLRQILQVK 592
QY 625 SKKGKMKDSETLKPNDFEESGTYFIAPDRYCNLDKISDNNTFEFLNFKVEIRNKMIDGES 564
DB 593 LPISKLDKDFEELPSSPESEGHVFIAPREYCKDLNADSDNTEFLKDFIEMKVTIDPSQ 652
QY 685 CNTDLINRVLLDAGFTNVLQVYVSWKQK-NIKGVKARFVVTGGITRVYKPEAGENWQEN 743
DB 653 CNFLHNLHLLDGTITQQLVERWRQDNLNTYSLAVFAATDGGITRVYKPEAGENWQEN 743
QY 744 PETVEDSFYKRSLDNDNYVFTAFYFNK-SGPGAYES---GIMVSKAVEIYIOCKLLKPAV 799
DB 713 PEPNASFYKRSLDNDNYVFTAFYFNK-SGPGAYES---GIMVSKAVEIYIOCKLLKPAV 799
QY 800 VGKIDVNSWENF-----TKTSIRDP--CAGP-----VCDCKRNSDMDVILDDGGFL 848
DB 773 VGKIDVNSWENF-----TKTSIRDP--CAGP-----VCDCKRNSDMDVILDDGGFL 848
QY 849 MANHDDYTNQIGRFFGEIDPGLMRHLVNTSYAFNKSVDYQSCVCEPAAKOGAGHRSAY 908
DB 832 LSNQNHQWQVGRFFSEVDANLMLYNNSTYTRKESYDQACAPQPPGNLGAAPRGVF 891

```

[3] SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN;  
 RX MEDLINE=98290545; PubMed=9628581;  
 Nagase T., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;  
 RA "Prediction of the coding sequences of unidentified human genes. IX. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";  
 RT DNA Res. 5:31-39(1998).  
 RL EMBL: AF040709; AAC70914.1; -;  
 DR EMBL: AF042792; AAB96913.1; -;  
 DR EMBL: AB011130; BAA25484.1; -;  
 DR InterPro: IPR004010; Cache.  
 DR InterPro: IPR002035; VWF\_A.  
 DR Pfam: PF02743; Cache; 1.  
 DR SMART: SM00327; VWA; 1.  
 DR PROSITE: P50234; VWF; 1.  
 SQ SEQUENCE 1145 AA; 129268 MW; 9ADA4807FC70971B CRC64;

Query Match 54.0%; Score 2887.5; DB 4; Length 1145;  
 Best Local Similarity 54.6%; Pred. No. 1.4e-167;  
 Matches 564; Conservative 164; Mismatches 264; Indels 41; Gaps 15;

7 LAULTLTLSQSLILGPPSPFPSSAVTIKSVKMDQEDLVTLAKTAGSVNQLVDIYEKYQD 66  
 44 LALLLPLLLAAPGASAYSFPQOHTMQHWARRLEQVGMRFPGVQQLREIYKDNRN 103  
 67 LYTVPEPNNAQLVEIARDIEKLLNSRSKALVRLALEAEKVQAAHQRDEAFASNEVYVN 126  
 104 LFEQNEPQKLVKAVAGDIESLDRKQVAKRLADAENFQAKHRWQDNKEEDIVYD 163  
 127 AKDDL--DPEKNDSEPGSO--RIKPVFIDDANFGROISYQHAHVHIPTDIYEGSTVLN 181  
 164 AKADAEIDDPSEDERGSKASTLRLEDFEDPNKKNVNSYAAVQIPTDIYKGSTVLN 223  
 182 ELNNTSALDVEYFKNNREDPELLMQVTSGLARYYPASPWNDSKTPNKIDLYDVR 241  
 224 ELNNTAELENVEMNRDPTLLMQVFGSATGVTRYYPATPW---RAPKKIDLYDVR 279  
 242 PWYIOGASPKDMLILVDVSGVSGLTCLKIRTSVSEMLETLSDDDPFVNVASFNSAODV 301  
 280 PWYIOGASPKDMLIIVDVSGVSGLTCLKMKTSVCEMLDLSDDVNVVASFNEKAQPV 339  
 302 SCFOHLVQANVRNKKVLKDVANNITAKGIDYKGFSPFAEQLLNYSRANCKIIMLF 361  
 340 SCFTHLVQANVRNKKVFEAQVQVAKGTTGKAGFEAFDQLQNSITRANCKIMTF 399  
 362 TDGGERAQEIFAKYN-RDKVRYFTFSVGHNDYDRGPIONMACENKGYIYEIPSIGAIR 420  
 400 TDGGERVQDVEKYNWPNRYVRYFTFSVGHNDYDTPLOWMACANKGYIYEIPSIGAIR 459  
 421 INTQEYLDVGLRPMVLADKAKOVQWNTVYLDALGLGVITGTLVPVNIT--GQNEKTN 478  
 460 INTQEYLDVGLRPMVLADKAKOVQWNTVYEDALGLGVITGTLVPVNLTDGPGEK--- 516  
 479 LKNQLILGVMDVLSLEDKRLTFRTELCPCNGYXFAIDPNGYVLLHPNLPKNPKSQBPV 538  
 517 -KNQLILGVMDIVANDIKRTPNTLPGANGYVFAIDNGYVLLHPNLPKQTTNFRP 575  
 539 TLDFDLAELENIDKIEIRNMKIDGESGEKTFRTLVKSQDERYDKGNRTYTWTPVNGTDY 598  
 576 TLDFDLAELENKEIRSMIDGNKGHKQIRTLVKSIDERYIDERTYNTVTPIRSTNY 635  
 599 SLALVLPYTSFYIYKAKIETITQARKSKGKMKDSETLKPNFEESGYTEFAPRDYCN 658  
 636 SLGLVLPYTSFYIYKAKIETITQARKSKGKMKDSETLKPNFEESGYTEFAPRDYCN 688  
 659 KISDNNTFLLNFEFTDKRTPNPNPCNTDLNRVLLDADAGFTNELVQVYWSKQK-NIKGV 717  
 689 NASDNNTFLLNFEFTDKRTPNPNPCNTDLNRVLLDADAGFTNELVQVYWSKQK-NIKGV 748  
 718 KARFVYVTDGGITRYVYKPEAGENQWNPEDYSDYFSKRSLDNDNVPYTFAPYFNK-SGPGAY 776



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QY 421 INTQEVLDVGRPMVLGADKAKOVQNTNYYLDALGLGLVITGTLVPFNIT--GQENENKTN 478
|||||
Db 460 INTQEVLDVGRPMVLGADKAKOVQNTNYYLDALGLGLVITGTLVPFNITQDGPGEK--- 516
|||||
QY 479 LKNQILGVMGVDVSLDIDKRLTPRTCLPCNGYFEALDNGYVLLHPNLQPNPKSQEPV 538
|||||
Db 517 -KNQILGVMGIDVALNDIKRLTPNTYLGANGYFEALDNGYVLLHPNLKLPOTNFPREV 575
|||||
QY 539 TLFDFDAELEDNKVEIRKMKWIDGESGKTFRTLKVSQDERYIDKGNRTYTWTPVNGTDY 598
|||||
Db 576 TLFDFDAELEDNKVEIRKMKWIDGESGKTFRTLKVSQDERYIDVETRYTWTPVIRSTNY 635
|||||
QY 599 SLALVLPYTFYIKAKIETITQAKSKGKMDSETLKPDPNEESGYTFIAPRDYCN 658
|||||
Db 636 SLGLVLPYTFYIKAKIETITQAKSKGKMDSETLKPDPNEESGYTFIAPRDYCN 695
|||||
QY 659 KISDNTEFLNNEFIDRKTPNPNPCNTDLINRVLLDAGFTNELYQNSKQK-NIKGV 717
|||||
Db 696 NASDNTEFLNNEFIDRKTPNPNPCNTDLINRVLLDAGFTNELYQNSKQK-NIKGV 755
|||||
QY 718 KARFVVDGGITRVYKPEAGENQENPEYEDSFYKRSNDNDNVFTAPYFNK-SQPGAY 776
|||||
Db 756 LAVFAATDGGITRVYKPEAGENQENPEYEDSFYKRSNDNDNVFTAPYFNK-SQPGAY 815
|||||
QY 777 ES---GLMYSKAVEIYQGLKLPVAVGVKIDVNSWENP-----TKTSIRD--CAGP- 825
|||||
Db 816 ENDTVGLVSTAVELSLGRTRLPVAVGVKIDVNSWENP-----TKTSIRD--CAGP- 874
|||||
QY 826 ---VCDCKRNSDVMDCVLLDDGGFLLMANHDDYTNQIGRFFGIDPSLMRHLVNSVYAF 882
|||||
Db 875 SHCEMDCEVNNEDLLCVLDDGGFLVLSNQHNDQVGRFFSEVDANLMLYNNSEYTR 934
|||||
QY 883 NKSYDVQSVCEPGAAPKQAGHRSAYVPSIADILHGWATAAAWSILQOFLLSLTFPR 942
|||||
Db 935 KESYDQAACAPQPPGNLGAAPRGVFTVADFLNLAWTSAAWSLSLFOQLLYGLIYHSW 994
|||||
QY 943 LEAVEMEDDDFTASLSKQSCITEQTQYFFDNDKSKSGVLDGNCGRIFHVEKLMNTNLI 1002
|||||
Db 995 FOADPAEAEQ-SPESTRSSCMKQTYQYFGVSANYNAILDCGNCRLFAOQLTNTNLL 1053
|||||
QY 1003 FIMVESKGTCPCD 1015
|||||
Db 1054 FVVAEKPLCSQCE 1066
|||||

RESULT 8
Q9EQG2 PRELIMINARY; PRT; 1156 AA.
AC Q9EQG2;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Voltage-dependent calcium channel alpha-2-delta-2 subunit.
GN CACNA2D2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TKDU;
RX MEDLINE=21015416; PubMed=11130987;
RA Barclay J., Rees M.;
RT *Genomic organization of the mouse and human alpha2delta2 voltage-
RL dependent calcium channel subunit genes.*;
RL Mamm. Genome 11:1142-1144(2000).
DR ENBL; AF247139; AAG47846.1; -.
DR MGD; MGI:1929813; CACNA2D2.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 1.
DR SMART; SM00327; VWA; 1.
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DR PROSITE; PS0234; VWA; 1.
SQ SEQUENCE 1156 AA; 130611 MW; A732545A2B302A52 CRC64;

Query Match 54.2%; Score 2900.5; DB 11; Length 1156;
Best Local Similarity 54.5%; Pred. No. 2.3e-168;
Matches 564; Conservative 168; Mismatches 268; Indels 35; Gaps 15;

QY 6 LIALTLTLFQSLIGP-SQEPFFPSAVTIKSWDKMOEDLVTLAKTASGVNQLVDIYEKY 64
|||||
Db 45 LLLLPPLLLPLLTAPGASAYSFPOQHTMQHARRLEQIDGVNMRIFGGVQOLREIKDN 104
|||||
QY 65 QDLVYVENNARQOLVEIAARDIEKLLSNRKAIVLALAEAKVQAAHQWREDFASNEVY 124
|||||
Db 105 RNLFEVQENEPQKLVKAGDIESLLDRKQVQALKRLADAENFQKARWQNIKEEDIMY 164
|||||
QY 125 YNAKDDL---DPEKNDSEPGSQ--RIKPVFIDDAFNGQISYQVAAHVHPIRDIYEGSTIV 179
|||||
Db 165 YDAKADAELDDPESEDMERGSKTSALRLDFIEDPNFKKNVSYTAVOIPDIDYKGSIVI 224
|||||
QY 180 LNELNWTLSALDEVFKKNEEDPSLLWQVFGSATGLARYYPASPWVDSNRTNPKIDLYDVR 239
|||||
Db 225 LNELNWTLEALENVFTENRRQDPTLLWQVFGSATGVTTRYYPATPW----RAPKKIDLYDVR 280
|||||
QY 240 RPPWYIOGASPKDMVIIIDVSGSVSGTLTKLRTSVSEMLETSLDDDFVNVASFNSAQ 299
|||||
Db 281 RPPWYIOGASPKDMVIIIDVSGSVSGTLTKLRTSVSEMLETSLDDDFVNVASFNSAQ 340
|||||
QY 300 DYSCFQHLVQANVRNKKVLKDAVNNTAKITDYKGFSAFQEQLLNYNVSRANCKNIIIM 359
|||||
Db 341 PVSCFTHLVQANVRNKKVKEAVQGMVAKGITGYKAGFAYAFDQOLNSNITRANCKNIM 400
|||||
QY 360 LFTDGGERAQEIFAKYN-KKKVVRVFTSVQGHNYDRGPIONMACENKGYEIPSTGA 418
|||||
Db 401 MFTDGGEDRVQDFEKKYNNPRTVRVFTSVQGHNYDVTPLQWNACTNKGYYEIPSTGA 460
|||||
QY 419 IRINTQEVLDVGRPMVLGADKAKOVQNTNYYLDALGLGLVITGTLVPFNIT--GQENK 476
|||||
Db 461 IRINTQEVLDVGRPMVLGADKAKOVQNTNYYLDALGLGLVITGTLVPFNITQDGPGEK- 519
|||||
QY 477 TNLKNQILGVMGVDVSLDIDKRLTPRTCLPCNGYFEALDNGYVLLHPNLQPNPKSQE 536
|||||
Db 520 ---KNQILGVMGIDVALNDIKRLTPNLTGANGYFEALDNGYVLLHPNLKLPQTNPRE 576
|||||
QY 537 PVTDLFDAELEDNKVEIRKMKWIDGESGKTFRTLKVSQDERYIDKGNRTYTWTPVNGT 596
|||||
Db 577 PVTDLFDAELEDNKVEIRKMKWIDGESGKTFRTLKVSQDERYIDVETRYTWTPVIRST 636
|||||
QY 597 DYSLALVLPYTFYIKAKIETITQAKSKGKMDSETLKPDPNEESGYTFIAPRDYCN 656
|||||
Db 637 NYSGLVLPYTFYIKAKIETITQAKSKGKMDSETLKPDPNEESGYTFIAPRDYCN 696
|||||
QY 657 DLKISDNTEFLNNEFIDRKTPNPNPCNTDLINRVLLDAGFTNELYQNSKQK-NIK 715
|||||
Db 697 DLNADSNSTEFLLKDFIELMEKVTYPSKOCNFFLLHNLIDTGTITQQLVVERVWRQDLNTY 756
|||||
QY 716 GVKAERFVTDGGITRVYKPEAGENQENPEYEDSFYKRSNDNDNVFTAPYFNK-SQPG 774
|||||
Db 757 SLALVFAATDGGITRVYKPEAGENQENPEYEDSFYKRSNDNDNVFTAPYFNK-SQPG 816
|||||
QY 775 AYES---GLMYSKAVEIYQGLKLPVAVGVKIDVNSWENP-----TKTSIRD--CAG 824
|||||
Db 817 ELENDTVGLVSTAVELSLGRTRLPVAVGVKIDVNSWENP-----TKTSIRD--CAG 875
|||||
QY 825 P-----VCDCKRNSDVMDCVLLDDGGFLLMANHDDYTNQIGRFFGIDPSLMRHLVNSVY 880
|||||
Db 876 PSSHCMDCEVNNEDLLCVLDDGGFLVLSNQHNDQVGRFFSEVDANLMLYNNSEY 935
|||||
QY 881 AFNKSYDVQSVCEPGAAPKQAGHRSAYVPSIADILHGWATAAAWSILQOFLLSLTFP 940
|||||
Db 936 TRKESYDQAACAPQPPGNLGAAPRGVFTVADFLNLAWTSAAWSLSLFOQLLYGLIYH 995
|||||
QY 941 RLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDKSKSGVLDGNCGRIFHVEKLMNTN 1000
|||||
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DE WUGSC:H_DJ0560014.1 protein (Fragment).
GN WUGSC:H_DJ0560014.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99063792; PubMed=9847074;
RA Sulston J.E., Waterston R.;
RT "Toward a complete human genome sequence.";
RL Genome Res. 8:1097-1108(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Mead K., Bauer C.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006145; AAD20938.1; -.
DR InterPro; IPR004010; Cache.
DR Pfam; PF02743; Cache; 1.
DR PROSITE; PS50234; VWFA; 1.
FT NON_TER
SQ SEQUENCE 745 AA; 84396 MW; BC07B53484B71EA4 CRC64;

Query Match 66.2%; Score 3542; DB 4; Length 745;
Best Local Similarity 99.0%; Pred. No. 7.9e-208;
Matches 665; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 347 YNVSFRANCKIIMLTGDEEERAEQIFAKYKDKKRVFTSVGQHNVDYDRGPQIMWACEN 406
DB 1 YNVSFRANCKIIMLTGDEEERAEQIFAKYKDKKRVFTSVGQHNVDYDRGPQIMWACEN 60
QY 407 KGYEIPISGAIRINTQYLDVLRPMVLGADKAKQVQWNVYLDALGLGVITGILPV 466
DB 61 KGYEIPISGAIRINTQYLDVLRPMVLGADKAKQVQWNVYLDALGLGVITGILPV 120
QY 467 FNITQENKNTLNKQILGVMGVDVSLDIKRLTPFTLCPNGYFAIDPNGVYLLHPN 526
DB 121 FNITQENKNTLNKQILGVMGVDVSLDIKRLTPFTLCPNGYFAIDPNGVYLLHPN 180
QY 527 LQPKPKSQEPTVLDLDAELNDLKVEIRNKMIDGEGEKTFTLVKQSDERYIDKGNR 586
DB 181 LQPKPKSQEPTVLDLDAELNDLKVEIRNKMIDGEGEKTFTLVKQSDERYIDKGNR 240
QY 587 TYTTPVNGTQSYLALVLPYTSFYIKAKIETITQARSKKGMKDSITLKPDPNFESGY 646
DB 241 TYTTPVNGTQSYLALVLPYTSFYIKAKIETITQARSKKGMKDSITLKPDPNFESGY 300
QY 647 TFIAPRDYCNLDKISDNTEFLNFEPIIDRKTPNPNPSCNTDLINRVLLDAGFTNELVN 706
DB 301 TFIAPRDYCNLDKISDNTEFLNFEPIIDRKTPNPNPSCNTDLINRVLLDAGFTNELVN 360
QY 707 YWSKQKNIKGKARVVTGDTGTRVYKPEACENQENPETVEDSFYKRSLDNDNVYFAP 766
DB 361 YWSKQKNIKGKARVVTGDTGTRVYKPEACENQENPETVEDSFYKRSLDNDNVYFAP 420
QY 767 YFNKSGPGAYESGIMVSKAVEIYIQGLLKPVAVYGIKIDNSWLENFTKTSIRDPACAGV 826
DB 421 YFNKSGPGAYESGIMVSKAVEIYIQGLLKPVAVYGIKIDNSWLENFTKTSIRDPACAGV 480
QY 827 CDCRNSDVCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLNLSVYAFNKS 886
DB 481 CDCRNSDVCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLNLSVYAFNKS 540
QY 887 DYQSVCEPGAAPKQAGHRSAYVPSIADILHIGHWATAAASWILQOFLLSITPPRLLEAV 946
DB 541 DYQSVCEPGAAPKQAGHRSAYVPSIADILHIGHWATAAASWILQOFLLSITPPRLLEAV 600

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QY 947 EMEDDDFATSLSKQSCITEQTOYFFDNDKSFSGVLDGNCGRIFHVEKLMNTNLIIFMV 1006
DB 601 EMEDDDFATSLSKQSCITEQTOYFFDNDKSFSGVLDGNCGRIFHVEKLMNTNLIIFMV 660
QY 1007 ESKGTCPCDTRL 1018
DB 661 ESKGTCPCDTRL 672

RESULT 7
Q9NY47
ID Q9NY47 PRELIMINARY; PRT; 1150 AA.
AC Q9NY47;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Calcium channel, alpha 2/delta subunit 2.
GN CACNA2D2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYROID;
RA Klugbauer N.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=THYROID;
RA Hobom M., Dai S., Marais E., Lacinova L.;
RT "Neuronal distribution and functional characterization of the calcium channel alpha2delta-2 subunit.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ251368; CAB86193.1; -.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50234; VWFA; 1.
SQ SEQUENCE 1150 AA; 129876 MW; 37B75F687AF5E73C CRC64;

Query Match 54.5%; Score 2915; DB 4; Length 1150;
Best Local Similarity 54.8%; Pred. No. 2.9e-169;
Matches 566; Conservative 166; Mismatches 267; Indels 34; Gaps 14;

QY 7 LALTTLTFLQSLILGPPSSQEPSPSAVTIKSWVDKMOEDLVTLAKTASGVQLVDIYKYQD 66
DB 44 LALLLLPLLLAAPGASAYSFPQOHTWQHWARDEVEVGVMRIFGVQQLREIYKDNRN 103
QY 67 LYTVPPNARQIVELIARDEIEKLLSNRSKALVRLALEAEKVQAAHQWRDFAASNEVYVN 126
DB 104 LFEVQENEPQKLEKAVAGDIESLLDRKQVQALKRLADAAENFOKARHQDNKEEDIVYD 163
QY 127 AKDDL--DPEKNDSEPGSQ--RIKPVFIDANFGRIQSYQHAHVHIPTDIEGSTIVLN 181
DB 164 AKADAEUDDPESEDDEVRGSKASTLRDLFEDPNFKKNVSYAAVQIPTDIYKGVSTVLN 223
QY 182 ELNWTLSALDEVEFKKREEDPSSLVQVFGSATGLARYVSPASPVWVDSNRSTNPKIDLYDVR 241
DB 224 ELNWTLEALNVFENRRQDPTLLWQVFGSATGTRYYPATPW----RAPKKIDLYDVR 279
QY 242 PWYIQGAASPDKMLILVDVSGSVSGITLKITSVSEMLETISDDDFVNVASFNSNAQDV 301
DB 280 PWYIQGAASPDKMVIIVDVSGSVSGITLKITSVSEMLETISDDDFVNVASFNEKAQPV 339
QY 302 SCFOHLVQANVRNKKVYLDKAVNNITAGTIDYKKGFSFAFQELLNLYNVSFRANCKIIMLF 361
DB 340 SCFTHLVQANVRNKKVYKAVQGMVAKGTGKAGFEYAFDQLQNSNITRANCKNIMWF 399
QY 362 TDGGEERAQEIFAKYN-KDKKRVFTSVGQHNVDYDRGPQIMWACENKGYEIPISGAIR 420
DB 400 TDGGEERVDQVFEKYNWPNRTVYRFTSVGQHNVDYDRGPQIMWACENKGYEIPISGAIR 459

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Db 541 LRKRRPNVQPKSQEPVTLDFDLAELENEIKVEIRNMKIDGESGEKTFRTLVKSQDERYI 600
QY 582 DGNRRYVTPVNGTDSIALVLPTYSFYIIKAKIETITQARSKKGMKDSFTLKPDNF 641
Db 601 DGNRRYVTPVNGTDSIALVLPTYSFYIIKAKIETITQARY-----SETLKPDNF 653
QY 642 EESGYTFIAPRDYCNLDKISDNNTFLLNPNFIDRKTPNPNPSCNTDLINRVLLDAGFTN 701
Db 654 EESGYTFIAPREVCNDLKPSDNNTFLLNPNFIDRKTPNPNPSCNTDLINRVLLDAGFTN 713
QY 702 ELVQNTWSKOKNTKGVKARVVDGTRVYPKEAGENWQENPETEYDSFYKRSNDNXY 761
Db 714 ELVQNTWSKOKNTKGVKARVVDGTRVYPKEAGENWQENPETEYDSFYKRSNDNXY 773
QY 762 VFTAPYFNKSGPAYESGIMVSKAVEIYTOGKLLKPAVVGKIDVNSWTENFTKTSIRDP 821
Db 774 VFTAPYFNKSGPAYESGIMVSKAVEIYTOGKLLKPAVVGKIDVNSWTENFTKTSIRDP 833
QY 822 CAGPVCCKRNSDVMDCVILDDGFLLMANHHDDYTNOIGRFFGEIDPSLMRHLVNTSVYA 881
Db 834 CAGPVCCKRNSDVMDCVILDDGFLLMANHHDDYTNOIGRFFGEIDPSLMRHLVNTSVYA 893
QY 882 FNKSYDQSCVCEGAPKQAGHRSAYVPSIADILHIGWATAAANSILQOFLLSLTFPR 941
Db 894 FNKSYDQSCVCEGAPKQAGHRSAYVPSIADILHIGWATAAANSILQOFLLSLTFPR 953
QY 942 LLEAVEMEDDFTASLSKQSCITEQTYFPDNDKSFSGVLDCGNCGRSRIFPHVEKLMNTNL 1001
Db 954 LLEAVEMEDDFTASLSKQSCITEQTYFPDNDKSFSGVLDCGNCGRSRIFPHVEKLMNTNL 1013
QY 1002 IFIMVESKGTCPDTRL 1018
Db 1014 VFIMVESKGTCPDTRL 1030

RESULT 5
Q8VHS9 PRELIMINARY; PRT; 1079 AA.
AC Q8VHS9;
AT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE L-type calcium channel alpha2/delta subunit.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=HEART;
RX MEDLINE=21601730; PubMed=11604404;
RA Yamada Y., Nagashima M., Tsutsuura M., Kobayashi T., Seki S.,
RA Makita N., Horio Y., Tohse N.;
RT "Cloning of a functional splice variant of L-type calcium channel
beta2 subunit from rat heart.";
RL J. Biol. Chem. 276:47163-47170(2001).
DR EMBL; AF400662; AAL47093.1;
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; WWF_A.
DR Pfam; PF02743; Cache; 1.
DR Pfam; PF00092; wva; 1.
DR SMART; SM00327; WVA; 1.
DR PROSITE; PS0234; WVA; 1.
SQ SEQUENCE 1079 AA; 122172 MW; DC4A3641195B546C CRC64;

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Query Match 96.08; Score 5135; DB 11; Length 1079;  
 Best Local Similarity 95.88; Pred. No. 8e-305;  
 Matches 975; Conservative 20; Mismatches 11; Indels 12; Gaps 2;

QY 1 MAAGCLLATLTTLFQSLIIGPSSQEPFPFSAVTKISWDKMQEDLVTAKTASGVNQLVDI 60  
 Db 1 MAAGCLLATLTTLFQSLIIGPSSQEPFPFSAVTKISWDKMQEDLVTAKTASGVNQLADI 60

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QY 61 YEKYODLVTPPNARQVLVEAARDIEKLLSNRSKALVRLALEAEKVOAAHQWREDFASN 120
Db 61 YEKYODLVTPPNARQVLVEAARDIEKLLSNRSKALVRLALEAEKVOAAHQWREDFASN 120
QY 121 EVVYNAKDDDDPEKNDSEPGSORIKPVFIIDANFGROISYQHAHVHIPTDIYEGSTIVL 180
Db 121 EVVYNAKDDDDPEKNESESGORIKPVFIIDANFGROISYQHAHVHIPTDIYEGSTIVL 180
QY 181 NELNWTNSALDEVFKKNREDEPSLLMQVFGSATGLARYYPASPVWDNSRTPNKIDLYDVR 240
Db 181 NELNWTNSALDEVFKKNREDEPSLLMQVFGSATGLARYYPASPVWDNSRTPNKIDLYDVR 240
QY 241 RPWYIQGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSLDDDDPVNVASNSNAQD 300
Db 241 RPWYIQGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSLDDDDPVNVASNSNAQD 300
QY 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEQLLNVNVRANCKIIML 360
Db 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEQLLNVNVRANCKIIML 360
QY 361 FTDGGEERAQELFAKYNKDKKVRVFTFSVGQHNDRGPQIOMMACENKGYIYEIPSIGAIR 420
Db 361 FTDGGEERAQELFAKYNKDKKVRVFTFSVGQHNDRGPQIOMMACENKGYIYEIPSIGAIR 420
QY 421 INTQEYLDVLRPMVLADKAKQVQWNTVYLDALGLVITGLTPVFNITQGNENKTNLK 480
Db 421 INTQEYLDVLRPMVLADKAKQVQWNTVYLDALGLVITGLTPVFNITQGNENKTNLK 480
QY 481 NQLILGVGVDSVLEDIKRLTPREFTLCPNGYFAIDPNGYVLLHPNLOPKNPKSQEPVTL 540
Db 481 NQLILGVGVDSVLEDIKRLTPREFTLCPNGYFAIDPNGYVLLHPNLOPKNPKSQEPVTL 540
QY 541 DFLDAELNDIKVEIRNMKIDGESGEKTFRTLVKSQDERYIDKGNRTYTPVNGTDSL 600
Db 541 DFLDAELNDIKVEIRNMKIDGESGEKTFRTLVKSQDERYIDKGNRTYTPVNGTDSL 600
QY 601 ALVLPYSFYIIKAKIETITQARSKKGMKDSFTLKPDNFESGYTFIAPREYCNLDKP 648
Db 601 ALVLPYSFYIIKAKIETITQARSKKGMKDSFTLKPDNFESGYTFIAPREYCNLDKP 648
QY 648 SDNTEFFLLNPNFIDRKTPNPNPSCNTDLINRVLLDAGFTNVLQVYWSKQNKIKGVKAR 720
Db 648 SDNTEFFLLNPNFIDRKTPNPNPSCNTDLINRVLLDAGFTNVLQVYWSKQNKIKGVKAR 720
QY 721 FVVTGGITRVYPKEAGENWQENPETEYDSFYKRSIDNDNYYVFTAPYFNKSGPAYESGI 780
Db 721 FVVTGGITRVYPKEAGENWQENPETEYDSFYKRSIDNDNYYVFTAPYFNKSGPAYESGI 780
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWTENFTKTSIRDPKAGVPCDCRNSDVMDCVI 840
Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWTENFTKTSIRDPKAGVPCDCRNSDVMDCVI 840
QY 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLNIVSYAFNKSIDYQSCVCEGAPKQ 900
Db 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLNIVSYAFNKSIDYQSCVCEGAPKQ 900
QY 901 GAGHRSAYVPSIADILHIGWATAAANSILQOFLLSLTPRLLLEAVEMEDDFTASLSKQ 960
Db 901 GAGHRSAYVPSIADILHIGWATAAANSILQOFLLSLTPRLLLEAVEMEDDFTASLSKQ 960
QY 961 SCITEQTYFPDNDKSFSGVLDCGNCGRSRIFHVEKLMNTNLIFIMVESKGTCPDTRL 1018
Db 961 SCITEQTYFPDNDKSFSGVLDCGNCGRSRIFHVEKLMNTNLIFIMVESKGTCPDTRL 1018
QY 961 SCITEQTYFPDNDKSFSGVLDCGNCGRSRIFHVEKLMNTNLIFIMVESKGTCPDTRL 1006

```

RESULT 6

Q9UDQ3

ID Q9UDQ3 PRELIMINARY; PRT; 745 AA.

AC Q9UDQ3;

DT 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)



661 SDNTEFLNFEIDRKTPNPNPCNTDNLINRILLDAGFTNVLQVYWSKQNIKGVKAR 720  
721 FVYDGGITRVTPKEAGENQWNPETEDSFYKRSILDNDNYVFTAPYFNKSPGAYESGI 780  
721 FVYDGGITRVTPKEAGENQWNPETEDSFYKRSILDNDNYVFTAPYFNKSPGAYESGI 780  
781 MYSKAVEIYIOCKLLKPAVVGKIDVNSWIEFTKTSIRDCAGVPVCDCKRNSDVMDCVI 840  
781 MYSKAVEIYIOCKLLKPAVVGKIDVNSWIEFTKTSIRDCAGVPVCDCKRNSDVMDCVI 840  
841 LDGGFLLMANHDDYTNOIGREFGIDPFSMLRHLVNIISVAFNKSIDYQSCVCEPAAPKQ 900  
841 LDGGFLLMANHDDYTNOIGREFGIDPFSMLRHLVNIISVAFNKSIDYQSCVCEPAAPKQ 900  
901 GAGHSAYVPSTADILHIGWATAAASILQOFLSLTFPRLLLEAVEMDDFTASLSKQ 960  
901 GAGHSAYVPSTADILHIGWATAAASILQOFLSLTFPRLLLEAVEMDDFTASLSKQ 960  
961 SCITEQTYFFDNDKSFSGVLDCGNCRIHFVEKLMNTNLIIFIMVESKGTCPDTRL 1018  
961 SCITEQTYFFDNDKSFSGVLDCGNCRIHFVEKLMNTNLIIFIMVESKGTCPDTRL 1018  
RESULT 4  
008532 PRELIMINARY; PRT: 1103 AA.  
AC 008532: 008533; 008534; 008535; 008536;  
DT 01-JUN-1998 (Tremblrel. 06, Created)  
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)  
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
DE Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta  
subunits precursor.  
GN CACNA2D1 OR CACNA2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N. A.  
RC TISSUE-BRAIN;  
RX MEDLINE=97113514; PubMed=8955374;  
RA Angelotti T., Hofmann F.;  
RL FEBS Lett. 397:331-337(1996).  
CC -1- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN  
EXCITATION-CONTRACTION COUPLING.  
CC -1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:  
ALPHA-1, ALPHA-2, BETA AND GAMMA.  
CC -1- SUBUNIT: ALPHA-2 AND DELTA FORM HETERODIMERS THAT ARE DISULFIDE-  
LINKED.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -1- ALTERNATIVE PRODUCTS: FIVE FORMS OF THE PROTEIN, ISOFORMS 2A-2E,  
ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THE  
SEQUENCE SHOWN HERE IS THAT OF ISOFORM 2A.  
CC -1- TISSUE SPECIFICITY: ISOFORM 2A IS EXPRESSED IN SKELETAL MUSCLE AND  
AORTA. 2B IS EXPRESSED IN BRAIN, 2C IS EXPRESSED IN HEART, 2D IS  
EXPRESSED IN HEART AND SMOOTH MUSCLE, AND 2E IS EXPRESSED IN  
SMOOTH MUSCLE. ALL FIVE ISOFORMS ARE EXPRESSED IN THE  
CARDIOVASCULAR SYSTEM.  
CC -1- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM  
A PRECURSOR FORM.  
CC -1- SIMILARITY: TO OTHER SPECIES ALPHA-2 SUBUNIT.  
DR EMBL; U73484; AAB50139.1; -  
DR EMBL; U73485; AAB50140.1; -  
DR EMBL; U73483; AAB50138.1; -  
DR EMBL; U73486; AAB50141.1; -  
DR EMBL; U73487; AAB50142.1; -  
DR MGD; MGI:88295; CACna2d1.  
DR InterPro: IPR004010; Cache.  
DR InterPro: IPR002035; VWF.A.  
DR Pfam: PF02743; Cache; 1.  
DR Pfam: PF00092; vwa; 1.  
DR SMART; SM00327; VWA; 1.  
DR PROSITE; PS0234; VWF.A; 1.

Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;  
Calcium channel; Glycoprotein; Phosphorylation; Signal;  
Alternative splicing.  
KW SIGNAL 1 24  
KW CHAIN 25 957  
KW CHAIN 958 1103  
KW TRANSMEM 446 469  
KW TRANSMEM 918 942  
KW TRANSMEM 1079 1098  
KW MOD\_RES 501 501  
KW MOD\_RES 845 845  
KW CARBOHYD 92 92  
KW CARBOHYD 136 136  
KW CARBOHYD 184 184  
KW CARBOHYD 324 324  
KW CARBOHYD 348 348  
KW CARBOHYD 475 475  
KW CARBOHYD 604 604  
KW CARBOHYD 613 613  
KW CARBOHYD 675 675  
KW CARBOHYD 781 781  
KW CARBOHYD 824 824  
KW CARBOHYD 888 888  
KW CARBOHYD 895 895  
KW CARBOHYD 985 985  
KW CARBOHYD 998 998  
KW VARSPLIC 531 549  
KW VARSPLIC 531 554  
KW VARSPLIC 644 644  
SQ SEQUENCE 1103 AA; 124629 MW; 103773B4735120D4 CRC64;  
Query Match 96.4%; Score 5159; DB 11; Length 1103;  
Best Local Similarity 94.5%; Pred. No. 2.8e-306;  
Matches 980; Conservative 22; Mismatches 9; Indels 26; Gaps 2;  
Y -> SKKGKMD (IN ISOFORMS 2A, 2D AND 2E).

QY 1 MAAGCLLALTLFQSLIGPSQEPFPPSAVTKSVWDMQEDLVTLAKTASGVQLADI 60  
DB 1 MAAGCLLALTLFQSLIGPSQEPFPPSAVTKSVWDMQEDLVTLAKTASGVQLADI 60  
QY 61 YEKYQDLYTVEPNNAOLVIAARDIEKLLNSRKALVRLALEAEKVAQAHOHREDFASN 120  
DB 61 YEKYQDLYTVEPNNAOLVIAARDIEKLLNSRKALVRLALEAEKVAQAHOHREDFASN 120  
QY 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFIDANFGRQISYOHAAVHPTDIYEGSTVL 180  
DB 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFIDANFGRQISYOHAAVHPTDIYEGSTVL 180  
QY 181 NELNWTSLADVEYFKKNREDEPSSLQVFGSATGLARYYPASPVVDNSRTPNKIDLYDVR 240  
DB 181 NELNWTSLADVEYFKKNREDEPSSLQVFGSATGLARYYPASPVVDNSRTPNKIDLYDVR 240  
QY 241 RPWYIQAASPKDMLILVDVSGVSGTLKIRTYSVEMLETSLDDDDFVNVASFNNAQD 300  
DB 241 RPWYIQAASPKDMLILVDVSGVSGTLKIRTYSVEMLETSLDDDDFVNVASFNNAQD 300  
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSAFQELINYNVSRANCKIIML 360  
DB 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSAFQELINYNVSRANCKIIML 360  
QY 361 FTDGGEERAQEIFAKYKNDKVRVFTFSVGHNYDRGPIQMACENKGYEIPSGAIR 420  
DB 361 FTDGGEERAQEIFAKYKNDKVRVFTFSVGHNYDRGPIQMACENKGYEIPSGAIR 420  
QY 421 INTQEYLDVLGRPMVLADGKAKQVQWNVYLDALGLVITGTLVPVNTIQENKNTLK 480  
DB 421 INTQEYLDVLGRPMVLADGKAKQVQWNVYLDALGLVITGTLVPVNTIQENKNTLK 480  
QY 481 NQLILGVMGVDVSLDIKRLTPRETLPNGYFAIDPNGYVLLHPNLQPK----- 530  
DB 481 NQLILGVMGVDVSLDIKRLTPRETLPNGYFAIDPNGYVLLHPNLQPKIGVIGPTIN 540  
QY 531 -----NPKSQFPVTLDFDLAELENDIKVEIRNKMIDGESGEKTFRTLVKSQDERYI 581

QY	121	EVVYNAKDDLPKNDSEPGSORIKPVFIDDANFCRQISYQHAHVHIPTDIYEGSTIVL	180
Db	121	EVVYNAKDDLPKNDSEPGSORIKPVFIEDANFCRQISYQHAHVHIPTDIYEGSTIVL	180
QY	181	NELNWTSAIDVFPKKNREEDPSLLWQVFGSATGLARYYPASVPWVNSRTPNKIDLYDVR	240
Db	181	NELNWTSAIDVFPKKNREEDPSLLWQVFGSATGLARYYPASVPWVNSRTPNKIDLYDVR	240
QY	241	RPWYIOGAASPKDMLILVDVSGVSGLTLLKIRTSYSEMLETLSDDDFVNVSFNSNAQD	300
Db	241	RPWYIOGAASPKDMLILVDVSGVSGLTLLKIRTSYSEMLETLSDDDFVNVSFNSNAQD	300
QY	301	VSCFQHLVQANVRNKKVLDKAVNNITAKGTTDYKKGFSFAFEOLLNYSRANCKNIIML	360
Db	301	VSCFQHLVQANVRNKKVLDKAVNNITAKGTTDYKKGFSFAFEOLLNYSRANCKNIIML	360
QY	361	FTDGGERAQEIFAKYKNDKKVVFVSVGQHNDRGPIQWACENKGYIYEIPISGAIR	420
Db	361	FTDGGERAQEIFAKYKNDKKVVFVSVGQHNDRGPIQWACENKGYIYEIPISGAIR	420
QY	421	INTQEYLDVLRPMVLADKAKQVQWNTNVDLALEGLVITGTLPVNITQGENKTNLK	480
Db	421	INTQEYLDVLRPMVLADKAKQVQWNTNVDLALEGLVITGTLPVNITQGENKTNLK	480
QY	481	NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYIFAIDPNGYVLLHPNLPKPKSQBPVTL	540
Db	481	NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYIFAIDPNGYVLLHPNLPKPKSQBPVTL	540
QY	541	DFLDAELENDDIKVEIRNKMIDGESGKTFRTLKVSQDERYIDKGNRTYTTVPNGTDYSL	600
Db	541	DFLDAELENDDIKVEIRNKMIDGESGKTFRTLKVSQDERYIDKGNRTYTTVPNGTDYSL	600
QY	601	ALVLPYTFYIYKAKIETITQARSKKGMKDSITLKPDPFESGYTFIAPROYCNDLKI	660
Db	601	ALVLPYTFYIYKAKIETITQARSKKGMKDSITLKPDPFESGYTFIAPROYCNDLKI	660
QY	661	SDNTEFLLNPNFEDIRKTPNPNPCNTDLNRLVLLDAGFTNQLVQVWSKQNKIKGVKAR	720
Db	661	SDNTEFLLNPNFEDIRKTPNPNPCNTDLNRLVLLDAGFTNQLVQVWSKQNKIKGVKAR	720
QY	721	ELVQVWSKQNKIKGVKARVVTGGITRVYPKEAGENQWNPETYEDSFYKRSLDNDY	780
Db	721	ELVQVWSKQNKIKGVKARVVTGGITRVYPKEAGENQWNPETYEDSFYKRSLDNDY	780
QY	781	VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGLKLPVAVGKIDVNSWIENTKTSIRDP	840
Db	781	VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGLKLPVAVGKIDVNSWIENTKTSIRDP	840
QY	822	CAGPVCDCKRNSDMVDCVILDDGGFLLMANHDDYTQIGRFFGEIDPSLMRHLNYSIYA	881
Db	841	CAGPVCDCKRNSDMVDCVILDDGGFLLMANHDDYTQIGRFFGEIDPSLMRHLNYSIYA	900
QY	882	FNKSYDYQSVCPGAPKOGAGHRSAYVPSIADILHIGWATAAWSLQOFLSLTFPR	941
Db	901	FNKSYDYQSVCPGAPKOGAGHRSAYVPSIADILHIGWATAAWSLQOFLSLTFPR	960
QY	942	LLEAVEMEDDDFTASLSKQSCITEQTYFFDNDKSFSGVLDGNCRSIFHVEKLMNTNL	1001
Db	961	LLEAVEMEDDDFTASLSKQSCITEQTYFFDNDKSFSGVLDGNCRSIFHVEKLMNTNL	1020
QY	1002	IFIMVESKGTCPCDTRL	1018
Db	1021	IFIMVESKGTCPCDTRL	1037
RESULT 3			
Q9ERS3	PRELIMINARY: PRT: 1091 AA.		
ID	Q9ERS3		
AC	Q9ERS3		
DT	01-MAR-2001 (TremBLrel. 16, Created)		
DT	01-MAR-2001 (TremBLrel. 16, Last sequence update)		
DT	01-JUN-2002 (TremBLrel. 21, Last annotation update)		

Voltage-gated calcium channel alpha2/delta-1 subunit.  
Rattus norvegicus (Rat).  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
NCBI\_TaxID=10116;  
[1]  
SEQUENCE FROM N.A.  
STRAIN=SPRAGUE-DAWLEY; TISSUE=SUPERIOR CERVICAL GANGLIA;  
Lin Y., Lipscombe D.;  
Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
EMBL: AF286488; AGS28164.1;  
DR InterPro: IPR004010; Cache.  
DR InterPro: IPR002035; VWF\_A.  
DR Pfam: PF02743; Cwch; 1.  
DR SMART: SM00327; VWA; 1.  
DR PROSITE: PS50234; VWF; 1.  
FT VARIANT 209 212 GSAT -> AADR.  
FT VARIANT 338 338 S -> T.  
FT VARIANT 599 600 SL -> RY.  
FT VARIANT 869 869 S -> R.  
SQ SEQUENCE 1091 AA; 123467 MW; C155088971628E19 CRC64;  
Query Match 97.8%; Score 5231; DB 11; Length 1091;  
Best Local Similarity 97.1%; Pred. No. 1, le-310;  
Matches 988; Conservative 20; Mismatches 10; Indels 0; Gaps 0;  
QY 1 MAAGCILLALTTLTFLFOSLLIGSPSPPEPPSAVTKSWDKMQEDLVTLAKTASGVNQLVDI 60  
Db 1 MAAGCILLALTTLTFLFOSLLIGSPSPPEPPSAVTKSWDKMQEDLVTLAKTASGVNQLADI 60  
QY 61 YKYQDLYTVENNARQOLVEIAARDIEKLLSNRKAALYALAEAKVQAAHQRREDFASN 120  
Db 61 YKYQDLYTVENNARQOLVEIAARDIEKLLSNRKAALYALAEAKVQAAHQRREDFASN 120  
QY 121 EVVYNAKDDLPKNDSEPGSORIKPVFIDDANFCRQISYQHAHVHIPTDIYEGSTIVL 180  
Db 121 EVVYNAKDDLPKNDSEPGSORIKPVFIEDANFCRQISYQHAHVHIPTDIYEGSTIVL 180  
QY 181 NELNWTSAIDVFPKKNREEDPSLLWQVFGSATGLARYYPASVPWVNSRTPNKIDLYDVR 240  
Db 181 NELNWTSAIDVFPKKNREEDPSLLWQVFGSATGLARYYPASVPWVNSRTPNKIDLYDVR 240  
QY 241 RPWYIOGAASPKDMLILVDVSGVSGLTLLKIRTSYSEMLETLSDDDFVNVSFNSNAQD 300  
Db 241 RPWYIOGAASPKDMLILVDVSGVSGLTLLKIRTSYSEMLETLSDDDFVNVSFNSNAQD 300  
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGTTDYKKGFSFAFEOLLNYSRANCKNIIML 360  
Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGTTDYKKGFSFAFEOLLNYSRANCKNIIML 360  
QY 361 FTDGGERAQEIFAKYKNDKKVVFVSVGQHNDRGPIQWACENKGYIYEIPISGAIR 420  
Db 361 FTDGGERAQEIFAKYKNDKKVVFVSVGQHNDRGPIQWACENKGYIYEIPISGAIR 420  
QY 421 INTQEYLDVLRPMVLADKAKQVQWNTNVDLALEGLVITGTLPVNITQGENKTNLK 480  
Db 421 INTQEYLDVLRPMVLADKAKQVQWNTNVDLALEGLVITGTLPVNITQGENKTNLK 480  
QY 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYIFAIDPNGYVLLHPNLPKPKSQBPVTL 540  
Db 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYIFAIDPNGYVLLHPNLPKPKSQBPVTL 540  
QY 541 DFLDAELENDDIKVEIRNKMIDGESGKTFRTLKVSQDERYIDKGNRTYTTVPNGTDYSL 600  
Db 541 DFLDAELENDDIKVEIRNKMIDGESGKTFRTLKVSQDERYIDKGNRTYTTVPNGTDYSL 600  
QY 601 ALVLPYTFYIYKAKIETITQARSKKGMKDSITLKPDPFESGYTFIAPROYCNDLKI 660  
Db 601 ALVLPYTFYIYKAKIETITQARSKKGMKDSITLKPDPFESGYTFIAPROYCNDLKI 660  
QY 661 SDNTEFLLNPNFEDIRKTPNPNPCNTDLNRLVLLDAGFTNQLVQVWSKQNKIKGVKAR 720  
Db 661 SDNTEFLLNPNFEDIRKTPNPNPCNTDLNRLVLLDAGFTNQLVQVWSKQNKIKGVKAR 720



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OM protein - protein search, using sw model

Run on: February 10, 2003, 14:13:55 ; Search time 39.7275 Seconds  
(without alignments)  
5279.867 Million cell updates/sec

Title: US-10-090-827-6  
Perfect score: 5349  
Sequence: 1 MAAGCLLALTTLFQSLLLIG.....TNLIFIMVESKGTCPDTRL 1018

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organalle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriaph:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5349	100.0	1091	6 077773	O77773 sus scrofa
2	5284.5	98.8	1110	4 Q9UIU0	Q9ui00 homo sapien
3	5231	97.8	1091	11 Q9ERS3	Q9ers3 rattus norv
4	5159	96.4	1103	11 O08532	O08532 mus musculu
5	5135	96.0	1079	11 O8VH59	O8vhs9 rattus norv
6	3542	66.2	745	4 Q9UDQ3	Q9udq3 homo sapien
7	2915	54.5	1150	4 Q9NY47	Q9ny47 homo sapien
8	2900.5	54.2	1156	11 Q9EQG2	Q9eqg2 mus musculu
9	2887.5	54.0	1143	4 Q9NY48	Q9ny48 homo sapien
10	2887.5	54.0	1145	4 Q9Y268	Q9y268 homo sapien
11	2875	53.7	1084	11 Q920H6	Q920h6 mus musculu
12	2866.5	53.6	1076	4 Q9UEW0	Q9uew0 homo sapien
13	2691	50.3	975	4 Q9NSA6	Q9nsa6 homo sapien
14	1112	20.8	1091	11 Q9Z1L5	Q9z1l5 mus musculu
15	1045	19.5	997	4 Q9NY16	Q9ny16 homo sapien
16	1021.5	19.1	1218	5 Q8T9C3	Q8t9c3 drosophila

17	941.5	17.6	2190	5	Q9NK64	Q9nk64 drosophila
18	926.5	17.3	2172	5	Q9VJW0	Q9vjw0 drosophila
19	899	16.8	1191	5	Q9VJN7	Q9vjn7 drosophila
20	897.5	16.8	1255	5	Q9NK83	Q9nk83 drosophila
21	875	16.4	170	4	Q9UDL7	Q9udl7 homo sapien
22	848.5	15.9	1022	5	Q9V6T7	Q9v6t7 drosophila
23	759.5	14.2	519	4	Q9NY18	Q9ny18 homo sapien
24	661	12.4	317	11	Q920H5	Q920h5 mus musculu
25	570.5	10.7	1148	5	Q17517	Q17517 caenorhabdi
26	549	10.3	842	5	Q95R75	Q95r75 drosophila
27	516.5	9.7	104	4	Q9UDH1	Q9udh1 homo sapien
28	515	9.6	100	6	Q9GLH1	Q9glh1 bos taurus
29	496.5	9.3	121	4	Q9UD82	Q9ud82 homo sapien
30	479	9.0	98	4	Q9UDU5	Q9udu5 homo sapien
31	467	8.7	97	4	Q9UD80	Q9ud80 homo sapien
32	404	7.6	77	4	Q95026	Q95026 homo sapien
33	330.5	6.2	1185	4	Q9HGT9	Q9hcj9 homo sapien
34	319.5	6.0	223	11	Q9R142	Q9r142 mus musculu
35	229	4.3	978	6	Q95KE0	Q95ke0 macaca fasc
36	217	4.1	1449	5	Q9V917	Q9v917 drosophila
37	201.5	3.8	886	11	Q91WG9	Q91wg9 mus musculu
38	190.5	3.6	1450	16	Q9CE07	Q9ce07 lactococcus
39	177.5	3.3	494	5	Q9U7P4	Q9u7p4 eufolliculi
40	170.5	3.2	1819	16	Q97K40	Q97k40 clostridium
41	167	3.1	796	17	Q9HJRO	Q9hjr0 thermoplasm
42	167	3.1	800	17	Q9FAH3	Q9fah3 thermoplasm
43	165	3.1	459	16	O25905	O25905 helicobacte
44	164.5	3.1	789	2	Q45793	Q45793 bacillus th
45	164	3.1	614	16	Q8XN21	Q8xn21 clostridium

#### ALIGNMENTS

RESULT 1

O77773 ID O77773 PRELIMINARY; PRT; 1091 AA.  
AC O77773; 1998 (TREMREL. 08, Created)  
DT 01-NOV-1998 (TREMREL. 08, Last sequence update)  
DT 01-NOV-1998 (TREMREL. 08, Last sequence update)  
DT 01-MAR-2002 (TREMREL. 20, Last annotation update)  
DE Voltage-dependent calcium channel alpha-2 delta subunit precursor.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9623;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN CORTEX;  
RX MEDLINE=98411353; PubMed=9738015;  
RA Brown J.P., Gee N.S.;  
RT "Cloning and deletion mutagenesis of the alpha2 delta calcium channel  
RT subunit from porcine cerebral cortex. Expression of a soluble form of  
RT the protein that retains [3H]gabapentin binding activity.";  
RL J. Biol. Chem. 273:25458-25465(1998).  
DR EMBL; AF077665; AAC36289.1;  
DR InterPro; IPR004010; Cache.  
DR InterPro; IPR002035; VWF\_A.  
DR Pfam; PF02743; Cache; 1.  
DR Pfam; PF00092; vwa; 1.  
DR SMART; SM00327; VWA; 1.  
DR PROSITE; PS50234; VWA; 1.  
KW Signal.  
FT SIGNAL 1 24  
FT CHAIN 25 1091  
FT CHAIN 25 1091  
SQ SEQUENCE 1091 AA; 123150 MW; 293DDC7EBE9E60E CRC64;

Query Match 100.0%; Score 5349; DB 6; Length 1091;  
Best Local Similarity 100.0%; Pred. No. 6.6e-318;  
Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLFQSLLLIGPSQEPFSAVTIKSWDKMEDLVTLAKTASGVNQLVDI 60



Search completed: February 10, 2003, 14:28:12  
Job time : 47.4836 secs

[illegible]

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Db 417 TNYVEDALGLVVTGTLPVNLTQDGPGEK-----KNQLILGVMGIDVALNDIKRLTPNY 472
QY 505 TLPNGYFFAIDPNGYVLLHNPQKPKSQEPVTLDFDLDAELNDIKVIRKMKIDGES 564
Db 473 TLGANGYVFAIDLNGYVLLHNPQKPKSQEPVTLDFDLDAELNDIKVIRKMKIDGNK 532
QY 565 GEKFRVLVKSQDRYIDKGNRYTTPVNGTQDYSALVLPYTFYFYKAKIETITQAR 624
Db 533 GHKQIRLVKSLDERYIDVTRVYTPVIRSTNYSLGLVLPYTFYVQANLSDQILQ-- 590
QY 625 SKGKMKDSETLKPNDFEESGYTFIAPRDYCNLDKISDNNTTELLNFENFIDRKTTNPS 684
Db 591 -----VKYFEFLPSPSESGHVFIAPREYCKDNLASNNTEFLKFNIEFLMEKVTDPDSQ 645
QY 685 QNTDLINRVLLDAGTFELVQNYWSKOK-NIKGVKARFVVTGDTIRVYKEAGENWOEN 743
Db 646 CNFELHNLILDITGITQOLVERWRDQDLNTYSLAVFAATDGGITRVFFPKAAEDWTEN 705
QY 744 PETEDSYFKRSLDNNDYVFTAPYFNK-SGPGAYES---GIMVSKAVEIYIOGKLLKPAV 799
Db 706 PEPENASYFRSLDNHGVFKPHQDALLRPLENDTVGLVSTAVELSLGRRTLRPAV 765
QY 800 VGKIDVNSWIENF-----FKTSIRDP--CAGP-----VCDCKRNSDVMDCVILDDGGFLL 848
Db 766 VGVKLDLEAWAEKFKVLASNRTHQDQPKC-GPNSHCEMDCEVNNEDLLCLVLDGGFLV 824
QY 849 MANHDDYTNQIGRFFGEIDPSLMRHLNIVSYAFNKSVDYQSVCEPGAAPKQAGHRSAY 908
Db 825 LSNQNHQDQVGRFSEVDANLMLYNNSTYRKESYDYQAACAPQPPGNLGAAPRGVF 884
QY 909 VPSIADILHIGWATAAWSILQOFLSLTPPRILLEAVEMEDDDFTASLSKQSCITRQTO 968
Db 885 VPTVADFLNLAWMTSAAWSLFQOLLYGLIYHSWFQADPAEAG-SPETRESSCVMKQTO 943
QY 969 YFFONDSFSGLDCGNCGRIFHVEKLMNTNLFIFVSKGTCPCDTRLLIOAEQ--TS 1026
Db 944 YFGSVNAYSNAIIDCGNCRLFAHQRTNLTNLLFVVAERPLCSQCRAGRLLOKETHCPA 1003
QY 1027 DGPDPDMVKOPRYRKPGDVCFDNNALDYDCG 1060
Db 1004 DGPEQCELQVPRYRRGPHICFDYNATEDSDCG 1037

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## RESULT 13

```

Q9NSA6 PRELIMINARY; PRT; 975 AA.
AC Q9NSA6;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE LUAC11.1 (Calcium channel, voltage-dependent, L type, alpha 2D subunit
  (K1AA0558)) (Fragment).
GN LUAC11.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Barlow K.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z84492; CAB41767.2; -.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS00234; VWFA; 1.
FT NON_TER
SQ SEQUENCE 975 AA; 110192 MW; C7874D46B8242BF CRC64;

```

Query Match 50.5%; Score 2829; DB 4; Length 975;  
 Best Local Similarity 57.0%; Pred. No. 1.4e-164;  
 Matches 543; Conservative 146; Mismatches 223; Indels 40; Gaps 15;

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QY 132 DPEKNDSEPGSQ--RIKPVFIDDAFNGRQISYQHAHVHPTDIYEGSTIVLNELNWTSA 189
Db 2 DPESEDVERGSKASTLRDLDFIEDPNFKNKVNSYAAVQIPTDIYKGSTVILNELNWTAL 61
QY 190 DEVFKKNEEDSLLHVOVFGSATGLARYYPASVWVDSNRTPNKIDLYDYRRRPWYIQAA 249
Db 62 ENVMFMRNQDPTLHVOVFGSATGVTYYPATPW----RAPKKIDLYDYRRRPWYIQAG 117
QY 250 SPKDMILVDVSGVSGTLKLRITSVSEMLETLDSDDFVNVASFNSNAQDVSCFQHLVQ 309
Db 118 SPKDMVILVDVSGVSGTLKLRITSVSEMLETLDSDDFVNVASFNSNAQDVSCFQHLVQ 177
QY 310 ANVRNKKVLUKDAVNNITAKITDYKKFGFAPEQLNLTNVSRANCKIIMLETFDGEGER 369
Db 178 ANVRNKKVFEKAVQGVAKGTTGYKAGFEYAFDQLQNSNITRANCKIMMFTDGEDRV 237
QY 370 QELFAKYN-KDKKVRVFTESVGHVNDYRGPIOMACENKNGYVEIPIPSIGAIRINTQEYL 428
Db 238 QDVFEEKYNWPNRTVFTFVSGQHNIDVTPLOWMACANKGYFEIPIPSIGAIRINTQEYL 297
QY 429 VLGPRMVLADGAKAQVQMTNVYIDALEGLVITGTLPVFNIT--GQENKNTLKNQILIG 486
Db 298 VLGPRMVLADGAKAQVQMTNVYIDALEGLVITGTLPVFNIT--GQENKNTLKNQILIG 353
QY 487 VMGVDSLSLEDIKRLPRFTLCPNGYFFAIDPNGYVLLHNPQKPKSQEPVTLDFDLAE 546
Db 354 VMGIDVALNDIKRLTPNYTGLANGYVFAIDLNGYVLLHNPQKPKSQEPVTLDFDLAE 413
QY 547 LENDIKVEIRNKMIDGEGKTFRTLVKSDERYIDKGNRTVTVTPVNGTQDYSALVLP 606
Db 414 LEDENKEELRRSMIDGNKHKQIRTLVKSLDERYIDVTRVYTPVIRSTNYSLGLVLP 473
QY 607 YSFYIIKAKIETITQARSKKMKMDSETLKPDPNFEESGYTFIAPRDYCNLDKISDNNT 666
Db 474 YSFYIQLANLSDQILQ-----VKYFEFLPSPSESGHVFIAPREYCKDNLASNNTE 526
QY 667 FLNPFNEFIDRTPNPNPSCNTDLINRVLLDAGTFELVQNYWSKOK-NIKGVKARFVVT 725
Db 527 FLKNFIELMEKVTDPDSKQCNFLHNLILDITGITQOLVERWRDQDLNTYSLAVFAAT 586
QY 726 GGITRVYPKAGBNQENPENYEDSYFKRSLDNNDYVFTAPYFNK-SGPGAYES---GIM 781
Db 587 GGITRVYFPNKAEDWTENPENENASYFRSLDNHGVFKPHQDALLRPLELENDTVGIL 646
QY 782 VSKAVEIYIOGKLLKPAVVGKIDVNSWIENF-----FKTSIRDP--CAGP-----VCDCK 830
Db 647 VSTAVELSLGRRTLRPAVVGKIDLEAWAEKFKVLASNRTHQDQPKC-GPNSHCEMDCE 705
QY 831 RNSDVMDCVTLDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLNIVSYAFNKSVDYQ 890
Db 706 VNNEDLLCVLIDGGFLVLSNQNHQDQVGRFSEVDANLMLYNNSTYRKESYDYQA 765
QY 891 VCEPGAAPKQAGHRSAYVPSIADILHIGWATAAWSILQOFLSLTPPRLEAVEMED 950
Db 766 ACAPQPPGNLGAAPRGVFTVADFLNLAWMTSAAWSLFQOLLYGLIYHSWFQADPAE 825
QY 951 DDTASLSKQSCITEQTOYFFDNDSKFSFVLDGNCGRIFHVEKLMNTNLFIFVSKG 1010
Db 826 EG-SPETRESSCVMKQTOYFVGSVNASYNAIIDCGNCRLFAHQRTNLTNLLFVVAEKPL 884
QY 1011 TCPDTRLLIOAEQ--TSDGPDPCDMVKOPRYRKPGDVCFDNNALDYDCG 1060
Db 885 CSQCEAGRLLQKETHCPADGPEQCELQVPRYRRGPHICFDYNATEDSDCG 936

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## RESULT 14

```

Q9Z1L5 PRELIMINARY; PRT; 1091 AA.
AC Q9Z1L5;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)

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DR EMBL; AF247141; AAL01650.1; --
DR MGD; MGI:1929813; Cacta2d2.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 1.
DR PROSITE; PS0234; VWF_A; 1.
SQ SEQUENCE 1084 AA; 123104 MW; 197D6B5B37EB9893 CRC64;

Query Match 53.8%; Score 3013; DB 11; Length 1084;
Best Local Similarity 54.7%; Pred. No. 9.3e-176;
Matches 577; Conservative 177; Mismatches 264; Indels 36; Gaps 15;

QY 33 IKSVDKMOEDLVTLAKTAGVGNQVLVDIYKYQDLYTVEPNNAQQLVEIAARDIEKLNS 92
Db 1 MOHWARRLEQEDIGVGNRIFGGVQQLREIYKDNRLFEYQENEPQKLVEKVGADIESLDR 60
QY 93 RSKALVRLALEAEKQVAAHQRREDFASNEVYVYNAKDDL---DPEKNDSEPGSO--RIKP 147
Db 61 KVOALKRLADAENFQKAHRQDNKKEHDIMYDAKADAELDDPESEMERGKSTSLRL 120
QY 148 VFIDANFGROISYOHAAVHIPTDIYEGSTIVLNLNMTSALDEVFKKNEEDPSLLQV 207
Db 121 DFIEDPNFKVNYSYTAQVQIPTDIYKGSTVILNLTWALENVFTENRRQDPTLLQV 180
QY 208 FGSATGLARYYPASPVDNSRTPNKIDLYDVRPRPWYIQGAASPKOMLILVDVSGSVGL 267
Db 181 FGSATGVTRYYPATPW-----RAPKKIDLYDVRPRPWYIQGAASPKOMVILVDVSGSVGL 236
QY 268 TLKLI RTSVSEMLETSLDDDDPVNVSANNAQDYSQFHLVQAVNRKKNVLDKAVNNITA 327
Db 237 TLKLMKTSVCEMLDTSLDDDDPVNVSANNAQDYSQFHLVQAVNRKKNVLEKAVQGVMA 296
QY 328 KGITDYKGFSEAFQOLLNWNVRANCKNIIMLTDTGGEERAQEIFAKYN-KDKKVRVFT 386
Db 297 KGITDYKGFSEAFQOLLNWNVRANCKNIIMLTDTGGEERAQEIFAKYN-KDKKVRVFT 356
QY 387 FSVGQHNVDYDRIOWMACENKGYEIPISGAIRINTQYLDVLRPVMVLAKGAKOVQ 446
Db 357 FSVGQHNVDYDRIOWMACENKGYEIPISGAIRINTQYLDVLRPVMVLAKGAKOVQ 416
QY 447 TNYVLDALGLVITGTLPVFNIT--GONENKTNLKNQILGVMGVDVSLDIKRLTPRF 504
Db 417 TNYVEDALGLVITGTLPVFNITQDGPGEK---KNQILGVMGIDVANDLKRITPNY 472
QY 505 TLCPNGYFAADPNQYVLLHPNLPKPKSQEPVTLDFDLDAELNDIKVIRKNMIDGES 564
Db 473 TLGANGYFAADLNGYVLLHPNLPKPKSQEPVTLDFDLDAELNDIKVIRKNMIDGES 532
QY 565 GEKTFRTLVKSDERYIDKGNRTYTPVNGTDYSLALVLPYTSFYIYKAKIETITQAR 624
Db 533 GHKQIRTLVSLDERYIDVIRNYTWYPIRSTNYSLGLVLPYTSFYIYKAKIETITQAR 592
QY 625 SKGKMKDSETLKPDNFEESGYTFIAPRDCNDLKI SDNNTEFLNLFNEPDRKTPNPS 684
Db 593 LPI SKLDFEFLPSSPESGCHVF IAPREYCKDLNADSDNTEFLKDFIELMEKVTDPDSK 652
QY 685 CNTDLINRLDAGTFELQVNTWSKQK-NIKGVKARFVYTDGGITRVPKKEGNNQEN 743
Db 653 CNPFLNHLIDGTITQOLVERVWRDOLNTYSLLAFAATDGGITRVPKKEGNNQEN 712
QY 744 PETYEDSKRSLDNDNYVFTAPYFNK-SGPAYES---GIMYSKAVEIYIOCKLKPAP 799
Db 713 PEPNASEFYRSLDNGHYIFKPHQDLSLRPLENDYTGVLVSTAVEISLGRTRLPAP 772
QY 800 VGKIDVNSIENP-----TKTSIRD--CAGP-----VCDCKRNSDVMBCVILDDGGFL 848
Db 773 VGKIDLEAWEAEKFKVLASNRTHQDQPKC-GPSSHCMECDCEVNEDLLCVLIDGGFLV 831
QY 849 MANHDDYTNQIGFFGIDPSLRHLVNIISYAFNKSIDYQSVCEPAGPKQAGHRSAY 908
Db 832 LSNQNHQDQVGRFFSEVDANLMLALNNSFYTRKESYDYQACAPQPPGNLGAAPRGVF 891
QY 909 VPSTADILHIGWATAAAWSILOQFLSLTFLPRLLAEVEMEDDDFTASLSKQSCITEQ 968
Db 872 VPTIADFLNLAWTSAARWSLFOQLLYGLYHSWFQADPAEAG-SPETRESSCVMKQTQ 950
QY 969 YFDNDSKFSGLVDCGNCRIHFVEKLMNTNLIIFIMVESKGTGCPDTRLLIAEQ--TS 1026
Db 951 YIFGSVNASYNAIIDCGNCISRLFAOQLTNTNLLFVVAEKLPLCSQCEAGRLQKETHCPA 1010
QY 1027 DGPDPDCDMVKOPRYKRGPDVCFDNNALDYDCG 1060
Db 1011 DGFEQELVORPRYRGRPHICFDYNATEDSDCG 1044

RESULT 12
Q9UEW0 PRELIMINARY; PRT; 1076 AA.
AC Q9UEW0;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
DE Alpha 2 delta calcium channel subunit isoform II.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wei M.-H., Latif F., Duh F.-M., Adreazzoli-Angeloni D., Kashuba V.,
RA Zabarovsky E., Johnson B., Lerman M.I.;
RT "A new alpha 2 delta subunit of the L-type voltage gated calcium
RT channel resides in the lung cancer critical region on 3p21.3.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF042793; AAB96914.1;
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS0234; VWF_A; 1.
SQ SEQUENCE 1076 AA; 122116 MW; BEC474836B7EDA85 CRC64;

Query Match 53.6%; Score 3004.5; DB 4; Length 1076;
Best Local Similarity 54.9%; Pred. No. 3.1e-175;
Matches 579; Conservative 173; Mismatches 259; Indels 43; Gaps 16;

QY 33 IKSVDKMOEDLVTLAKTAGVGNQVLVDIYKYQDLYTVEPNNAQQLVEIAARDIEKLNS 92
Db 1 MOHWARRLEQEDIGVGNRIFGGVQQLREIYKDNRLFEYQENEPQKLVEKVGADIESLDR 60
QY 93 RSKALVRLALEAEKQVAAHQRREDFASNEVYVYNAKDDL---DPEKNDSEPGSO--RIKP 147
Db 61 KVOALKRLADAENFQKAHRQDNKKEHDIMYDAKADAELDDPESEMERGKSTSLRL 120
QY 148 VFIDANFGROISYOHAAVHIPTDIYEGSTIVLNLNMTSALDEVFKKNEEDPSLLQV 207
Db 121 DFIEDPNFKVNYSYTAQVQIPTDIYKGSTVILNLTWALENVFTENRRQDPTLLQV 180
QY 208 FGSATGLARYYPASPVDNSRTPNKIDLYDVRPRPWYIQGAASPKOMLILVDVSGSVGL 267
Db 181 FGSATGVTRYYPATPW-----RAPKKIDLYDVRPRPWYIQGAASPKOMVILVDVSGSVGL 236
QY 268 TLKLI RTSVSEMLETSLDDDDPVNVSANNAQDYSQFHLVQAVNRKKNVLDKAVNNITA 327
Db 237 TLKLMKTSVCEMLDTSLDDDDPVNVSANNAQDYSQFHLVQAVNRKKNVLEKAVQGVMA 296
QY 328 KGITDYKGFSEAFQOLLNWNVRANCKNIIMLTDTGGEERAQEIFAKYN-KDKKVRVFT 386
Db 297 KGITDYKGFSEAFQOLLNWNVRANCKNIIMLTDTGGEERAQEIFAKYN-KDKKVRVFT 356
QY 387 FSVGQHNVDYDRIOWMACENKGYEIPISGAIRINTQYLDVLRPVMVLAKGAKOVQ 446
Db 357 FSVGQHNVDYDRIOWMACENKGYEIPISGAIRINTQYLDVLRPVMVLAKGAKOVQ 416
QY 447 TNYVLDALGLVITGTLPVFNIT--GONENKTNLKNQILGVMGVDVSLDIKRLTPRF 504
Db 417 TNYVEDALGLVITGTLPVFNITQDGPGEK---KNQILGVMGIDVANDLKRITPNY 472
QY 505 TLCPNGYFAADPNQYVLLHPNLPKPKSQEPVTLDFDLDAELNDIKVIRKNMIDGES 564
Db 473 TLGANGYFAADLNGYVLLHPNLPKPKSQEPVTLDFDLDAELNDIKVIRKNMIDGES 532
QY 565 GEKTFRTLVKSDERYIDKGNRTYTPVNGTDYSLALVLPYTSFYIYKAKIETITQAR 624
Db 533 GHKQIRTLVSLDERYIDVIRNYTWYPIRSTNYSLGLVLPYTSFYIYKAKIETITQAR 592
QY 625 SKGKMKDSETLKPDNFEESGYTFIAPRDCNDLKI SDNNTEFLNLFNEPDRKTPNPS 684
Db 593 LPI SKLDFEFLPSSPESGCHVF IAPREYCKDLNADSDNTEFLKDFIELMEKVTDPDSK 652
QY 685 CNTDLINRLDAGTFELQVNTWSKQK-NIKGVKARFVYTDGGITRVPKKEGNNQEN 743
Db 653 CNPFLNHLIDGTITQOLVERVWRDOLNTYSLLAFAATDGGITRVPKKEGNNQEN 712
QY 744 PETYEDSKRSLDNDNYVFTAPYFNK-SGPAYES---GIMYSKAVEIYIOCKLKPAP 799
Db 713 PEPNASEFYRSLDNGHYIFKPHQDLSLRPLENDYTGVLVSTAVEISLGRTRLPAP 772
QY 800 VGKIDVNSIENP-----TKTSIRD--CAGP-----VCDCKRNSDVMBCVILDDGGFL 848
Db 773 VGKIDLEAWEAEKFKVLASNRTHQDQPKC-GPSSHCMECDCEVNEDLLCVLIDGGFLV 831
QY 849 MANHDDYTNQIGFFGIDPSLRHLVNIISYAFNKSIDYQSVCEPAGPKQAGHRSAY 908
Db 832 LSNQNHQDQVGRFFSEVDANLMLALNNSFYTRKESYDYQACAPQPPGNLGAAPRGVF 891
QY 909 VPSTADILHIGWATAAAWSILOQFLSLTFLPRLLAEVEMEDDDFTASLSKQSCITEQ 968
Db 872 VPTIADFLNLAWTSAARWSLFOQLLYGLYHSWFQADPAEAG-SPETRESSCVMKQTQ 950
```

DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)  
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
 DE KIA0558 protein.  
 GN KIA0558.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN;  
 RA Sekido Y., Duh F.-M., Latif F., Ding J., Lin J., Mathis M.,  
 RA Minna J.D.;  
 RT "Gene 26, a new candidate human tumor suppressor gene located in the  
 RT 3p21.3 small cell lung cancer homozygous deletion region homologous to  
 RT a voltage gated calcium channel alpha 2/ delta subunit";  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Wei M.-H., Latif F., Duh F.-M., Adreazoli-Angeloni D., Kashuba V.,  
 RA Zabarovsky E., Johnson B., Lerman M.I.;  
 RT "A new alpha 2 delta subunit of the L-type voltage gated calcium  
 RT channel resides in the lung cancer critical region on 3p21.3";  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN;  
 RA Nagase T., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.,  
 RA Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. IX.  
 RT The complete sequences of 100 new cDNA clones from brain which can  
 RT code for large proteins in vitro";  
 RL DNA res. 5:31-39(1998).  
 DR EMBL: AF040709; AAC70914.1; -;  
 DR EMBL: AF042792; AAB96913.1; -;  
 DR EMBL: AB011130; BAA25484.1; -;  
 DR InterPro: IPR004010; Cache.  
 DR InterPro: IPR002035; VWF\_A.  
 DR Pfam: PF02743; Cache; 1.  
 DR SMART: SM00327; VWA; 1.  
 DR PROSITE: PS50234; VWEA; 1.  
 SQ SEQUENCE 1145 AA, 129268 MW, 9ADA4807FC70971B CRC64;  
 Query Match 54.0%; Score 3025.5; DB 4; Length 1145;  
 Best local similarity 54.4%; Pred. No. 1.7e-176;  
 Matches 588; Conservative 174; Mismatches 275; Indels 43; Gaps 16;  
 Qy 7 LALTLTLFQSLIGPSSOEPPSAVTIKSVKMDKEDLVTLAKTAGVGNOLVDIYEKYD 66  
 Db 44 LMLLLPLPLLAAPGASAYFPQOHTMOWHARRLEQEVGVGMIFGVQOLREIYKDNRN 103  
 Qy 67 LYTVEPNARQLVETIARDIEKLSNRSKALVRLALEAEKVQAAHAWHREDFASNEVYYN 126  
 Db 104 LFEQENEPQKLVKQVAGDIESLDRKQALRLADAAENFQKAHRMODNKEEDIVYD 163  
 Qy 127 AKDDL---DPKNDSEPGSQ--RIKVPFIDDANFGROISTQHAAYHIPTDIYEGSTIVLN 181  
 Db 164 AKADAELDDPSEIVERGSKASTLRLDFIEDPNFKKNVNTSYAAVQIPTDIYKGSTVILN 223  
 Qy 182 ELNNTSALDEYFKKREEDPSLWQVGSATGLARYVPSAPWVDNSTRPNKIDLYDVR 241  
 Db 224 ELNTEALENVFMENRQDPTLLMQVGSATGVTRYYPATPW----RAPKKIDLYDVR 279  
 Qy 242 PWYIQGAASPKDMLILVDVSGVSGSLTKLRTSVSEMLETSLDDDDFVNVASFNNSAQDV 301  
 Db 280 PWYIQGASSPKDMLIIVDVSGVSGSLTKLTKTSVCEMLDTLSDDDYVNVASFNEKAQV 339  
 Qy 302 SCFOHLVQANVRNKKVLKDVANNITAGITDYKKGFSAEQLLNWNVSRANCKIIMLF 361  
 Db 340 SCFTHLVQANVRNKKVKEAYGVQAVKGTGKAGFYAFDQNSNITRANCKNIMMF 399  
 Qy 362 TDGGEARQAEIFAKYN-KDKKVRVFTFSVGHNYDRGPFIQWACENKGYGYEIPSGAIR 420

Db 400 TDGGEDRVQDFEYKYNPNRVRVFTSVGQHNDVTPLOWMACANKGYIFEISGAIR 459  
 Qy 421 INTQYLDVLGRPMVLADGKAKQVQWTVNYLDALGLVITGTLVPFNIT--GQENKNTN 478  
 Db 460 INTQYLDVLGRPMVLADGKAKQVQWTVNYEDALGLVITGTLVPFNLTQDGPGEK--- 516  
 Qy 479 LKNQILGVMGVDVSLEDIKRLTPFTLCPNGYFAIDPNGYVLLHPNLQPKNPKSQEPV 538  
 Db 517 -KNQILGVMGIDVALNDIKRLTPFTLCPNGYFAIDPNGYVLLHPNLQPKNPKSQEPV 575  
 Qy 539 TLDLDALENDIKVEIRKNMIDGESGKFTFTLVKSODERYIDKGNRTYTWTPVNGTDY 598  
 Db 576 TLDLDALENDIKVEIRKNMIDGESGKFTFTLVKSODERYIDKGNRTYTWTPVNGTDY 635  
 Qy 599 SLALVPTYSFYIKAKIETITQARSKKGMKDSSETLKPDNFEESGYTFIAPRDYCNLD 658  
 Db 636 SLGLVLPYSTFYIQLANLSDQILQ-----VKYFEFLPSSFESEGHVFIAPREYCKDL 688  
 Qy 659 KISDNNTFELNFEFIDRKTPNPNPSCNTDLNRLVLLDAGFTNELVQNYWSKQK-NIGV 717  
 Db 689 NASDNNTFELNFEFIDRKTPNPNPSCNTDLNRLVLLDAGFTNELVQNYWSKQK-NIGV 748  
 Qy 718 KARFVVTVGGITRVYPKEAGENQWQENPETYEDSFYKRSILDNDNYVFTAPYFNK-SGPGAY 776  
 Db 749 LAVFAATDGGITRVYPKEAGENQWQENPETYEDSFYKRSILDNDNYVFTAPYFNK-SGPGAY 808  
 Qy 777 ES---GIMVSKAVEIYIOCKLKPAAVGIKIDVNSWIENF-----TKTSIRDP--CAGP- 825  
 Db 809 ENDTVGILVSTAVELSLGRRTLRPAVGVGLDLAEAKFKVLASNRTHQDPQKCG-CPN 867  
 Qy 826 ---VDCRKNSDVMDCVILDDGGFLLMANHDDYTNOIGRFTGEIDPSLMRLHVLNVSYAF 882  
 Db 868 SHCEMDCEVNNEDLLCVLDDGGFLLVSNQHWQVGRFFSEVDANLMLALYNNNSFYTR 927  
 Qy 883 NKSYDQSVCEPGAAPKOGAGHRSAYVPSIADILHIGWATAAAWSILQQFLLSLTFPRL 942  
 Db 928 KESYDQACAPQPPGNLGAAPRGVFTVADFLNLAWTSAAMSLFQQLLYGLIYHSW 987  
 Qy 943 LEAVEMEDDDFTASISKOSCTEQTQYFFDNDKSKFSFVGLDCGNSRIFHVKMLNNTLI 1002  
 Db 988 FQADPAEAEG-SPETRESSCVNMKQTYVFGSVNAYNAIDICGNSRIFHVKMLNNTLI 1046  
 Qy 1003 FIMVESKGTCPCDTRLIIQAEQ--TSDGPDPCDMVKQPRYKGPVDFDNNALDYDTGCG 1060  
 Db 1047 FYVAEKPLCSQCEAGRLQKETHCPADGPEQCELVQPRYKGPVDFDNNALDYDTGCG 1106  
 RESULT 11  
 Q920H6 PRELIMINARY; PRT; 1084 AA.  
 AC Q920H6;  
 DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE Voltage-dependent calcium channel alpha-2-delta-2 mutant subunit  
 DE 2.  
 GN CACNA2D2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=TKDU;  
 RA MEDLINE=21380284; PubMed=11487633;  
 RA Barclay J., Balaguero N., Mione M., Ackerman S.L., Letts V.A.,  
 RA Brobeck J., Cantl C., Meir A., Page K.M., Kusumi K., Perez-Reyes E.,  
 RA Lander E.S., Frankel W.N., Gardiner R.M., Dolphin A.C., Rees M.;  
 RT "Ducky mouse phenotype of epilepsy and ataxia is associated with  
 RT mutations in the Cacna2d2 gene and decreased calcium channel current  
 RT in cerebellar Purkinje cells";  
 RL J. Neurosci. 21:6095-6104(2001).

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QY 659 KISDNTEFLNFEIDRKTNNPNSCWTDLNVRLLDAGFNELVQNVWSKOK-NIKGV 717
Db 689 NASDNTFELKNFIELEMEKVTDSKQCNFLHNLHILDTGITQQLVERWRDQDLNTYSL 748
QY 718 KARFVYDGGITRVYKPEAGENKQENPETYDSFYKRSLDNDNYVFTAPYFNK-SGPGAY 776
Db 749 LAVEAATDGGITRVYFNKKAEDWTENPEFNASFYRSLDNGHYVFKPQDALLRPLEL 808
QY 777 ES---GIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENF-----TKTSIRD--CAGP- 825
Db 809 ENDTGILVSTAVELSLGRTRLRPAVVGKLDLEAWAEKFKVLASNRTHQDQPKC-GPN 867
QY 826 ---VCDCKRNSDVMDCVILDDGFFLLMHNDYTNQIGRFGCEIDPSLMRHLVNSVAF 882
Db 868 SHCEMCEVNNEDLCVLDDGGFFVLSNQHWDOVGRFFSEVDANLMLALYNSFTYR 927
QY 883 NKSYDQSVCEPGAAPKQAGHRSAYVPSIADILHIGWATAAANSILQQLFLLSUTPEPL 942
Db 928 KESYDQAACAPPPGNLGAAPRGVFTVADFLNLAWTSAAAWSLFQQLLYGLIYHSW 987
QY 943 LEAVEMEDDDFTASLSKQSCITEQTYFFDNDKSFSGVLCGNGSRIFHVEKLMNTNLI 1002
Db 988 FOADPAEAG-SPETRESSCMVKQTYFYFGSVNASYNALIDCGNCSRLFHAQRLTNTLL 1046
QY 1003 FTWVESKGTCPDTRLLQAEQSDGPPCDMVKQPRYKGPDYCFDNNALDYDTCG 1060
Db 1047 FVVAEKPLCSQCEAGRLQKETHSDGPEQCELVQPRYRRGPHCFDYNATEDSDCG 1104

RESULT 9
Q9EOG2
ID Q9EOG2 PRELIMINARY; PRT; 1156 AA.
AC Q9EOG2;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Voltage-dependent calcium channel alpha-2-delta-2 subunit.
GN CACNA2D2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TKDU;
RX MEDLINE=21015416; PubMed=11130987;
RA Barclay J., Rees M.;
RT "Genomic organization of the mouse and human alpha2delta2 voltage-
RT dependent calcium channel subunit genes.";
RL Mann. Genome 11:1142-1144(2000).
DR EMBL; AF247139; AAC47846.1;
DR MGI; MGI:1929813; CACNA2D2.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS00234; VWFA; 1.
SQ SEQUENCE 1156 AA; 130611 MW; A732545A2B302A52 CRC64;

Query Match 54.2%; Score 3038.5; DB 11; Length 1156;
Best Local Similarity 54.3%; Pred. No. 2.8e-177;
Matches 588; Conservative 178; Mismatches 279; Indels 37; Gaps 16;

QY 6 LALTLTLFQSLGIP--SSOEPPPSAVTIKSWYDKWQEDLVTLAKTAGVQNLVDIYKY 64
Db 45 LLLLPPLLLPLTAPGASYPSPQHTMOHWARRLEIDGVYMRIFGGVQQLREIYKDN 104
QY 65 QDLTYTPNNARQLVETAAADIEKLLSNRSKALVRLALEAEKVQAAHOREDPASNEVY 124
Db 105 RNLFEVQENEPQKLVKAVAGDIESLDRKQVAKLRADAEAFQKRAHRQWDNIKESDIMY 164
QY 125 YNAKDDL--DPEKNDSPEGSQ--RTKVPFDIDNFGROIYSOHAHAAVHIPTDIYEGSTIV 179

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Db 165 YDARADAEALDDPESDMERGSKTSALRLDFIEDFNFKVNYSTAVQIPDITKSGTVI 224
QY 180 LNELNWTSALEDEVFKKREEDPSLLMQVFGSATGLARYYPASPWVDRSNRPNKIDLYDVR 239
Db 225 LNELNWTSALESNVFIENRRQDPTLLWQVFGSATGVTRYYPATPW---RAPKKIDLYDVR 280
QY 240 RRPWYIOGAASPDKMLILVDVSGVSGLTGLIRTSVSEMLETSLSDDDFVNVASFNSAQ 299
Db 281 RRPWYIOGASSPKDMVILVDVSGVSGLTGLIRTSVSEMLETSLSDDDFVNVASFNEKAQ 340
QY 300 DVSFQHLVQANVRNKKVLKDAVNNITAKGITYDKKGFSAFQELLNYSRANCKIIM 359
Db 341 PVSCTHLVQANVRNKKVFEAVQGVAKGTTGKAGFEAFDQLOQNSNITRANCKMIM 400
QY 360 LFTDGGEEAEIYAKYN-RDKKVRVFTFSVQGHNYDRGFIOWMACENKGYEIPSIGA 418
Db 401 MFTDGGEDRQDVDFEKNWPNRTVRFVTSVQGHNYDVTPLQWMACTNKGYEIPSIGA 460
QY 419 IRINTQBYLDVLRPMVLADKAKQVQWNTVYLDALGLVITGTLPVFNIT--GQENK 476
Db 461 IRINTQBYLDVLRPMVLADKAKQVQWNTVYEDALGLVITGTLPVFNITQDGGPEK- 519
QY 477 TNLKNQILGVMGVDSLEDIKRLTPRFTLCPNGYFYFAIDPNGYVLLHPLNPKPKSQE 536
Db 520 ---KNQILGVMGIDVALNDIKRLTPNYTLGANGYFAIDNGYVLLHPLNPKPQTTNFE 576
QY 537 PVTLDLDALENDIKVEIKNMIDGESGKTFRTLVKSQDERYIDKGNRTYTWTPVNGT 596
Db 577 PVTLDLDALENDIKVEIKNMIDGESGKTFRTLVKSQDERYIDKGNRTYTWTPVNGT 636
QY 597 DYSALVLPTYFYIYAKIETITQARSKKGMKQSETLKPDNFESEGYTFETAPDYCN 656
Db 637 NYSGLVLPYSTYLYLQANLRDQILQVKLPISKLDFEFLPSFSEGHVFTAPREYCK 696
QY 657 DLKISDNNTFELNFEIDRKTNNPNSCWTDLNVRLLDAGFNELVQNVWSKOK-NIK 715
Db 697 DLNASDNSTEFKDFIELMEKVTDSKQCNFLHNLHILDTGITQQLVERWRDQDLNTY 756
QY 716 GVKARFVYDGGITRVYKPEAGENKQENPETYDSFYKRSLDNDNYVFTAPYFNK-SGPG 774
Db 757 SLLAFAAATDGGITRVYFNKKAEDWTENPEFNASFYRSLDNGHYVFKPQDALLRPL 816
QY 775 AYES---GIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENF-----TKTSIRD--CAG 824
Db 817 ELENDTVGLVSTAVELSLGRTRLRPAVVGKLDLEAWAEKFKVLASNRTHQDQPKC-G 875
QY 825 P----VCDCKRNSDVMDCVILDDGFFLLMHNDYTNQIGRFGCEIDPSLMRHLVNSY 880
Db 876 PSHCEMCEVNNEDLCVLDDGGFFVLSNQHWDOVGRFFSEVDANLMLALYNSPY 935
QY 881 AFNKSYDQSVCEPGAAPKQAGHRSAYVPSIADILHIGWATAAANSILQQLFLLSUTFP 940
Db 936 TRKESYDQAACAPPPGNLGAAPRGVFTVADFLNLAWTSAAAWSLFQQLLYGLIYH 995
QY 941 RLLEAVEMEDDDFTASLSKQSCITEQTYFFDNDKSFSGVLCGNGSRIFHVEKLMNTN 1000
Db 996 SFWQADPAEAG-SPETRESSCMVKQTYFYFGSVNASYNALIDCGNCSRLFHAQRLTNTN 1054
QY 1001 LIFIMVESKGTCPDTRLLQAEQ--TSDGPPCDMVKQPRYKGPDYCFDNNALDYDTCG 1058
Db 1055 LIFVVAEKPLCSQCEAGRLQKETHCPADGPEQCELVQPRYRRGPHCFDYNATEDSD 1114
QY 1059 CG 1060
Db 1115 CG 1116

RESULT 10
Q9Y268
ID Q9Y268 PRELIMINARY; PRT; 1145 AA.
AC Q9Y268;
DT 01-NOV-1999 (Tremblrel. 12, Created)

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QY 901 GAGHSAYVPSIADILHIGHWATAAAWSILQOFLLSILTPRLLEAVEMEDDDFTASLSKQ 960  
 DB 889 GAGHSAYVPSITDILQIHWATAAAWSILQOFLLSILTPRLLEAVEMEDDDFTASLSKQ 948  
 QY 961 SCITEQTYFFDNDKSFSGVLDCGNCGRIFHVEKLMNTNLIFIMVESGTCPCDTRLLI 1020  
 DB 949 SCITEQTYFFKNDTKSFSGLLDCGNCGRIFHVEKLMNTNLIFIMVESGTCPCDTRLLM 1008  
 QY 1021 QAEQTSDDGPPCDMVKQPRYKGPVDFCFDNNALDYTCGGVS 1063  
 DB 1009 QAEQTSDDGPPCDMVKQPRYKGPVDFCFDNNVLEDYTCGGVS 1051  
 RESULT 6  
 ID Q9UDQ3 PRELIMINARY; PRT; 745 AA.  
 AC Q9UDQ3;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE WUGSC:H.DJ0560014.1 protein (Fragment).  
 GN WUGSC:H.DJ0560014.1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99063792; PubMed=9847074;  
 RA Sulston J.E., Waterston R.;  
 RT "Toward a complete human genome sequence.";  
 RL Genome Res. 8:1097-1108(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Mead K., Bauer C.;  
 RP SEQUENCE FROM N.A.  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC006145; AAD20938.1; -;  
 DR InterPro; IPR004010; Cache.  
 DR InterPro; IPR002035; VWF\_A.  
 DR Pfam; PF02743; Cache; 1.  
 DR PROSITE; PS50234; VWA; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 745 AA; 84396 MW; BC07B53484B71EA4 CRC64;

Query Match 67.6%; Score 3786; DB 4; Length 745;  
 Best Local Similarity 98.7%; Pred. No. 2.5e-223;  
 Matches 708; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
 QY 347 YNVSFRANCKIIMLFTDGGEEAQQEIEFAKYNKDKKVRVFTSVGQHNDRGPIQWACEN 406  
 DB 1 YNVSFRANCKIIMLFTDGGEEAQQEIEFAKYNKDKKVRVFTSVGQHNDRGPIQWACEN 60  
 QY 407 KGYEYEPSIGAIRINTEQYLDVLRPWLGRVLAGDKAKQVQNTNYLDALGLVITGLTPV 466  
 DB 61 KGYEYEPSIGAIRINTEQYLDVLRPWLGRVLAGDKAKQVQNTNYLDALGLVITGLTPV 120  
 QY 467 FNITGQENKTNLKNQILGVMGVDVSLDILKRLTPRTLCPCNGYFFAIDPNGYVLLHPN 526  
 DB 121 FNITGQENKTNLKNQILGVMGVDVSLDILKRLTPRTLCPCNGYFFAIDPNGYVLLHPN 180  
 QY 527 LQPNKPSQEPVTLDFDALENDIKVEIRKNMIDGSGEKTFRTLVKSODERYIDKGNR 586  
 DB 181 LQPNKPSQEPVTLDFDALENDIKVEIRKNMIDGSGEKTFRTLVKSODERYIDKGNR 240  
 QY 587 TYTTPVNGTDSYALVLPYTSFYIKAKTEETITQARSKKGKWKDSETLKPNPFESGY 646  
 DB 241 TYTTPVNGTDSYALVLPYTSFYIKAKTEETITQARSKKGKWKDSETLKPNPFESGY 300

QY 647 TFIAPRDYCNLDKISDNNTEFLNNEFIDRKTNNPNSCNTDLNLRVLLDAGFTNELVQN 706  
 DB 301 TFIAPRDYCNLDKISDNNTEFLNNEFIDRKTNNPNSCNTDLNLRVLLDAGFTNELVQN 360  
 QY 707 YWSKOKNIGVKARVVTGGITRVYPKEAGENMOENPETYEDSFYKRSLNDNDYVETAP 766  
 DB 361 YWSKOKNIGVKARVVTGGITRVYPKEAGENMOENPETYEDSFYKRSLNDNDYVETAP 420  
 QY 767 YFNKSGPCAYESGIMVSKAVEIYIQGLLKPAVVGIIKIDVNSWIENFTKTSIRDPGAPV 826  
 DB 421 YFNKSGPCAYESGIMVSKAVEIYIQGLLKPAVVGIIKIDVNSWIENFTKTSIRDPGAPV 480  
 QY 827 CDCKRNSDVMDCVILDDGGFLMANHDDYTQIGRFFGEIDPSLMRHLVNISYAFNKS 886  
 DB 481 CDCKRNSDVMDCVILDDGGFLMANHDDYTQIGRFFGEIDPSLMRHLVNISYAFNKS 540  
 QY 887 DYQSVCEGPAAPKOGAGHRSAYVPSIADILHIGHWATAAAWSILQOFLLSILTPRLLEAV 946  
 DB 541 DYQSVCEGPAAPKOGAGHRSAYVPSIADILHIGHWATAAAWSILQOFLLSILTPRLLEAV 600  
 QY 947 EMEDDDFTASLSKQSCITEQTYFFDNDKSFSGVLDCGNCGRIFHVEKLMNTNLIFIMV 1006  
 DB 601 EMEDDDFTASLSKQSCITEQTYFFDNDKSFSGVLDCGNCGRIFHVEKLMNTNLIFIMV 660  
 QY 1007 ESKGTCPCDTRLLIQAQETSDGPPCDMVKQPRYKGPVDFCFDNNALDYTCGGVS 1063  
 DB 661 ESKGTCPCDTRLLIQAQETSDGPPCDMVKQPRYKGPVDFCFDNNVLEDYTCGGVS 717

## RESULT 7

ID Q9NY47 PRELIMINARY; PRT; 1150 AA.  
 AC Q9NY47;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Calcium channel, alpha 2/delta subunit 2.  
 GN CACNA2D2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=THYROID;  
 RA Klugbauer N.;  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=THYROID;  
 RA Hobom M., Dai S., Marais E., Lacinova L.;  
 RT "Neuronal distribution and functional characterization of the calcium channel alpha2delta-2 subunit";  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ251368; CAB86193.1; -;  
 DR InterPro; IPR004010; Cache.  
 DR InterPro; IPR002035; VWF\_A.  
 DR Pfam; PF02743; Cache; 1.  
 DR SMART; SM00327; VWA; 1.  
 DR PROSITE; PS50234; VWA; 1.  
 SQ SEQUENCE 1150 AA; 129876 MW; 37B75F687AFE573C CRC64;

Query Match 54.7%; Score 3066; DB 4; Length 1150;  
 Best Local Similarity 54.8%; Pred. No. 5.8e-179;  
 Matches 591; Conservative 175; Mismatches 278; Indels 34; Gaps 14;  
 QY 7 LATLTLFOSLILIGSSQEPFSAVTIKSWDKMQEDLVTLAKTAGSNQVLDIYERYQD 66  
 DB 44 LMLLPLPLPLAAPGASAYSFQOHTMQHARRLEQVDGVMIRFGVQQLREIYKDRN 103  
 QY 67 LYTVPNNARQLVETAAARDIEKLLSNRSKALVRLALEAKVQAAHQWREDFASNEVYYN 126  
 DB 104 LFEVQENEPQKLVKAGVDIESLLDRKQVQALKRLADAAENFQKAHRWQDNKEEDIVYD 163

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Db 361 FTDCGEEAQQEIAFYKNDKVRVFTFSVGOHNDGPIQWACENKGYIETPSTGAI 420
QY 421 INTQYLDVLGRPMVLADGAKAKQVQNTVYLDALGLGLVITGTLPVFNITGQENKTNLK 480
Db 421 INTQYLDVLGRPMVLADGAKAKQVQNTVYLDALGLGLVITGTLPVFNITGQENKTNLK 480
QY 481 NQLILGVMGVDVSLIEDIKRLTPRTFLCPNGYIYFAIDPNGYVLLHPLNLPK- 530
Db 481 NQLILGVMGVDVSLIEDIKRLTPRTFLCPNGYIYFAIDPNGYVLLHPLNLPK- 540
QY 531 -----NPKSQEPVTLDFDAELENDIKVEIRNKMIDGESGKTFRTLVKSQERYI 581
Db 541 LRKRRPNVQNPQKQEPVTLDFDAELENDIKVEIRNKMIDGESGKTFRTLVKSQERYI 600
QY 582 DKGNTYVTPVNGTDSLALVLPYTFYIYKAKIETITQAKSKGKMDSETLKPDNF 641
Db 601 DKGNTYVTPVNGTDSLALVLPYTFYIYKAKIETITQAKSKGKMDSETLKPDNF 653
QY 642 EESGTYTAPRYCNDLKI SDNTEFLNFEFIDRKTNNPSCNTDLINRVLLDAGFTN 701
Db 654 EESGTYTAPRYCNDLKI SDNTEFLNFEFIDRKTNNPSCNTDLINRVLLDAGFTN 713
QY 702 ELVQYWSKQNIKGVKARFVVDGGLITRVYPKEAGENWQENPETEDSYKRSNDNY 761
Db 714 ELVQYWSKQNIKGVKARFVVDGGLITRVYPKEAGENWQENPETEDSYKRSNDNY 773
QY 762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRD 821
Db 774 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRD 833
QY 832 CAGPVCDCRNSDMVDCVILDDGGLFMANHDDYTNOIGRFFGIDPSLMRHLNLSIYA 881
Db 834 CAGPVCDCRNSDMVDCVILDDGGLFMANHDDYTNOIGRFFGIDPSLMRHLNLSIYA 893
QY 882 FNKSYDQSVCEPCGAPKQAGHSAYVPSIADILHIGWATAAASIILOQLLSLTFPR 941
Db 894 FNKSYDQSVCEPCGAPKQAGHSAYVPSIADILHIGWATAAASIILOQLLSLTFPR 953
QY 942 LLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDKSFSGVLDGNCGRIFHVEKLMNTN 1001
Db 954 LLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDKSFSGVLDGNCGRIFHVEKLMNTN 1013
QY 1002 IFIMVESKGTCPDTRLLIQAEQISDGPDCDMVKQPRYKGPVCFDNNALDYTCGG 1061
Db 1014 IFIMVESKGTCPDTRLLIQAEQISDGPDCDMVKQPRYKGPVCFDNNALDYTCGG 1073
QY 1062 VS 1063
Db 1074 VS 1075

RESULT 5
Q8VHS9 PRELIMINARY; PRT; 1079 AA.
AC Q8VHS9;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE L-type calcium channel alpha2/delta subunit.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=HEART;
RX MEDLINE=21601730; PubMed=11604404;
RA Yamada Y., Negashima M., Tsutsuura M., Kobayashi T., Seki S.,
RA Makita N., Horio Y., Tohse N.
RT "Cloning of a functional splice variant of L-type calcium channel
RT beta2 subunit from rat heart."
RL J. Biol. Chem. 276:47163-47170(2001).
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DR EMBL; AF400662; AAL47093.1; -.
DR InterPro; IPR004010; Cache.
DR Pfam; PF02743; Cache; 1.
DR Pfam; PF00092; vwa; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50234; VWFA; 1.
SQ SEQUENCE 1079 AA; 122172 MW; DC4A3641195B546C CRC64;

Query Match
Best Local Similarity 96.1%; Score 5381; DB 11; Length 1079;
Matches 1018; Conservative 21; Mismatches 12; Indels 12; Gaps 2;

QY 1 MAAGCLLALTFLFOSLLIGPSSQPPSPFSAVITKSWDKMQEDLVTLAKTASGVNQLVDI 60
Db 1 MAAGCLLALTFLFOSLLIGPSSQPPSPFSAVITKSWDKMQEDLVTLAKTASGVNQLVDI 60
QY 61 YKQYODLVTEPNNAQOLVEIAARDIEKLLSNRSKALVRLALEAKVQAAHQRWDFASN 120
Db 61 YKQYODLVTEPNNAQOLVEIAARDIEKLLSNRSKALVRLALEAKVQAAHQRWDFASN 120
QY 121 EYVYNAKDDLDPEKNDSEPSQRIKPVFIDANFGROIYQHAHVHIPTDIYEGSTIVL 180
Db 121 EYVYNAKDDLDPEKNDSEPSQRIKPVFIDANFGROIYQHAHVHIPTDIYEGSTIVL 180
QY 181 NELNWTLSALDEVFKNREDEPDLWQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240
Db 181 NELNWTLSALDEVFKNREDEPDLWQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240
QY 241 RPWYIQGAASPKDMLLVDVSGVSLTLKLTSTVSEMLETLSDDDDFNVASFNSNAQD 300
Db 241 RPWYIQGAASPKDMLLVDVSGVSLTLKLTSTVSEMLETLSDDDDFNVASFNSNAQD 300
QY 301 VSCFOHLVQANVRNKKVLKADVNNITAKITDYKKGFSFAFQOLLNMYNVRANCKNIIML 360
Db 301 VSCFOHLVQANVRNKKVLKADVNNITAKITDYKKGFSFAFQOLLNMYNVRANCKNIIML 360
QY 361 FTDGGERAQEIFAKYKNDKVRVFTFSVGOHNDGPIQWACENKGYIETPSTGAI 420
Db 361 FTDGGERAQEIFAKYKNDKVRVFTFSVGOHNDGPIQWACENKGYIETPSTGAI 420
QY 421 INTQYLDVLGRPMVLADGAKAKQVQNTVYLDALGLGLVITGTLPVFNITGQENKTNLK 480
Db 421 INTQYLDVLGRPMVLADGAKAKQVQNTVYLDALGLGLVITGTLPVFNITGQENKTNLK 480
QY 481 NQLILGVMGVDVSLIEDIKRLTPRTFLCPNGYIYFAIDPNGYVLLHPLNLPKQSPVTL 540
Db 481 NQLILGVMGVDVSLIEDIKRLTPRTFLCPNGYIYFAIDPNGYVLLHPLNLPK- 535
QY 541 DFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSQERYIDKGNRTYTWTPVNGTDSL 600
Db 536 DFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSQERYIDKGNRTYTWTPVNGTDSL 595
QY 601 ALVLPTYSYFIYKAKIETITQAKSKGKMDSETLKPONFESGYTFTIAPRDYCNLKI 660
Db 596 ALVLPTYSYFIYKAKIETITQAKSKGKMDSETLKPONFESGYTFTIAPRDYCNLKI 648
QY 661 SDNTEFLNFEFIDRKTNNPSCNTDLINRVLLDAGFTNVLQYWSKQNIKGVKAR 720
Db 649 SDNTEFLNFEFIDRKTNNPSCNTDLINRVLLDAGFTNVLQYWSKQNIKGVKAR 708
QY 721 FVYTDGGLITRVYPKEAGENWQENPETEDSYKRSNDNYVFTAPYFNKSGPGAYESGI 780
Db 709 FVYTDGGLITRVYPKEAGENWQENPETEDSYKRSNDNYVFTAPYFNKSGPGAYESGI 768
QY 781 MVS KAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPCAGPVCDCRNSDMVDCVI 840
Db 769 MVS KAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPCAGPVCDCRNSDMVDCVI 828
QY 841 LDGGFLFMANHDDYTNOIGRFFGIDPSLMRHLNLSIYAFNKSVDYQSVCEPCGAPKQ 900
Db 829 LDGGFLFMANHDDYTNOIGRFFGIDPSLMRHLNLSIYAFNKSVDYQSVCEPCGAPKQ 888
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Db 541 DFLDALENDIKVIRKMKIDGESGEKTRTLVKSDERYIDKGNRTYTWTVPNGTDSL 600
QY 601 ALVLPTSYFYIKAKIETITQARSKKGMKDSKTLKPNFESGYTFIAPRDYCNLDKI 660
Db 601 ALVLPTSYFYIKAKIETITQARSKKGMKDSKTLKPNFESGYTFIAPREYCNLDKP 660
QY 661 SDNTEFLNNEFIDRKTPNPNPSCNTDLINRVLLDAGFTNVLQVYNSKQKNIKGVKAR 720
Db 661 SDNTEFLNNEFIDRKTPNPNPSCNTDLINRVLLDAGFTNVLQVYNSKQKNIKGVKAR 720
QY 721 FVYTDGGITRVYPKEAGENQENPETEDSFYKRSILDNDNYVFTAPYENKSGPGAYESGI 780
Db 721 FVYTDGGITRVYPKEAGENQENPETEDSFYKRSILDNDNYVFTAPYENKSGPGAYESGI 780
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTKTSIRDPCAGVCDCKRNSDVMDCVI 840
Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTKTSIRDPCAGVCDCKRNSDVMDCVI 840
QY 841 LDDGGFLLMANHDDYTNQIGREFGEIDPSLMRHLNYSVYAFNKSYDYOSVCEGPAAPKQ 900
Db 841 LDDGGFLLMANHDDYTNQIGREFGEIDPSLMRHLNYSVYAFNKSYDYOSVCEGPAAPKQ 900
QY 901 GAGHSAYVPSIADILHIGWATAAASWILQOFLLSLTFPRLLLEAVEMEDDFTASLSKQ 960
Db 901 GAGHSAYVPSIADILHIGWATAAASWILQOFLLSLTFPRLLLEAVEMEDDFTASLSKQ 960
QY 961 SCITQTOYFFDNDKSGSVGLDCGNCRIHFVEKLMNTNLFIMVESKGTCPDTRLLI 1020
Db 961 SCITQTOYFFDNDKSGSVGLDCGNCRIHFVEKLMNTNLFIMVESKGTCPDTRLLI 1020
QY 1021 QAEQTSDDGPDPCDMVKQPRYKRGPDVCFDNNALDYDCGGVS 1063
Db 1021 QAEQTSDDGPDPCDMVKQPRYKRGPDVCFDNNALDYDCGGVS 1063

RESULT 4
O08532 PRELIMINARY; PRT: 1103 AA.
AC O08532; O08534; O08535; O08536;
DT 01-JUN-1998 (Tremblrel. 06, created)
DT 01-JUN-1998 (Tremblrel. 06, last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, last annotation update)
DE Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta
DE subunits precursor.
GN CACNA2D1 OR CACNA2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=97113514; PubMed=8955374;
RA Angelotti T.; Hofmann F.;
RL PERS Lett. 397:331-337(1996).
CC -1- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN
CC EXCITATION-CONTRACTION COUPLING.
CC -1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:
CC ALPHA-1, ALPHA-2, BETA AND GAMMA.
CC -1- SUBUNIT: ALPHA-2 AND DELTA FORM HETERODIMERS THAT ARE DISULFIDE-
CC LINKED.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: FIVE FORMS OF THE PROTEIN, ISOFORMS 2A-2E,
CC ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THE
CC SEQUENCE SHOWN HERE IS THAT OF ISOFORM 2A.
CC -1- TISSUE SPECIFICITY: ISOFORM 2A IS EXPRESSED IN SKELETAL MUSCLE AND
CC AORTA, 2B IS EXPRESSED IN BRAIN, 2C IS EXPRESSED IN HEART, 2D IS
CC EXPRESSED IN HEART AND SMOOTH MUSCLE, AND 2E IS EXPRESSED IN
CC SMOOTH MUSCLE. ALL FIVE ISOFORMS ARE EXPRESSED IN THE
CC CARDIOVASCULAR SYSTEM.
CC -1- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM
CC A PRECURSOR FORM.
CC -1- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.

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DR EMBL; U73484; AAB50139.1; -
DR EMBL; U73485; AAB50140.1; -
DR EMBL; U73483; AAB50138.1; -
DR EMBL; U73486; AAB50141.1; -
DR EMBL; U73487; AAB50142.1; -
DR MGI; MGI:88295; Cagca2d1.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 1.
DR Pfam; PF00032; vwa; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS0234; VWFA; 1.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Calcium channel; Glycoprotein; Phosphorylation; Signal;
KW Alternative splicing.
FT SIGNAL 1 24
FT CHAIN 25 957
FT CHAIN 958 1103
FT TRANSMEM 446 469
FT TRANSMEM 918 942
FT TRANSMEM 1079 1098
FT MOD_RES 501 501
FT MOD_RES 845 845
FT CARBOHYD 92 92
FT CARBOHYD 136 136
FT CARBOHYD 184 184
FT CARBOHYD 324 324
FT CARBOHYD 348 348
FT CARBOHYD 475 475
FT CARBOHYD 604 604
FT CARBOHYD 613 613
FT CARBOHYD 675 675
FT CARBOHYD 781 781
FT CARBOHYD 824 824
FT CARBOHYD 888 888
FT CARBOHYD 895 895
FT CARBOHYD 985 985
FT VARSPPLIC 531 549
FT VARSPPLIC 531 554
FT VARSPPLIC 644 644
FT SQ SEQUENCE 1103 AA; 124629 MW; 103773B4735120D4 CRC64;

Query Match 96.5%; Score 5405; DB 11; Length 1103;
Best Local Similarity 94.5%; Pred. No. 0;
Matches 1023; Conservative 23; Mismatches 10; Indels 26; Gaps 2;

QY 1 MAAGCLLALTTLTFLQSLIGPSOEPPPSAVTIKSWDKMQEDLVTLAKTASGVQLVDI 60
Db 1 MAAGCLLALTTLTFLQSLIGPSOEPPPSAVTIKSWDKMQEDLVTLAKTASGVQLADI 60
QY 61 YEKYQDLYTVEPNARQLVEIARDIEKLLSNRSKALVRLALEAEKVQAAHQRREDFASN 120
Db 61 YEKYQDLYTVEPNARQLVEIARDIEKLLSNRSKALVRLALEAEKVQAAHQRREDFASN 120
QY 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFIIDANFGRQISYQHAHVHIPTDIYEGSTIVL 180
Db 121 EYVYNAKDDLDPERNESEPGSQRIKPVFIIDANFGRQISYQHAHVHIPTDIYEGSTIVL 180
QY 181 NELNWTSALEDEVFKKRNREDPSLLWQVFGSATGLARYYPASVPWVNSRTPNKIDLYDVR 240
Db 181 NELNWTSALEDEVFKKRNREDPSLLWQVFGSATGLARYYPASVPWVNSRTPNKIDLYDVR 240
QY 241 RPWYIQGAASPKDMLILVDVSGVSGLTLLKRTSVSEMLETSLDSDDFVNVASFNSAQD 300
Db 241 RPWYIQGAASPKDMLILVDVSGVSGLTLLKRTSVSEMLETSLDSDDFVNVASFNSAQD 300
QY 301 VSCFOHLVOANYRNKVKLVKDAVNNITAKGIDTKKGFSAFEPQLLNNVSRANCKNIIML 360
Db 301 VSCFOHLVOANYRNKVKLVKDAVNNITAKGIDTKKGFSAFEPQLLNNVSRANCKNIIML 360
QY 361 FTDGGERAQEIFAKYKNDKVRVFTFFSQHNDYRGPIQWACENKGYEYIPEISGAIR 420

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QY 61 YEKYQDLYTVEPNNAQVLAARDIEKLLSNRSKALVRLAEAEKVQAAHQWREDFASN 120
Db 61 YEKYQDLYTVEPNNAQVLAARDIEKLLSNRSKALVRLAEAEKVQAAHQWREDFASN 120
QY 121 EVVYNAKDDLPKNDSEPGSQRIPKFVTDANFGRQISYQHAHVHIPTDIYEGSTIVL 180
Db 121 EVVYNAKDDLPKNDSEPGSQRIPKFVTDANFGRQISYQHAHVHIPTDIYEGSTIVL 180
QY 181 NELNWTALDEVFKKNEEDPSLLQWVFGSATGLARYYPASPWVDSRTPNKIDLYDVR 240
Db 181 NELNWTALDEVFKKNEEDPSLLQWVFGSATGLARYYPASPWVDSRTPNKIDLYDVR 240
QY 241 RPWYIQGAASPKDMLILVDVSGVSGLTILKIRTSVSEMLETISDDDFVNVASFNSNAQ 300
Db 241 RPWYIQGAASPKDMLILVDVSGVSGLTILKIRTSVSEMLETISDDDFVNVASFNSNAQ 300
QY 301 VSCFQHLVQANVRNKKVLDVANNITAKGTDYKKGFSFAFQOLLNYSRANCNKIIML 360
Db 301 VSCFQHLVQANVRNKKVLDVANNITAKGTDYKKGFSFAFQOLLNYSRANCNKIIML 360
QY 361 FTDCGEERAQEIFAKYKNDKKVRVFTFSVGHNYDRGPIQWACENKGYIYEIPSGAIR 420
Db 361 FTDCGEERAQEIFAKYKNDKKVRVFTFSVGHNYDRGPIQWACENKGYIYEIPSGAIR 420
QY 421 INTQYLDVLRPMVLAGDKAKOVQNTVYLDALGLVITGLTPVFNITGQENKTNLK 480
Db 421 INTQYLDVLRPMVLAGDKAKOVQNTVYLDALGLVITGLTPVFNITGQENKTNLK 480
QY 481 NQILGVMGVDVSLIEDIKRLTPRTLCPCNGYYPFADIPNGVYLLHPNLQPKNSQBPVTL 540
Db 481 NQILGVMGVDVSLIEDIKRLTPRTLCPCNGYYPFADIPNGVYLLHPNLQPKNSQBPVTL 540
QY 541 DFLDAELNDIKVEIRNKMIDGESGKTRFTLVKSODERYIDKGNRTYTWTPVNGTDSL 600
Db 541 DFLDAELNDIKVEIRNKMIDGESGKTRFTLVKSODERYIDKGNRTYTWTPVNGTDSL 600
QY 61 YEKYQDLYTVEPNNAQVLAARDIEKLLSNRSKALVRLAEAEKVQAAHQWREDFASN 120
Db 61 YEKYQDLYTVEPNNAQVLAARDIEKLLSNRSKALVRLAEAEKVQAAHQWREDFASN 120
QY 121 EVVYNAKDDLPKNDSEPGSQRIPKFVTDANFGRQISYQHAHVHIPTDIYEGSTIVL 180
Db 121 EVVYNAKDDLPKNDSEPGSQRIPKFVTDANFGRQISYQHAHVHIPTDIYEGSTIVL 180
QY 181 NELNWTALDEVFKKNEEDPSLLQWVFGSATGLARYYPASPWVDSRTPNKIDLYDVR 240
Db 181 NELNWTALDEVFKKNEEDPSLLQWVFGSATGLARYYPASPWVDSRTPNKIDLYDVR 240
QY 241 RPWYIQGAASPKDMLILVDVSGVSGLTILKIRTSVSEMLETISDDDFVNVASFNSNAQ 300
Db 241 RPWYIQGAASPKDMLILVDVSGVSGLTILKIRTSVSEMLETISDDDFVNVASFNSNAQ 300
QY 301 VSCFQHLVQANVRNKKVLDVANNITAKGTDYKKGFSFAFQOLLNYSRANCNKIIML 360
Db 301 VSCFQHLVQANVRNKKVLDVANNITAKGTDYKKGFSFAFQOLLNYSRANCNKIIML 360
QY 361 FTDCGEERAQEIFAKYKNDKKVRVFTFSVGHNYDRGPIQWACENKGYIYEIPSGAIR 420
Db 361 FTDCGEERAQEIFAKYKNDKKVRVFTFSVGHNYDRGPIQWACENKGYIYEIPSGAIR 420
QY 421 INTQYLDVLRPMVLAGDKAKOVQNTVYLDALGLVITGLTPVFNITGQENKTNLK 480
Db 421 INTQYLDVLRPMVLAGDKAKOVQNTVYLDALGLVITGLTPVFNITGQENKTNLK 480
QY 481 NQILGVMGVDVSLIEDIKRLTPRTLCPCNGYYPFADIPNGVYLLHPNLQPKNSQBPVTL 540
Db 481 NQILGVMGVDVSLIEDIKRLTPRTLCPCNGYYPFADIPNGVYLLHPNLQPKNSQBPVTL 540
QY 541 DFLDAELNDIKVEIRNKMIDGESGKTRFTLVKSODERYIDKGNRTYTWTPVNGTDSL 600
Db 541 DFLDAELNDIKVEIRNKMIDGESGKTRFTLVKSODERYIDKGNRTYTWTPVNGTDSL 600
```

```
RESULT 3
QYERS3
ID QYERS3 PRELIMINARY; PRT; 1091 AA.
AC QYERS3;
DT 01-MAR-2001 (TREMREL. 16, Created)
DT 01-MAR-2001 (TREMREL. 16, Last sequence update)
DT 01-JUN-2002 (TREMREL. 21, Last annotation update)
DE Voltage-gated calcium channel alpha2/delta-1 subunit.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=SUPERIOR CERVICAL GANGLIA;
RA Lin Y., Lipscombe D.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF286488; AAG28164.1; -.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 1.
DR Pfam; PF00092; vwa; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50234; VWF; 1.
FT VARIANT 209 212 GSAT -> AADR.
FT VARIANT 338 338 S -> T.
FT VARIANT 599 600 SL -> RY.
FT VARIANT 869 869 S -> R.
SQ SEQUENCE 1091 AA; 123467 MW; CL55088971628E19 CRC64;

Query Match 97.8%; Score 5477; DB 11; Length 1091;
Best Local Similarity 97.0%; Pred. No. 0;
Matches 1031; Conservative 21; Mismatches 11; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLFQSLILGPSQRPSPSAVTIKSWDKMQEDLVTLAKTAGSVNQLVDI 60
Db 1 MAAGCLLALTLFQSLILGPSQRPSPSAVTIKSWDKMQEDLVTLAKTAGSVNQLADI 60
QY 61 YEKYQDLYTVEPNNAQVLAARDIEKLLSNRSKALVRLAEAEKVQAAHQWREDFASN 120
Db 61 YEKYQDLYTVEPNNAQVLAARDIEKLLSNRSKALVRLAEAEKVQAAHQWREDFASN 120
QY 121 EVVYNAKDDLPKNDSEPGSQRIPKFVTDANFGRQISYQHAHVHIPTDIYEGSTIVL 180
Db 121 EVVYNAKDDLPKNDSEPGSQRIPKFVTDANFGRQISYQHAHVHIPTDIYEGSTIVL 180
QY 181 NELNWTALDEVFKKNEEDPSLLQWVFGSATGLARYYPASPWVDSRTPNKIDLYDVR 240
Db 181 NELNWTALDEVFKKNEEDPSLLQWVFGSATGLARYYPASPWVDSRTPNKIDLYDVR 240
QY 241 RPWYIQGAASPKDMLILVDVSGVSGLTILKIRTSVSEMLETISDDDFVNVASFNSNAQ 300
Db 241 RPWYIQGAASPKDMLILVDVSGVSGLTILKIRTSVSEMLETISDDDFVNVASFNSNAQ 300
QY 301 VSCFQHLVQANVRNKKVLDVANNITAKGTDYKKGFSFAFQOLLNYSRANCNKIIML 360
Db 301 VSCFQHLVQANVRNKKVLDVANNITAKGTDYKKGFSFAFQOLLNYSRANCNKIIML 360
QY 361 FTDCGEERAQEIFAKYKNDKKVRVFTFSVGHNYDRGPIQWACENKGYIYEIPSGAIR 420
Db 361 FTDCGEERAQEIFAKYKNDKKVRVFTFSVGHNYDRGPIQWACENKGYIYEIPSGAIR 420
QY 421 INTQYLDVLRPMVLAGDKAKOVQNTVYLDALGLVITGLTPVFNITGQENKTNLK 480
Db 421 INTQYLDVLRPMVLAGDKAKOVQNTVYLDALGLVITGLTPVFNITGQENKTNLK 480
QY 481 NQILGVMGVDVSLIEDIKRLTPRTLCPCNGYYPFADIPNGVYLLHPNLQPKNSQBPVTL 540
Db 481 NQILGVMGVDVSLIEDIKRLTPRTLCPCNGYYPFADIPNGVYLLHPNLQPKNSQBPVTL 540
QY 541 DFLDAELNDIKVEIRNKMIDGESGKTRFTLVKSODERYIDKGNRTYTWTPVNGTDSL 600
Db 541 DFLDAELNDIKVEIRNKMIDGESGKTRFTLVKSODERYIDKGNRTYTWTPVNGTDSL 600
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Db 1 MAAGCLLALTLTLFQSLIGSPSEPFPASVTIKSWDKMOEDLVTAKTASGVNQLVDI 60  
QY 61 YEKYODLYTVPNNARQLVEIAARDIEKLLSNRSKALVRLALEAEKQVAAHQRREDFASN 120  
Db 61 YEKYODLYTVPNNARQLVEIAARDIEKLLSNRSKALVRLALEAEKQVAAHQRREDFASN 120  
QY 121 EYVYVNAKDDLDPEKNSEPGSQRIKPVFIDANFGRQISYQHAHVHPTDIYEGSTIVL 180  
Db 121 EYVYVNAKDDLDPEKNSEPGSQRIKPVFIDANFGRQISYQHAHVHPTDIYEGSTIVL 180  
QY 181 NELNWTSSALDEVFVKNREEDPSLLWQVFGSATGLARYYPASPPWVDSNRTPNKIDLYDVR 240  
Db 181 NELNWTSSALDEVFVKNREEDPSLLWQVFGSATGLARYYPASPPWVDSNRTPNKIDLYDVR 240  
QY 241 RPWTIOGAASPKDMLILVDVSGVSGITLKLIRTSVSEMLETISDDDFVNVASFNSNAQD 300  
Db 241 RPWTIOGAASPKDMLILVDVSGVSGITLKLIRTSVSEMLETISDDDFVNVASFNSNAQD 300  
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDTYKKGFSFAFEQLLNVSRANCKNIIML 360  
Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDTYKKGFSFAFEQLLNVSRANCKNIIML 360  
QY 361 FTDGGEERAQEIFAKYKNDKVRVFTSVGOHNYDRGPIQWMAKENGYYEIPSTGAIR 420  
Db 361 FTDGGEERAQEIFAKYKNDKVRVFTSVGOHNYDRGPIQWMAKENGYYEIPSTGAIR 420  
QY 421 INTOEYLDVLRPMVLADGAKAQVQVNTVYLDALGLVITGTLPVFNITQENKNTNLK 480  
Db 421 INTOEYLDVLRPMVLADGAKAQVQVNTVYLDALGLVITGTLPVFNITQENKNTNLK 480  
QY 481 NOLLILGVMGVDVSLDKRTPFTLCPNGYIFAIDPNGVYLLHNPQLPKPKSQEPVTL 540  
Db 481 NOLLILGVMGVDVSLDKRTPFTLCPNGYIFAIDPNGVYLLHNPQLPKPKSQEPVTL 540  
QY 541 DFLDAELENDIKVEIRNKMIDGESGKFTFLVKSDODERYIDKNGTYTWPVNGTDYSL 600  
Db 541 DFLDAELENDIKVEIRNKMIDGESGKFTFLVKSDODERYIDKNGTYTWPVNGTDYSL 600  
QY 601 ALVLPYTSFYIYIAKIBETITQARSKGKMKDSETLKPNFESGTYTFIAPRDYCNLDKI 660  
Db 601 ALVLPYTSFYIYIAKIBETITQARSKGKMKDSETLKPNFESGTYTFIAPRDYCNLDKI 660  
QY 661 SDNTEFLNFEFIDKTPNPNPSCNTDLNRLVLLDAGFTNELVQVWSKQNIKGVKAR 720  
Db 661 SDNTEFLNFEFIDKTPNPNPSCNTDLNRLVLLDAGFTNELVQVWSKQNIKGVKAR 720  
QY 721 FVVTGDIITRVYKPEAGENMOENPETEYDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
Db 721 FVVTGDIITRVYKPEAGENMOENPETEYDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
QY 781 MVSKAVEIYI 840  
Db 781 MVSKAVEIY 840  
QY 841 LDGGLFLLMANHDDYTNQIGRFGEDIPSLMRHLVNIYVAFNKSVDYOSVCEPGAAPKQ 900  
Db 841 LDGGLFLLMANHDDYTNQIGRFGEDIPSLMRHLVNIYVAFNKSVDYOSVCEPGAAPKQ 900  
QY 901 GAGHRSAYVPSIADILHIGWATAAAMSILQOFLSLTPRLLAEVEMEDDDFTASLSKQ 960  
Db 901 GAGHRSAYVPSIADILHIGWATAAAMSILQOFLSLTPRLLAEVEMEDDDFTASLSKQ 960  
QY 961 SCITEOTQVFFDNDKSFSGVLDGCGNCSRIYHVEKLMNTNLFIMVESGTCPCDTRLLI 1020  
Db 961 SCITEOTQVFFDNDKSFSGVLDGCGNCSRIYHVEKLMNTNLFIMVESGTCPCDTRLLI 1020  
QY 1021 QAEQTSDDGPDPCDMVKQPRYKGPDPVCFDNNALDLYTDCGGVS 1063  
Db 1021 QAEQTSDDGPDPCDMVKQPRYKGPDPVCFDNNALDLYTDCGGVS 1063

RESULT 2

Q9UIU0  
ID Q9UIU0 PRELIMINARY; PRT: 1110 AA.  
AC Q9UIU0;  
DT 01-MAY-2000 (TREMELrel. 13, Created)  
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)  
DT 01-MAR-2002 (TREMELrel. 20, Last annotation update)  
DE Dihydropyridine receptor alpha 2 subunit.  
GN CACNA2D1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20005942; PubMed=10534405;  
RA Schleithoff L., Mehrke G., Reutlinger B., Lehmann-Horn F.;  
RT "Genomic structure and functional expression of a human alpha(2)/delta  
calcium channel subunit gene (CACNA2).";  
RL Genomics 61:201-209(1999).  
DR EMBL: AF083854; AAF03259.1; JOINED.  
DR EMBL: AF083817; AAF03259.1; JOINED.  
DR EMBL: AF083818; AAF03259.1; JOINED.  
DR EMBL: AF083819; AAF03259.1; JOINED.  
DR EMBL: AF083820; AAF03259.1; JOINED.  
DR EMBL: AF083821; AAF03259.1; JOINED.  
DR EMBL: AF083822; AAF03259.1; JOINED.  
DR EMBL: AF083823; AAF03259.1; JOINED.  
DR EMBL: AF083824; AAF03259.1; JOINED.  
DR EMBL: AF083825; AAF03259.1; JOINED.  
DR EMBL: AF083826; AAF03259.1; JOINED.  
DR EMBL: AF083827; AAF03259.1; JOINED.  
DR EMBL: AF083828; AAF03259.1; JOINED.  
DR EMBL: AF083829; AAF03259.1; JOINED.  
DR EMBL: AF083830; AAF03259.1; JOINED.  
DR EMBL: AF083831; AAF03259.1; JOINED.  
DR EMBL: AF083832; AAF03259.1; JOINED.  
DR EMBL: AF083833; AAF03259.1; JOINED.  
DR EMBL: AF083834; AAF03259.1; JOINED.  
DR EMBL: AF083835; AAF03259.1; JOINED.  
DR EMBL: AF083836; AAF03259.1; JOINED.  
DR EMBL: AF083837; AAF03259.1; JOINED.  
DR EMBL: AF083838; AAF03259.1; JOINED.  
DR EMBL: AF083839; AAF03259.1; JOINED.  
DR EMBL: AF083840; AAF03259.1; JOINED.  
DR EMBL: AF083841; AAF03259.1; JOINED.  
DR EMBL: AF083842; AAF03259.1; JOINED.  
DR EMBL: AF083843; AAF03259.1; JOINED.  
DR EMBL: AF083844; AAF03259.1; JOINED.  
DR EMBL: AF083845; AAF03259.1; JOINED.  
DR EMBL: AF083846; AAF03259.1; JOINED.  
DR EMBL: AF083847; AAF03259.1; JOINED.  
DR EMBL: AF083848; AAF03259.1; JOINED.  
DR EMBL: AF083849; AAF03259.1; JOINED.  
DR EMBL: AF083850; AAF03259.1; JOINED.  
DR EMBL: AF083851; AAF03259.1; JOINED.  
DR EMBL: AF083852; AAF03259.1; JOINED.  
DR EMBL: AF083853; AAF03259.1; JOINED.  
DR InterPro: IPR004010; Cache.  
DR InterPro: IPR002035; VWF\_A.  
DR Pfam: PF02743; Cache; 1.  
DR Pfam: PF00092; vwa; 1.  
DR SMART: SM00327; VWA; 1.  
DR PROSITE: PS0234; VVFA; 1.  
DR Receptor.  
SQ SEQUENCE 1110 AA; 125307 MW; 8358DC6AD489C074 CRC64;

Query Match 98.7%; Score 5528.5; DB 4; Length 1110;  
Best Local Similarity 97.2%; Pred. No. 0;  
Matches 1052; Conservative 5; Mismatches 6; Indels 19; Gaps 1;  
QY 1 MAAGCLLALTLTLFQSLIGSPSEPFPASVTIKSWDKMOEDLVTAKTASGVNQLVDI 60  
Db 1 MAAGCLLALTLTLFQSLIGSPSEPFPASVTIKSWDKMOEDLVTAKTASGVNQLVDI 60

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 10, 2003, 14:13:55 ; Search time 41.4836 Seconds  
(without alignments)  
5279.867 Million cell updates/sec

Title: US-10-090-827-8  
Perfect score: 5602  
Sequence: 1 MAAGCLLALTLTFLQSLIG.....PDVCFDNNALDYDCGGVS 1063

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues 671580  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_prodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5602	100.0	1091	6 077773	077773 sus scrofa
2	5528.5	98.7	1110	4 Q9UIU0	Q9uiu0 homo sapien
3	5477	97.8	1091	11 Q9ERS3	Q9ers3 rattus norv
4	5405	96.5	1103	11 Q08532	Q08532 mus musculu
5	5381	96.1	1079	11 Q8VHS9	Q8vhs9 rattus norv
6	3786	67.6	745	4 Q9UDQ3	Q9udq3 mus musculu
7	3066	54.7	1150	4 Q9NY47	Q9ny47 homo sapien
8	3038.5	54.2	1143	4 Q9NY48	Q9ny48 homo sapien
9	3038.5	54.2	1156	11 Q9PQG2	Q9eqg2 mus musculu
10	3025.5	54.0	1145	4 Q9Y268	Q9y268 homo sapien
11	3013	53.8	1084	11 Q9Z0H6	Q9z0h6 mus musculu
12	3004.5	53.6	1076	4 Q9UEW0	Q9uew0 homo sapien
13	2829	50.5	975	4 Q9NSA6	Q9nsa6 homo sapien
14	1145.5	20.4	1091	11 Q9Z1L5	Q9z1l5 mus musculu
15	1074.5	19.2	997	4 Q9NV16	Q9ny16 homo sapien
16	1034	18.5	1218	5 Q8T9C3	Q8t9c3 drosophila

17	945	16.9	2190	5	Q9NK64	Q9nk64 drosophila
18	930	16.6	2172	5	Q9VJM0	Q9vjm0 drosophila
19	906.5	16.2	1191	5	Q9VJN7	Q9vjn7 drosophila
20	905	16.2	1255	5	Q9NK83	Q9nk83 drosophila
21	875	15.6	170	4	Q9UDL7	Q9udl7 homo sapien
22	861	15.4	1022	5	Q9V6T7	Q9v6t7 drosophila
23	759.5	13.6	519	4	Q9NV18	Q9nv18 homo sapien
24	661	11.8	317	11	Q9Z0H5	Q9z0h5 mus musculu
25	579.5	10.3	1148	5	Q17517	Q17517 caenorhabdi
26	561.5	10.0	842	5	Q95R75	Q95r75 drosophila
27	516.5	9.2	104	4	Q9UD81	Q9ud81 homo sapien
28	515	9.2	100	6	Q9GLH1	Q9glh1 bos taurus
29	496.5	8.9	121	4	Q9UD82	Q9ud82 homo sapien
30	479	8.6	98	4	Q9UDU5	Q9udu5 homo sapien
31	470.5	8.4	223	11	Q9R142	Q9r142 mus musculu
32	467	8.3	97	4	Q9UD80	Q9ud80 homo sapien
33	404	7.2	77	4	Q95026	Q95026 homo sapien
34	335	6.0	1185	4	Q9HCG9	Q9hcj9 homo sapien
35	233.5	4.2	978	5	Q95XE0	Q95xe0 macaca fasc
36	221	3.9	1449	5	Q9V917	Q9v917 drosophila
37	201.5	3.6	886	11	Q91WG9	Q91wg9 mus musculu
38	190.5	3.4	1450	16	Q9CE07	Q9ce07 lactococcus
39	177.5	3.2	494	5	Q9U7P4	Q9u7p4 eufoillculi
40	170.5	3.0	1819	16	Q97K40	Q97k40 clostridium
41	167	3.0	796	17	Q9HJRO	Q9hjr0 thermoplas
42	167	3.0	800	17	Q97AH3	Q97ah3 thermoplas
43	165	2.9	459	16	O25905	O25905 helicobacte
44	164.5	2.9	789	2	O45793	O45793 bacillus th
45	164	2.9	614	16	Q8XN21	Q8xn21 clostridium

## ALIGNMENTS

RESULT 1

077773 ID 077773 PRELIMINARY; PRT: 1091 AA.

AC 077773;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE Voltage-dependent calcium channel alpha-2 delta subunit precursor.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN CORTEX;  
RX MEDLINE=98411353; PubMed=9738015;  
RA Brown J.P., Gee N.S.;  
RT "Cloning and deletion mutagenesis of the alpha2 delta calcium channel subunit from porcine cerebral cortex. Expression of a soluble form of the protein that retains [3H]gabapentin binding activity.";  
RL J. Biol. Chem. 273:25458-25465(1998).  
DR EMBL; AF077665; AAC36289.1; -  
DR InterPro; IPR004010; Cache.  
DR Pfam; PF02743; Cache; 1.  
DR Pfam; PF00092; vwa; 1.  
DR SMART; SM00327; VWA; 1.  
DR PROSITE; PS50234; VWFA; 1.  
KW Signal.  
FT SIGNAL.  
FT CHAIN.  
FT SIGNAL.  
FT CHAIN.  
SQ SEQUENCE 1091 AA; 123150 MW; 293DDC7EBE9EE60E CRC64;

POTENTIAL.  
VOLTAGE-DEPENDENT CALCIUM CHANNEL ALPHA-2  
DELTA SUBUNIT.  
1 24  
25 1091

Query Match 100.0%; Score 5602; DB 6; Length 1091;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAAGCLLALTLTFLQSLIGSPSPFPFPFSAVTKSWDKMQEDLVTLAKTASGVNQLVDI 60

100

100

Page 13

QY	1044	PDVCFDNN	ALEDYTD	CGG	1061
		:	:   :		
Db	958	PESCHGFH	PEENARE	CCG	975

Search completed: February 10, 2003, 14:28:17  
Job time : 46.7178 secs

DE	Calcium channel alpha-2-delta-C subunit.
GN	CACNA2D3.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=BRAIN;
RA	Klugbauer N., Lacinova L., Marais E., Hobom M., Hofmann F.;
RT	"Molecular diversity of the calcium channel alpha2delta subunit.";
RL	J. Neurosci. 19:648-691(1999).
DR	EMBL; AJ010949; CAA09423.1; -.
DR	MGD; MGI:1338890; Cacna2d3.
DR	InterPro; IPR004010; Cache.
DR	InterPro; IPR002035; VWF_A.
DR	Pfam; PF02743; Cache: 2.
DR	SMART; SM00327; VWA: 1.
DR	PROSITE; PS02334; VWF: 1.
SEQ	SEQUENCE 1091 AA; 122777 MW; 7ABE2BDA10077A0A CRC64;
Query Match 20.3%; Score 1145.5; DB 11; Length 1091;	
Best Local Similarity 28.6%; Pred. No. 1.7e-61;	
Matches 322; Conservative 234; Mismatches 437; Indels 133; Gaps	
QY	3 ACCLALTLTLFQSLILIGPSSQBPFPSSAVTIKSWDKMQEDLVTLAKTASGVNQLDYIE 62
DB	14 ASALLA-TALLYAALGDVVRSEQOIPLSV-VKLWASAFGEIKSAIKYSGSLLQKKVK 71
QY	63 KYODLYTEPNNARQLVEIARDLEKLLSNRSKALVRLALEAKYVQAQHWREDPASVNE 122
DB	72 EYEKDVAEEIDGQLVKKLAKIWEEMFHKRSKAVRLVEAAEHLKHEFDADL---QY 128
QY	123 VYNNAK---DDLOPEKNDSEPGSQRIKPVFIDDAFNGRQISYQAAVHIPTDIYEGSTVL 180
DB	129 EYFNALINERDKDGNLELKGKEFI--LAPNDHFNNLPVNISLSVDQVFTNMYNKDPAIV 186
QY	181 NELNWTLSALDEVFKKNEEDPSLLWQVFGSATGLARYYPASPVDWNSRTPNKIDLYDVR 240
DB	187 NGVTWSESLNKVFDNEDRPSLWQVFGSAKGFQYQGIKWEPE--NGVIAFDGRN 243
QY	241 RPWYIQGAASPDKMLILVDYSGVSGYTLKLRITSYSEMLETISDDDFVNVASFNSNAQD 300
DB	244 RKWYIQAATSPKVVILVDYSGMKGLRLTIKQTVSSILDTLGGDDFNIIITNEELHY 303
QY	301 VS-CFQ-HLQVANYRNKKVLKADVNNITAKIFTDYKKGSFAFEQLLNVSRAN--CNK 356
DB	304 VEPCLNGTLQVADRTNKEHEHRLDKLFAKIGIMLDIALNEAFNILSDPNHTGQGSICSQ 363
QY	357 IIMLFTGGGERAQEIAFKN-KDKKRVFTFSVGQHNDRGPQIOWMACENKGYEYIIPS 415
DB	364 AIMLITDGAVDYDTIFAKYNWFRKVRIFTYDIGEAAFAFADNLKMWACANKGFTQTST 423
QY	416 IGATIRINQEYLDVLGRPMVLADGAKAQVQWTVNYLD-----ALELGLVI--TGTLL 464
DB	424 LADYQENMVEYLVHLSRPKVI--DQEHVDVWVTEAYIDSTLPAQKLADDOGLVMTTYAM 481
QY	465 PVFENITQGENKTNLKNQLILGVMGVDVSLIEDIKRLTPRTLCPGNYFYAIDPNGYVLH 524
DB	482 PVFS-----KQNETRSKG-ILLGVVGDVPVKELKTIPIKYKLGIGHYAFATNNGYILLTH 536
QY	525 PNLPQ---KNPKSQEP--VPLDPLDAELENLKVLRNKMIDGESGKERTFLVKSQDER 579
DB	537 PELRLPEEGCKRRKPNYSVDLSSEVWEDEDRDV-LRNAVWNRKTGK--FSNEVK----K 589
QY	580 YIDKGNFT-----YVWTPVNGVDYSALVLPT-YSFYIYIKAK--IEETITQARSKKGM 630
DB	590 TVDKGKRLVYMTINDYYTIDIKGTPPSLGVALSNGHKGKVFYFRNCVNTIEGSL----- 639
QY	631 KDSETLKPDNFEESGVFTFIAPROYCN-DLKISDNTEFLLNFEETIDRKTTPNPSCNFDL 689
DB	640 -----HDLHPDVSADENSGVNTDLPHEHRLHSQLEAIKYLKGGKEL-LQCCOKEL 690

Db 417 TNYVEDALGLGLVVTGTLTPVFNLTQDGPGEK-----KNQLLGVMGIDVALNDIKRLTPNY 472  
QY 505 TLCPNGYYFAIDPNGVYVLLHNPQKPKSQEPVTLDFDLAELENDIKVEIRKMKIDGES 564  
Db 473 TLGANGYVFAIDNGVYVLLHNPQKPKSQEPVTLDFDLAELENDIKVEIRKMKIDGES 532  
QY 565 GEKTFEFLVKSODERYIDKGNRTYVTPVNGTDYSIALVLPYSFYIKAKIEETITQAR 624  
Db 533 GHKOIRTLVKSODERYIDKGNRTYVTPVNGTDYSIALVLPYSFYIKAKIEETITQAR 590  
QY 625 SKGKMKDSETLKPDPNFESEGYTFIAPRDYCNLDKISDNNTEFLNFEIDIRKTPNNPS 684  
Db 591 -----VKYFEFLPSPSESGHVFIAPREYCKDLNASDNNTEFLKNEFELMEKVTDPDSKO 645  
QY 685 CNTDLINRVLLDAGTNELVONTWSKQK-NIKGVKARFVVTGGITRVYPKAGENWQEN 743  
Db 646 CNFELLHNLIDTGTQQLVERVWRDQDLNTYSLLAFAATDGGITRVYPKAAEDWTEN 705  
QY 744 PETYEDSFYKRSLDNDNYVFTAPYENK-SGPGAYES---GIMYSKAVEIYIOGKLLKPAV 799  
Db 706 PEPFNASFYRRSLDNGHYVFKPHQDALLRPLELENDTVGILVSTAVELSLGRTRLRPAV 765  
QY 800 VGKIDVNSWIEF-----TKTSIRDP--CAGP-----VCDCKRNSDVMDCVILDDGGFLL 848  
Db 766 VGVKLDLEAWEAEKFKVLASNRTHQDQPKC-GPNSHCMDCEVNNEDLLCVLIDGGFELV 824  
QY 849 MANHDDYTNIGRFGFIDPDSLMRHLVNSVYAFNKSVDYQSVCEPGAAPKQAGHRSAY 908  
Db 825 LSNQNHQWQVGRFSEVDANLALYNSFYRKESYDQAACAPQPPGNLGAAPRGVF 884  
QY 909 VPSTADILHIGWATAAWSILQFLLSLTFPRLLEAVEMEDDDFTASLSKOSCITEQ 968  
Db 885 VPTVADFLNLAWTSAAAWSLFQOILYGLIYHSWFQADPAEAG-SPEFRESCVMKQTO 943  
QY 969 YFFDNDKSFSGVLDGNCGRIFHEVEKLMNTNLIFINVESTKGCPCDTRLLIQAEQ--TS 1026  
Db 944 YFGSVNASYNAIICDNCGRSLFHAQRLTNTLFFVVAEKPLCSQCEAGRLQKETHCPA 1003  
QY 1027 DGPPDCMVKOPRYKRGPDVCFDNNALDYDCG 1060  
Db 1004 DGPEQCELVORPRYRRGHICFDYNATEDSDCG 1037

RESULT 13  
Q9NSA6 PRELIMINARY; PRT; 975 AA.  
AC Q9NSA6  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE LUAC11.1 (Calcium channel, voltage-dependent, L type, alpha 2D subunit (K1AA0558)) (Fragment).  
GN LUAC11.1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Barlow K.;  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; 284492; CAB41767.2; --  
DR InterPro; IPR004010; Cache.  
DR InterPro; IPR002035; VWF\_A.  
DR Pfam; PF02743; Cache; 1.  
DR SMART; SM00327; VWA; 1.  
DR PROSITE; PS0234; VWF; 1.  
FT NON\_TER 1  
SQ SEQUENCE 975 AA; 110192 MW; C7874D46B88242BF CRC64;  
Query Match 50.1%; Score 2829; DB 4; Length 975;  
Best Local Similarity 57.0%; Pred. No. 1.1e-164;  
Matches 543; Conservative 146; Mismatches 223; Indels 40; Gaps 15;

QY 132 DPEKNDSEPGSQ--RIKPVFIDDFANFRQISYQAAHVHIPTDIYEGSTIVLNLNWTFSAL 189  
Db 2 DPESEDVERGSKASTLRDLDFIEDFNKNVNSYAAQVPTDIYKGVTLNLNWTFSAL 61  
QY 190 DEVFKKNEEDPSLLQWFGSATGLARYYPASPVWVNSRTPNKKIDLDVRRRPWYIOGAA 249  
Db 62 ENVMENRQDPTLLIQWFGSATGVTRYYPATPW----RAPKKIDLDVRRRPWYIOGAS 117  
QY 250 SPKMDLILVDYSGVSGLTLLKIRTSYSEMLETISDDDFVNVASFNSNAQDVSCFHLVQ 309  
Db 118 SPKMDLILVDYSGVSGLTLLKIRTSYSEMLETISDDDFVNVASFNSNAQDVSCFHLVQ 177  
QY 310 ANVRNKKVLDKAVNNITAKGITDYKKGFSFAFEQQLLNVSRANCKIIMLFTDGGERA 369  
Db 178 ANVRNKKVLEKAVQGVAKGTTGYKAGFEYAFDQLQNSNITRANCKIMMFTDGGEDRV 237  
QY 370 QEIFAKYN-KDKKRVFTFSQGHNYDRGPIOWMACENKGYEYIPIPSIGAIRINTQEYLD 428  
Db 238 QDVPEKYWNPRTVRVFTFSVQGHNYDVTPLQWMACANKGYEYIPIPSIGAIRINTQEYLD 297  
QY 429 VLGRPMVLGADKAKOVQNTNVLDALEGLVITGTLPVENIT--QONENKTNLKNQLILG 486  
Db 298 VLGRPMVLGADKAKOVQNTNVEDALGLVYVGTGTLPVENITQDGPGEK-----KNQLILG 353  
QY 487 VMGVDSLEIDIKRLTPRFTLCPNGYFFAIDPNGYVLLHNPQKPKSQEPVTLDFDLAE 546  
Db 354 VMGIDVALNDIKRLTPNTLGVANGYVFAIDNGVYVLLHNPQKPKSQEPVTLDFDLAE 413  
QY 547 LENDIKVEIRKMKIDGESGEKTFRTLVKSODERYIDKGNRTYVTPVNGTDYSIALVLP 606  
Db 414 LEDENKEEIRRMIDGNKGHKQIRTLVKSODERYIDVTRNYVTPVIRSTNYSLGLVLP 473  
QY 607 YSFYIKAKIETIIOAKSKKMKDSETLKPDPNFESEGYTFIAPRDYCNLDKISDNNTE 666  
Db 474 YSTFYLOANLSQIILQ-----VKYFEFLPSPSESGHVFIAPREYCKDLNASDNNTE 526  
QY 667 FLNNEFTIDRTPNPNCSNTDLINRVLLDAGTNELVONTWSKQK-NIKGVKARFVVT 725  
Db 527 FLKNTIELMEKVTDPDSKQCNFLLHNLIDTGTQQLVERVWRDQDLNTYSLLAFAATD 586  
QY 726 GGITRVYPKAGENWQENPETYEDSFYKRSLDNDNYVFTAPYENK-SGPGAYES---GIM 781  
Db 587 GGITRVYPKAGENWQENPETYEDSFYKRSLDNDNYVFTAPYENK-SGPGAYES---GIM 781  
QY 782 VSKAVEIYIOGKLLKPAVVGKIDVNSWIEF-----TKTSIRDP--CAGP-----VCDCK 830  
Db 647 VSTAVELSLGRTRLRPAVVGKIDVNSWIEF-----TKTSIRDP--CAGP-----VCDCK 830  
QY 831 RNSDVMDCVILDDGGFLLMANHDDYTNQIGRFGFIDPDSLMRHLVNSVYAFNKSVDYQ 890  
Db 706 VNNEDLLCVLIDGGFLLVLSNQNHQWQVGRFSEVDANLALYNSFYRKESYDQA 765  
QY 891 VCEPGAAPKQAGHRSAYVPSIADILHIGWATAAWSILQFLLSLTFPRLLEAVEMED 950  
Db 766 ACAPQPPGNLGAAPRGVFVPTVADFLNLAWTSAAAWSLFQOILYGLIYHSWFQADPA 825  
QY 951 DDEFTASLSKOSCITEQTYFFDNDKSFSGVLDGNCGRIFHEVEKLMNTNLIFINVEST 1010  
Db 826 EG-SPEFRESCVMKQTOYFGSVNASYNAIICDNCGRSLFHAQRLTNTLFFVVAEKPL 884  
QY 1011 TCPDTRLLIQAEQ--TSDGPPDCMVKOPRYKRGPDVCFDNNALDYDCG 1060  
Db 885 CSQCEAGRLQKETHCPADGPEQCELVORPRYRRGHICFDYNATEDSDCG 936  
RESULT 14  
Q9Z1L5 PRELIMINARY; PRT; 1091 AA.  
AC Q9Z1L5  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DR EMBL; AF247141; AAL01650.1; --  
 DR MGD; MGI:1929813; Caccna2d2.  
 DR InterPro; IPR004010; Cache.  
 DR InterPro; IPR002035; VWF\_A.  
 DR Pfam; PF02743; Cache; 1.  
 DR PROSITE; PS50234; VWF\_A; 1.  
 SQ SEQUENCE 1084 AA; 123104 MW; 197D65B37EB9893 CRC64;

Query Match 53.3%; Score 3013; DB 11; Length 1084;  
 Best Local Similarity 54.9%; Pred. No. 7.2e-176;  
 Matches 577; Conservative 177; Mismatches 264; Indels 36; Gaps 15;

QY 33 IKSVDKMGEDLVTLAKTAGVGNQVLVDIYKQDYVTEPNNAQOLVIEIARDIEKLNS 92  
 DB 1 MHWARRLEQEDIGVGNRIFGGVQQLREIYKDNRLFEVQENEPQKLVKAGVAGDIESLDR 60

QY 93 RSKALVRLALEAEKVQAAHOREDPASNEVYVYNAKDDL---DPEKNDSEPGSO--RIKP 147  
 DB 61 KYQALKRLADAAENFQKAHRQDNKIKEEDIMYDADAKADAEALDDPESEDMERGKSTSLRL 120

QY 148 VFIDANFGRQISYQAAHVIPTDIYEGSTIVLNLNWTSSALDEVFKNREEDPSLLMQV 207  
 DB 121 DFIEDPNFKNKVNSYTAQVPTDIYKGSTVILNLTALNTEALENVFTENRRQDPTLLQV 180

QY 208 FGSATGLARYYPASPDVNSRTPNKIDLYVRRRPWTIOGAASPKDMLILVDVSGVSG 267  
 DB 181 FGSATGVTRYYPATPW----RAPKIDLYVRRRPWTIOGASSPKDMLIVDVGSGVSG 236

QY 268 TLKLI RTSVSEMLETSLDDDDFVNVASFNSNAQDSCFQHLVQANVRNKKVLKDAVNNTA 327  
 DB 237 TLKLMKTSVCEMLDTSDDDDVNVASFNEKAQPVSCFTHLVQANVRNKKVFEKAVQGMVA 296

QY 328 KGITDYKKGFSFAEQLLNLYNVSRANCKNIIMLFTDGGEEARAEIFAKYN-KDKKVRVFT 386  
 DB 297 KGTGTYKAGFYAFDQLNSNITRANCKNIMMFTDGGEDRVQDVFKEKPNRTVRF 356

QY 387 FSVGHNTYDRGPIQWACENKGYEIPSGAIRINTQEYLDVLRPMVLGAKAKQVOW 446  
 DB 357 FSVGHNTYDVTPLQWMACTNKGYEIPSGAIRINTQEYLDVLRPMVLGAKAKQVOW 416

QY 447 TNYVDALEGLVITGLTPVENIT--GQENKTNLKNQILGVMGVDVSLIEDIKRLTPRF 504  
 DB 417 TNYVDALEGLVITGLTPVENIT--GQENKTNLKNQILGVMGVDVSLIEDIKRLTPRF 504

QY 417 TNYVDALEGLVITGLTPVENIT--GQENKTNLKNQILGVMGVDVSLIEDIKRLTPRF 504  
 DB 417 TNYVDALEGLVITGLTPVENIT--GQENKTNLKNQILGVMGVDVSLIEDIKRLTPRF 504

QY 505 TLPNGYFAIDPNGYVLLHPNLPKPKSOEPTVTLDFDAELNDIKVIRKNKIDGES 564  
 DB 473 TLGANGYFAIDPNGYVLLHPNLPKPKSOEPTVTLDFDAELNDIKVIRKNKIDGES 564

QY 565 GEKTRTLVKSQDRYIDKGNRTYTWTPVNGTDYSLALVLPYTSFYIYKAKIETITQAR 624  
 DB 533 GHKQIRTLVKSQDRYIDKGNRTYTWTPVNGTDYSLALVLPYTSFYIYKAKIETITQAR 624

QY 625 SKKCKMKDSETLKPDNFEESGYFIAPRDCNDLKTSNDNTEFLNFPNEDIRKTPNPS 684  
 DB 593 LPISKLDKDFEFLPSSPSESGHYFIAPRDCNDLKTSNDNTEFLNFPNEDIRKTPNPS 684

QY 685 CNTDLINRLDAGFTNELQVYWSKQK-NIKGVKARFVVTGGLITRVYPKEAGENQWEN 743  
 DB 653 CNPFLHNLILDTGITOQLVERVWRDQDLNLTYSLLAVFAATDGGITRVYPKEAGENQWEN 712

QY 744 PEYEDSFYKRSNDNMYETAPYFNK-SGPGAYES---GIMYSKAVEIYIOGKILKPAP 799  
 DB 713 PEPFNASFYRSRSDNHYIFKPPHQDLSLLRPLENDTVGVLVSTAVELSLGRRTLRPAV 772

QY 800 VGKIDNWSIENF-----TKTSIRDP--CAGP-----VDCRKNSDVMDCVILDDGGFL 848  
 DB 773 VGKIDNWSIENF-----TKTSIRDP--CAGP-----VDCRKNSDVMDCVILDDGGFL 848

QY 849 MANHDDYTNQIGRFFRIPSLMRHLVNI SVYAFNKSQYQVCEPCEAPKACAGHRSAY 908  
 DB 832 LSNQNHQDQVGRFESEVDANLMLALYNYSFYTRKESYDIQACAPQPPGNLGAAPRGVY 891

QY 909 VPSIADILHIGWATAAANSILQQFLLSLTFPRLLEAVEMEDDDDETASLSKQSCITEQ 968

DB 892 VPTIADFLNLAWTSAANSLFQQLLYGLYHSWFQDPAEAG-SPETRESSCMVKQTQ 950  
 QY 969 YFFDNDKSGVGLDCGNCGRIFHEVKLMNTNLIFINVESKGTCPDCTRLIIQAEQ--TS 1026  
 DB 951 YIFGVSANYNATIDCGNCGRIFHEVKLMNTNLIFINVESKGTCPDCTRLIIQAEQ--TS 1026  
 QY 1027 DGPDPCCDMVKOPRYRKGPDVCFDNNALEDYDCG 1060  
 DB 1011 DGPQCELVQPRYRRRPHICFDYNATEDSDCG 1044

RESULT 12  
 Q9UEW0 PRELIMINARY; PRT; 1076 AA.  
 AC Q9UEW0;  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
 DE Alpha 2 delta calcium channel subunit isoform II.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wei M.-H., Latif F., Duh F.-M., Adreazzoli-Angeloni D., Kashuba V.,  
 RA Zabarovsky E., Johnson B., Lerman M.I.;  
 RT "A new alpha 2 delta subunit of the L-type voltage gated calcium  
 RT channel resides in the lung cancer critical region on 3p21.3";  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF042793; AAB96914.1;  
 DR InterPro; IPR004010; Cache.  
 DR InterPro; IPR002035; VWF\_A.  
 DR Pfam; PF02743; Cache; 1.  
 DR SMART; SM00327; VWA; 1.  
 DR PROSITE; PS50234; VWF\_A; 1.  
 SQ SEQUENCE 1076 AA; 122116 MW; BEC474836B7EDA85 CRC64;

Query Match 53.2%; Score 3004.5; DB 4; Length 1076;  
 Best Local Similarity 54.9%; Pred. No. 2.4e-175;  
 Matches 579; Conservative 173; Mismatches 259; Indels 43; Gaps 16;

QY 33 IKSVDKMGEDLVTLAKTAGVGNQVLVDIYKQDYVTEPNNAQOLVIEIARDIEKLNS 92  
 DB 1 MHWARRLEQEDIGVGNRIFGGVQQLREIYKDNRLFEVQENEPQKLVKAGVAGDIESLDR 60

QY 93 RSKALVRLALEAEKVQAAHOREDPASNEVYVYNAKDDL---DPEKNDSEPGSO--RIKP 147  
 DB 61 KYQALKRLADAAENFQKAHRQDNKIKEEDIMYDADAKADAEALDDPESEDMERGKSTSLRL 120

QY 148 VFIDANFGRQISYQAAHVIPTDIYEGSTIVLNLNWTSSALDEVFKNREEDPSLLMQV 207  
 DB 121 DFIEDPNFKNKVNSYTAQVPTDIYKGSTVILNLTALNTEALENVFTENRRQDPTLLQV 180

QY 208 FGSATGLARYYPASPDVNSRTPNKIDLYVRRRPWTIOGAASPKDMLILVDVSGVSG 267  
 DB 181 FGSATGVTRYYPATPW----RAPKIDLYVRRRPWTIOGASSPKDMLIVDVGSGVSG 236

QY 268 TLKLI RTSVSEMLETSLDDDDFVNVASFNSNAQDSCFQHLVQANVRNKKVLKDAVNNTA 327  
 DB 237 TLKLMKTSVCEMLDTSDDDDVNVASFNEKAQPVSCFTHLVQANVRNKKVFEKAVQGMVA 296

QY 328 KGITDYKKGFSFAEQLLNLYNVSRANCKNIIMLFTDGGEEARAEIFAKYN-KDKKVRVFT 386  
 DB 297 KGTGTYKAGFYAFDQLNSNITRANCKNIMMFTDGGEDRVQDVFKEKPNRTVRF 356

QY 387 FSVGHNTYDRGPIQWACENKGYEIPSGAIRINTQEYLDVLRPMVLGAKAKQVOW 446  
 DB 357 FSVGHNTYDVTPLQWMACTNKGYEIPSGAIRINTQEYLDVLRPMVLGAKAKQVOW 416

QY 447 TNYVDALEGLVITGLTPVENIT--GQENKTNLKNQILGVMGVDVSLIEDIKRLTPRF 504  
 DB 417 TNYVDALEGLVITGLTPVENIT--GQENKTNLKNQILGVMGVDVSLIEDIKRLTPRF 504

DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)  
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
 DE KIAA0558 protein.  
 GN KIAA0558.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN;  
 RA Sekido Y., Duh F.-M., Latif F., Ding J., Lin J., Mathis M.,  
 RA Minna J.D.;  
 RA "Gene 26, a new candidate human tumor suppressor gene located in the  
 RA 3p21.3 small cell lung cancer homozygous deletion region homologous to  
 RT a voltage gated calcium channel alpha 2/ delta subunit";  
 RT Submitted (Oct-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Wei M.-H., Latif F., Duh F.-M., Adreazzoli-Angeloni D., Kashuba V.,  
 RA Zabarovsky E., Johnson B., Lerman M.I.;  
 RA "A new alpha 2 delta subunit of the L-type voltage gated calcium  
 RT channel resides in the lung cancer critical region on 3p21.3";  
 RT Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN;  
 RX MEDLINE=98290545; PubMed=9628581;  
 RA Nagase T., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.,  
 RA Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. IX.  
 RT The complete sequences of 100 new cDNA clones from brain which can  
 RT code for large proteins in vitro.";  
 RL DNA Res. 5:31-39(1998).  
 DR EMBL; AF040709; AAC70914.1; -;  
 DR EMBL; AF042792; AAB96913.1; -;  
 DR EMBL; AB011130; BAA25484.1; -;  
 DR InterPro; IPR004010; Cache.  
 DR InterPro; IPR002035; VWF\_A.  
 DR Pfam; PF02743; Cache; 1.  
 DR SMART; SM00327; VWA; 1.  
 DR PROSITE; PS0234; VWF; 1.  
 SQ SEQUENCE 1145 AA; 129268 MW; 9ADA4807FC70971B CRC64;  
  
 Query Match 53.5%; Score 3025.5; DB 4; Length 1145;  
 Best Local Similarity 54.4%; Pred. No. 1.4e-176;  
 Matches 588; Conservative 174; Mismatches 275; Indels 43; Gaps 16;  
  
 QY 7 LALTLTQSLIGPSSQPPSATYIKSWDKMQEDLVTLAKTAGSVNQLVDIYKQD 66  
 DB 44 LWLPLPLLAAPGASAYSFPQOHTMQHARRLQEQVDGVMRTFGVQQLREIYKDRN 103  
  
 QY 67 LVTVPNARQLVETAAARDIEKLLSNRSKALVRLALEAEKVQAAHQWEDFASNEVYYN 126  
 DB 104 LEVEQENEPKLVKVGADIESLLDRKQVALKRLAADAENFQKAHRWQDNKEEDIVYD 163  
  
 QY 127 AKDDL--DPEKNDSEPGSQ--RIKVFIDDFANFQRTSYQHAHVHPTDIEGSTIVLN 181  
 DB 164 AKADAELDDPESEDVERGSKASTLRDELDFENFKNKYNSYAAVQIPTDIYKGVSTVLN 223  
  
 QY 182 ELNWTLSALDEVFKKREEDPSLLQVFGSATGLARYYPASPVWDSRTPNKLIDYDVR 241  
 DB 224 ELNWTLEALNFMENRQDPTLLQVFGSATGTTRYYPATPW----RAPKILIDYDVR 279  
  
 QY 242 PWYIOGASPKDMILVDYSGVSGGLTKLIRTSVSEMLETSDDDFFNVASFNSAODV 301  
 DB 280 PWYIOGASPKDMYIIVDYSVSGVSGGLTKLMTKTSVCEMLDTLSDDDYVNSAFNEKAQV 339  
  
 QY 302 SCFOHLVQANVRNKKVKLDVANNITAKGTDYKKGFSFAFQGLLYNVRANCNKIIMLF 361  
 DB 340 SCFTHLVQANVRNKKVKFAVGAKGTGYKAGFAFDQLQNSNITRANCNKIIMWF 399  
  
 QY 362 TDGGEERAQEIFAKYN-KDKKVRVTFVSGVQHNYDRGPQIOWMACENKGYEIPISGAIR 420

DB 400 TDGEDRVQDVEFEKYNWPNRTYRVETSVGQHNVDVTLQWMACANKGYEIPISGAIR 459  
 QY 421 INTOEYLDVLRPMVLGAKAKOVQWNTVYLDALGLVITGTLVPFNIT--GQENKTN 478  
 DB 460 INTOEYLDVLRPMVLGAKAKOVQWNTVYLDALGLVITGTLVPFNITQDGPGEK--- 516  
 QY 479 LKNQILGYMGVDSLEDIKRLTPRTFLCPNGYYPFAIDPNGVYLLHPNLPKNPSQBPV 538  
 DB 517 -KNQILGYMGIDVALNDIKRLTPNLTGANGYVEAIDLNGVYLLHPNLPKPTNRPVP 575  
 QY 539 TLDLDAELENDIKVEIRNKMIDGESGEXTFTLVKSQDERYIDKGNRYTWTVPVNGTDY 598  
 DB 576 TLDLDAELENDIKVEIRNKMIDGESGEXTFTLVKSQDERYIDKGNRYTWTVPVNGTDY 635  
 QY 599 SLALVLPYTFYIYAKIEETITQARKSKKMKRDSSTLKPDPNPFESGYFFIAPRDYCNLD 658  
 DB 636 SLGLVLPYTFYIYAKIEETITQARKSKKMKRDSSTLKPDPNPFESGYFFIAPRDYCNLD 688  
 QY 659 KISDNTEFLNPFIDRKTNNPSCNTDLNRLVLLDAGFTNELVQNTWSKQK-NIKGV 717  
 DB 689 NASDNTEFLNPFIDRKTNNPSCNTDLNRLVLLDAGFTNELVQNTWSKQK-NIKGV 748  
 QY 718 KARFVYTDGSTRVYPKEAGENWQENPEYEDSFYKRSLDNDNYVFTAPYFNK-SGPGAY 776  
 DB 749 LAVFAATDGGITRVPFNKAEDWTEPEFNASTYRSRSLDNHGYVFKPPHQDALLRPLEL 808  
 QY 777 ES---GIMYSKAVEIYIOGKLKLPVAVGKIDVNSWIEF-----TKTSIRDP--CAGP- 825  
 DB 809 ENDTVGILYSTAVELSLGRRTLRPAVVGKLDLEAWAEKFKVLASNRTHQDQPKC-GPN 867  
 QY 826 ---VCCKRNSVMDVILDDGGFLMANHDDYTNIGRFFGEIDPSLRLHLVNSIYAF 882  
 DB 868 SHCEMDVENEDLLCVLDDGGFLVLSNQNHQMDQVGRFFSEVDANLMLYNNSFYTR 927  
 QY 883 NKSYDYQSVCEPGAAPKQAGHRSAYVPSIADILHIGWATAAAWSILOQLLSLTFPRL 942  
 DB 928 KESYDQACAPOPPGNLGAPRGVFPVADVADFLNLAWTSAASWSLFOQLLYGLIYHSW 987  
 QY 943 LEAVEMEDDDFTASLSKQSCITEQTYFFDNDSKSGVLTDCGNCSTRIFHEVKLMTNLI 1002  
 DB 988 FQADPAEAEG-SPETRESSCVMKQTQYFGSVNAYNAIIDCGNCSTRIFHEVKLMTNLI 1046  
 QY 1003 FIVESKGTGCTCDRLRLIOAEQ--TSDGPDPCDMVQKPYRKGPDVCFNNALEDYDCG 1060  
 DB 1047 FVVAEKLPCSQCAGRLQLQKETHCPADGPEQCELVOPRTRRGPHICFDYNATEDSDCG 1106  
  
 RESULT 11  
 Q920H6 PRELIMINARY; PRT; 1084 AA.  
 AC Q920H6;  
 DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE Voltage-dependent calcium channel alpha-2-delta-2 mutant subunit 2.  
 GN CACNA2D2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=TKDU;  
 RX MEDLINE=21380284; PubMed=11487633;  
 RA Barclay J., Balaguero N., Mione M., Ackerman S.L., Letts V.A.,  
 RA Brodbeck J., Cantl C., Meir A., Page K.M., Kusumi K., Perez-Reyes E.,  
 RA Lander E.S., Frankel W.N., Gardiner R.M., Dolphin A.C., Rees M.;  
 RT "Ducky mouse phenotype of epilepsy and ataxia is associated with  
 RT mutations in the CACNA2D2 gene and decreased calcium channel current  
 RT in cerebellar Purkinje cells.";  
 RL J. Neurosci. 21:6095-6104(2001).



QY 659 KISDNTEFLNFEIDRTPNPNPSCNTDLINRVLLDAGFTNELVQYWSKQK-NIKGV 717  
Db 689 NASDNTEFLNFEIDRTPNPNPSCNTDLINRVLLDAGFTNELVQYWSKQK-NIKGV 717  
QY 718 KARFVTDGGITRYYPKAEENQWENPEYEDSYKSLDNDYVFTAPYFNK-SGPAY 776  
Db 749 LAVFAATDGGITRYYPKAEENQWENPEYEDSYKSLDNDYVFTAPYFNK-SGPAY 776  
QY 777 ES---GIMVSKAVEIYIQGLKLPVAVGIIKIDVNSWLENF-----TKTSIRDP--CAGP- 825  
Db 809 ENDVGTILVSTAVELSLGRRTLRPAVGVKIDLEAWAEKFKVLASNRTHQDQPKC-GPN 867  
QY 826 ---VCDCKRNSDVMDCVILDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNIYSYAF 880  
Db 868 SHCEMDCVNNEDLLCVLDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNIYSYAF 880  
QY 883 NKSYDYQSVCEPAAKPGQAGHRSAYVPSIADILHIGWATAAASLQOFLSLTFPRL 942  
Db 928 KESYDQAACAPQPPGNLGAAPRGVFTVADFLNLAWTSAANLQOFLSLTFPRL 942  
QY 943 LEAVEMEDDDFTASLSKOSCIETQYTFDNDKSGFSGVLDGCGNCSRIHFHVEKLMNTNLI 1002  
Db 988 FOADPAEAEAG-SPETRESSCVMKQYIFGVSNAYNALIDCGNCSRLFHQAQRLTNLL 1046  
QY 1003 FIMVESKGTCPCTRLLIQAEQTSDDGPDQDMYQPRYKRGPDVCFDNNALDYEYTDG 1060  
Db 1047 FVVAEKPLCSQCEAGRLLOKQETHCPADGPEOCELVQPRYRGRPHICFDYNATEDSDG 1104

RESULT 9  
Q9EQG2 PRELIMINARY; PRT; 1156 AA.  
ID Q9EQG2  
AC Q9EQG2  
DT 01-MAR-2001 (T-EMBLrel. 16, Created)  
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)  
DE Voltage-dependent calcium channel subunit genes.  
GN CACNA2D2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=TKDU;  
RX MEDLINE=21015416; PubMed=11130987;  
RA Barclay J., Rees M.;  
RT "Genomic organization of the mouse and human alpha2delta2 voltage-  
RT dependent calcium channel subunit genes.";  
RL Mamm. Genome 11:1142-1144(2000).  
DR MGD; AF247139; AAG47846.1;  
DR MGD; MGI:1929813; CACNA2D2.  
DR InterPro; IPR004010; Cache.  
DR InterPro; IPR002035; VWF\_A.  
DR Pfam; PF02743; Cache; 1.  
DR SMART; SM00327; VWA; 1.  
DR PROSITE; PS0234; VWA; 1.  
SQ SEQUENCE 1156 AA; 130611 MW; A732545A2B302A52 CRC64;

Query Match 53.8%; Score 3038.5; DB 11; Length 1156;  
Best Local Similarity 54.3%; Pred. No. 2.2e-177;  
Matches 588; Conservative 178; Mismatches 279; Indels 37; Gaps 16;

QY 6 LIALTLTQSLILGIP-SQOEPFPAVTKSWDKMQEDLVTLAKTASGVNQLVDIYKY 64  
Db 45 LILLPLLLPLLTAPGASVFPQOHTQHWARLEIDGVNRIFGVQQLREIYKDN 104  
QY 65 QDLVTEPNPNAQLVEIARDIEKLLNSRKSALVRLALEAEKVOAAHOREDFASNEVY 124  
Db 105 RNLFVEQENPQKLVKGVAGDIESLDRKQALKRLADAENFQKAHWQNDIKEEDIMY 164  
QY 125 YNAKODL---DPEKNDSEPGSQ--RIKPVFIDANFGRQISYQHAHVHIPTDIYEGSTIV 179

Db 165 YDAKADAEELDDPESEDMERGSKTSALRLDFIEDPNFKKNVYSYAVQIPTDIYKGSTVI 224  
QY 180 LNELNWTSDALDEVFKKKNREEDPSLLMQVFGSATGLARYYPASPVWDSNTPKIDLYDVR 239  
Db 225 LNELNWTALENVFENRRQDPTLLMQVFGSATGLARYYPASPVWDSNTPKIDLYDVR 280  
QY 240 RRPWYIOGAASPKDMLLVDVSGVSGGLTKLIRTSVSEMLETLSDDDFVNVASNSNAQ 299  
Db 281 RRPWYIOGAASPKDMLLVDVSGVSGGLTKLIRTSVSEMLETLSDDDFVNVASNSNAQ 340  
QY 300 DYSFQHLVQANVRNKKVLKDAVNNTAKGIDYKDKSFAFEQOLLNVNVRANCKIIM 359  
Db 341 PVSCFTHLVQANVRNKKVKEAVQGVAKGTTGYKAGEYAFDQQLQNSNTRANCNMIM 400  
QY 360 LFTDGEERAQAEIPAKYN-KDKKRVVFTFSGOHNYDRGIOWMACENKGYEIPISIGA 418  
Db 401 MFTDGEDRVQDVFKEYNPNRTVFTFSGOHNYDRGIOWMACENKGYEIPISIGA 460  
QY 419 IRINTQEYLDVLRPMVLGADKAKOVQNTVNYLDALGLVITGLPVFNIT--GQENK 476  
Db 461 IRINTQEYLDVLRPMVLGADKAKOVQNTVNYLDALGLVITGLPVFNIT--GQENK 519  
QY 477 TNLKNOLILGVMGVDSLEDKRLTPRETLPNGYFFAIDPNGYVLLHNPQNPXSOE 536  
Db 520 ---KNOLILGVMGIDVALNDIKRLTPRETLPNGYFFAIDPNGYVLLHNPQNPXSOE 576  
QY 537 PVTDLFQDAELNDIKVEIRNKMIDGESGKFTFRLVKSQDERYIDKGNRTYVTPVNGT 596  
Db 577 PVTDLFQDAELNDIKVEIRNKMIDGESGKFTFRLVKSQDERYIDKGNRTYVTPVNGT 636  
QY 597 DYSLALVLTYSFYIKAKIETITQARSKGMKDSLETKLPDNFEESGYFFIAPROYCN 656  
Db 637 NYSGLVLPYSTYVYLOANLRDQILQVLPISKLDFELLPSSFESGHHVFIAPREYCK 696  
QY 657 DLKISDNTEFLNFEIDRTPNPNPSCNTDLINRVLLDAGFTNELVQYWSKQK-NIK 715  
Db 697 DLNASDNSTEFKDFIELMEKVTDPKOCNNFLHNLILDTGITQQLVERVWRDQDLNTY 756  
QY 716 GVKARFVTDGGITRYYPKAEENQWENPEYEDSYKSLDNDYVFTAPYFNK-SGP 774  
Db 757 SLLAVFAATDGGITRYYPKAEENQWENPEYEDSYKSLDNDYVFTAPYFNK-SGP 816  
QY 775 AYES---GIMVSKAVEIYIQGLKLPVAVGIIKIDVNSWLENF-----TKTSIRDP--CAG 824  
Db 817 ELENVTGVLVSTAVELSLGRRTLRPAVGVKIDLEAWAEKFKVLASNRTHQDQPKC-G 875  
QY 825 P---VCDCKRNSDVMDCVILDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNIYSY 880  
Db 876 PSSHCEMDCVNNEDLLCVLDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNIYSY 935  
QY 881 AFNKSVDYQSVCEPAAKPGQAGHRSAYVPSIADILHIGWATAAASLQOFLSLTFP 940  
Db 936 TRKESYDQAACAPQPPGNLGAAPRGVFTVADFLNLAWTSAANLQOFLSLTFP 995  
QY 941 RLLAEVEMEDDDFTASLSKOSCIETQYTFDNDKSGFSGVLDGCGNCSRIHFHVEKLMNTN 1000  
Db 996 SWFQADPAEAEAG-SPETRESSCVMKQYIFGVSNAYNALIDCGNCSRLFHQAQRLTN 1054  
QY 1001 LIFTMVESKGTCPCTRLLIQAEQ--TSDGPDQDMYQPRYKRGPDVCFDNNALDYEYTD 1058  
Db 1055 LFFVVAEKPLCSQCEAGRLLOKQETHCPADGPEOCELVQPRYRGRPHICFDYNATEDSD 1114  
QY 1059 CG 1060  
Db 1115 CG 1116

RESULT 10  
Q9Y268  
ID Q9Y268  
AC Q9Y268;  
DT 01-NOV-1999 (T-EMBLrel. 12, Created)

QY 127 AKDDL---DPEKNDSPGSG--RIKPVFIDDANFGRIQISYQHAHVHPTDIIYEGSTIVLN 181  
Db 164 AKDAELDDPESEDEVERGSKASTLRDIEDPNFKNVISYAAVQIPTDIYKGTIVLN 223  
QY 182 ELNWTGALDEKFKNEEDPSSLQWFGSATGLARYYPASPWNDSRTNPKIDLDYVRRR 241  
Db 224 ELNWTGALDEKFKNEEDPSSLQWFGSATGLARYYPASPWNDSRTNPKIDLDYVRRR 279  
QY 242 PWYIOGAASPKDMLILVDYSGVSGTLKIRTSVSEMLETSLDDDFVNVASFNSAQDV 301  
Db 280 PWYIOGAASPKDMLILVDYSGVSGTLKIRTSVSEMLETSLDDDFVNVASFNSAQDV 339  
QY 302 SCFQHLVQANVRNKKVYLDKAVNNITAKGTDYKKGFSFAFEQOLLNVNVRANCNKIIMLF 361  
Db 340 SCFTHLVQANVRNKKVYLDKAVNNITAKGTDYKKGFSFAFEQOLLNVNVRANCNKIIMLF 399  
QY 362 TDGGEERAQEIFAKYN-KDKKVRVFTSVGOHNYDRGPIOWMACENKGYEIPSGAIR 420  
Db 400 TDGGEERAQEIFAKYN-KDKKVRVFTSVGOHNYDRGPIOWMACENKGYEIPSGAIR 459  
QY 421 INTQYLDLVGRPMVLADKAKOVQNTNYLDALGLVITGLPVFNIT--GQENKTN 478  
Db 460 INTQYLDLVGRPMVLADKAKOVQNTNYLDALGLVITGLPVFNIT--GQENKTN 516  
QY 479 LKNOLILGVMGVDSLEIDKRLTPRETLCPNGYFAIDPNGYVLLHPNLPKPKSQEPV 538  
Db 517 LKNOLILGVMGVDSLEIDKRLTPRETLCPNGYFAIDPNGYVLLHPNLPKPKSQEPV 575  
QY 539 TLDFDLAELENDIKVEIRNKMIDGESSEKTRFRLVKSQDERYIDKGNRTYTPWVTNGTDY 598  
Db 576 TLDFDLAELENDIKVEIRNKMIDGESSEKTRFRLVKSQDERYIDKGNRTYTPWVTNGTDY 635  
QY 599 SLALVLPYTFYIKAKIETIQAKSKGKMDSEYLPKDPNFEESGYTPIAPRDCNDL 658  
Db 636 SLGLVLPYTFYIKAKIETIQAKSKGKMDSEYLPKDPNFEESGYTPIAPRDCNDL 695  
QY 659 KISDNTEFLNFEFIDRTPNPNPSCNTDLINRVLDDAGFTNELVONYSKOK-NIKGV 717  
Db 696 NASDNTEFLNFEFIDRTPNPNPSCNTDLINRVLDDAGFTNELVONYSKOK-NIKGV 755  
QY 718 KARFVTDGGLTRVYKPEAGENQENPETYEDSEYKSLDNNDNVFTAPYFNK-SGPAY 776  
Db 756 LAVFAATDGGITRVYKPEAGENQENPETYEDSEYKSLDNNDNVFTAPYFNK-SGPAY 815  
QY 777 ES---GIMVSKAVEIYIOGKLLKPAVYGIKIDVNSWENF-----TKTSIRDP--CAGP- 825  
Db 816 ENDVIGILVSTAVELSLGRTRLPVAVGVKLDLEAWAEKPKVLASNRTHODQPKC-GPN 874  
QY 826 ---VCDCKRNSDVMDCVLDGGFLLMANHDDYTNQIGRFFGEIDPMSLRHLVNSIVAF 882  
Db 875 SHCEMDCEVNNEDLILVDGGFLVLSNQHNQHWQYGRFFSEYDANLMLALYNNSTYR 934  
QY 883 NKSVDYQSVCPGAAPKOGAGHRSAYVPSIADILHIGWATAAAWSILQOFLSLSTPRL 942  
Db 935 KESVDYQACAPQPPGNGUAPRGVFTVADFLNLAWTSAAWSLFQOULLYLIHWS 994  
QY 943 LEAVEMEDDDFTASLSKSCITEQTYFFDNDKDSFSGVLDCGNCGRIFHVEKLMNTNLI 1002  
Db 995 FQADPARAEG-SPEPRESSCVMKQTYFYFSGVSNASYNALIDCGNCSRLFAHRLTNTNLL 1053  
QY 1003 FIMVESKTCPCDTRLLIQAQGTSDGPPCDMVQKQPRYKRGPDVCFDNNALEDYDCG 1060  
Db 1054 FVVAEKPLCSQCEAGRLQKTHSDGPQCELVQPRYRGRPHCFIDYNATEDTSDCG 1111

RESULT 8

Q9NY48 PRELIMINARY; PRF: 1143 AA.

AC Q9NY48

DT 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)

DE Calcium channel, alpha 2/delta subunit 2.  
GN CACNA2D2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=HEART;  
RA Klugbauer N.;  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=HEART;  
RA Hobom M., Dai S., Marais E., Lacinova L.;  
RT "Neuronal distribution and functional characterization of the calcium  
channel alpha2delta-2 subunit";  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ251367; CAB86192.1; -;  
DR InterPro; IPR004010; Cache.  
DR InterPro; IPR002035; VWF\_A.  
DR Pfam; PF02743; Cache; 1.  
DR SMART; SM00327; VWA; 1.  
DR PROSITE; PS0234; VWF\_A; 1.  
DR PROSITE; PS1143 AA; 129085 MW; 492556C9919A0CE5 CRC64;  
SQ SEQUENCE 1143 AA; 129085 MW; 492556C9919A0CE5 CRC64;  
  
Query Match 53.8%; Score 3038.5; DB 4; Length 1143;  
Best Local Similarity 54.6%; Pred. No. 2.2e-177;  
Matches 589; Conservative 173; Mismatches 275; Indels 41; Gaps 15;

QY 7 LALTILFQSLILGSSQEPFSAVTIKSWDKMQEDLVTLAKTAGVNLQVLDIYKQD 66  
Db 44 LMLLPLLLAPGASVFFQOHTMQRRLSEQVDGVNRIEGVQOQLREIYKDRN 103  
QY 67 LVTPEPNARQLVEIAARDIEKLLSNRKALVLALEAEKVOAAHQWREDFASNEVYTN 126  
Db 104 LFEVOENEPQKLVKAGVAGDIESLLDRKQVQALRAAENFQKARHWDNIKEEDIVYD 163  
QY 127 AKDDL---DPEKNDSPGSG--RIKPVFIDDANFGRIQISYQHAHVHPTDIIYEGSTIVLN 181  
Db 164 AKDAELDDPESEDEVERGSKASTLRDIEDPNFKNVISYAAVQIPTDIYKGTIVLN 223  
QY 182 ELNWTGALDEKFKNEEDPSSLQWFGSATGLARYYPASPWNDSRTNPKIDLDYVRRR 241  
Db 224 ELNWTGALDEKFKNEEDPSSLQWFGSATGLARYYPASPWNDSRTNPKIDLDYVRRR 279  
QY 242 PWYIOGAASPKDMLILVDYSGVSGTLKIRTSVSEMLETSLDDDFVNVASFNSAQDV 301  
Db 280 PWYIOGAASPKDMLILVDYSGVSGTLKIRTSVSEMLETSLDDDFVNVASFNSAQDV 339  
QY 302 SCFQHLVQANVRNKKVYLDKAVNNITAKGTDYKKGFSFAFEQOLLNVNVRANCNKIIMLF 361  
Db 340 SCFTHLVQANVRNKKVYLDKAVNNITAKGTDYKKGFSFAFEQOLLNVNVRANCNKIIMLF 399  
QY 362 TDGGEERAQEIFAKYN-KDKKVRVFTSVGOHNYDRGPIOWMACENKGYEIPSGAIR 420  
Db 400 TDGGEERAQEIFAKYN-KDKKVRVFTSVGOHNYDRGPIOWMACENKGYEIPSGAIR 459  
QY 421 INTQYLDLVGRPMVLADKAKOVQNTNYLDALGLVITGLPVFNIT--GQENKTN 478  
Db 460 INTQYLDLVGRPMVLADKAKOVQNTNYLDALGLVITGLPVFNIT--GQENKTN 516  
QY 479 LKNOLILGVMGVDSLEIDKRLTPRETLCPNGYFAIDPNGYVLLHPNLPKPKSQEPV 538  
Db 517 LKNOLILGVMGVDSLEIDKRLTPRETLCPNGYFAIDPNGYVLLHPNLPKPKSQEPV 575  
QY 539 TLDFDLAELENDIKVEIRNKMIDGESSEKTRFRLVKSQDERYIDKGNRTYTPWVTNGTDY 598  
Db 576 TLDFDLAELENDIKVEIRNKMIDGESSEKTRFRLVKSQDERYIDKGNRTYTPWVTNGTDY 635  
QY 599 SLALVLPYTFYIKAKIETIQAKSKGKMDSEYLPKDPNFEESGYTPIAPRDCNDL 658  
Db 636 SLGLVLPYTFYIKAKIETIQAKSKGKMDSEYLPKDPNFEESGYTPIAPRDCNDL 698

[illegible]

```
ET PROPEP      647 886      BY SIMILARITY.
FT DOMAIN      279 439      VWFA.
FT CARBOHYD     88      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD    577 577      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT BINDING     646      CHONDROITIN 4-SULFATE, CROSS-LINK SITE
                        (BY SIMILARITY).
SQ SEQUENCE     886 AA; 99018 MW; AC0594C6852576B8 CRC64;

Query Match      3.1%; Score 164.5; DB 1; Length 886;
Best Local Similarity 23.2%; Pred. No. 0.03;
Matches 66; Conservative 56; Mismatches 112; Indels 51; Gaps 11;

QY 202 SLLQVFGSATGLARYYPASPDVNSRT-PNKID-----LYDVRRR-PWTIOGA-- 248
Db 208 SALTQSGKKGHSFKPS---LDOQRSCPTDLSLLNGDFTIYDYNRSPGNVQVNG 264
QY 249 -----ASPKMLILVDVSGVSGTLTKLIRTSVSEMLETISDDDFVNVASFNS 296
Db 265 YVHFFAFOGLPVYPKNIVFIDISGSMAGRKIQOTRVALLKILDDMKQDDYLNFLFST 324
QY 297 NAQDVSCFQHLVQANVRKKVLDVANNITAKITDYKKGFSFAFEOLLN----YNVSRA 352
Db 325 GY--TTWRDLSVQATPANLEARTFVRSISDQGMTNINDGLRIRMLTDAREQHTVPER 382
QY 353 NCKNTIMLFTDG---GEERAQEIFNKYDKKVRVFSVG-QHNYERGPQIOMACENK 407
Db 383 STSIIIML-TGDANTGSRPEKIQENVKKAIEGRFPLINLFGNNLNYNFLETMALENH 441
QY 408 GYVYRPSIGAIRINTQBYDLVLRPMVLADGKAKQVQWTVNYLD 452
Db 442 GVARIEDSDANLQOGFYEVANPLL-----TNVEYE 475

RESULT 10
ID POLYESTHER STANDARD; PRT; 1829 AA.
AC Q33845;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE DNA polymerase (nc 2.7.7.7).
GN POL.
OS Thermococcus sp. (strain TV).
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Thermococcus.
OX NCBI_TaxID=110163;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98094267; PubMed=9434178;
RA Niehaus F., Frey B., Antranikian G.
RT "Cloning and characterisation of a thermostable alpha-DNA polymerase
RT from the hyperthermophilic archaeon Thermococcus sp. TV.,"
RL Gene 204:153-158(1997).
CC -I- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + {DNA}(N).
CC -I- PMW: THIS PROTEIN UNDERGOES A PROTEIN SELF SPLICING THAT INVOLVES
CC A POST-TRANSLATIONAL EXCISION OF THE THREE INTERVENING REGION
CC (INTERNS) FOLLOWED BY PEPTIDE LIGATION.
CC -I- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Y13030; CAA73475.1; -.
DR HSSP; P56689; ITGO.
DR InterPro; IPR002064; DNA_pol_B.
DR InterPro; IPR003586; Hedgehog_hintc.
DR InterPro; IPR003587; Hedgehog_hintn.
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DR InterPro; IPR002203; Intein.
DR InterPro; IPR004042; Intein_endonuc.
DR InterPro; IPR004578; pol2.
DR Pfam; PF00136; DNA_pol_B; 4.
DR Pfam; PF03104; DNA_pol_B_exo; 1.
DR PRINTS; PR00379; INTEIN.
DR SMART; SM00305; Hintc; 3.
DR SMART; SM00306; Hintn; 3.
DR SMART; SM00486; POLBC; 1.
DR TIGRFAMs; TIGR00592; pol2; 2.
DR PROSITE; PS00116; DNA_POLYMERASE_B; FALSE_NEG.
DR PROSITE; PS00818; INTEIN_C_TER; 3.
DR PROSITE; PS00819; INTEIN_ENDONUCLEASE; 2.
DR PROSITE; PS00817; INTEIN_N_TER; 3.
KW Transferrase; DNA-directed DNA polymerase; DNA replication;
KW DNA-binding; Hydrolase; Endonuclease; Autocatalytic cleavage;
KW Protein splicing.
FT CHAIN 1 409 DNA POLYMERASE, 1ST PART (POTENTIAL).
FT CHAIN 410 769 INTEIN I.
FT CHAIN 770 855 DNA POLYMERASE, 2ND PART (POTENTIAL).
FT CHAIN 856 1392 INTEIN II.
FT CHAIN 1393 1441 DNA POLYMERASE, 3RD PART (POTENTIAL).
FT CHAIN 1442 1598 INTEIN III.
FT CHAIN 1599 1829 DNA POLYMERASE, 4TH PART (POTENTIAL).
SQ SEQUENCE 1829 AA; 211875 MW; A113A8BC57EB9CB3 CRC64;

Query Match      3.0%; Score 161; DB 1; Length 1829;
Best Local Similarity 20.1%; Pred. No. 0.14;
Matches 172; Conservative 101; Mismatches 301; Indels 282; Gaps 39;

QY 16 SLLIGPSSEPEPS-----AVTIKSV-----DKMQEDLVTLA 48
Db 229 TLLLRDKEHPKIRHMGDSFAVEIKRIHFDLPVVRTINLPYTLAEYEAVALGKT 288
QY 49 KTASGVNQLVDIYEKYQDL-----YVPEPNAQLVEIAARDIEKLLNSRKALVSLALE 103
Db 289 KSKLGAEEITAIWETESMKLAQYSME--DARATVEL-----GREFFPMEAE 334
QY 104 AEKVQAAHWRDEFAS--NEVVY-----NAKDDLDPKNDSEPGSQRIKPVFI----- 150
Db 335 LAKLIGQSYMDVSRSTGNLVVELRVAYERNELAPNKPDEEYRRRLRTYLGKYKE 394
QY 151 EDANFGRLSYQHAHVHIPTD---IYEGSTIV---LNELNWTSALDEVFKKNREEDPSL 203
Db 395 PERGLMENTAYLDFRCH--PADTKVIIVKGGIVNISDKEGDYILGIDG----- 441
QY 204 LMQVFGSATGLARYYPASPDVNSR---TPN-KIDLYDVRRRPWTIOGAASPKDMLILVD 259
Db 442 -WQ---RVKKVWKYHVEGKLININGLKCTPNHKVPVVTENDRQTRI-----RDSLAKSF 491
QY 260 VSGSVGLTKLIRTSVSEMLETISDDDFVNVASFNS----- 297
Db 492 LSGKVAG---KIITTKL-----FEKIAFEKPKPSBEELKGLSGIILAEGTL 537
QY 298 -ADVSCF-----QHLVQANV-RNKKVLKDAV-----NNITAGK--- 329
Db 538 LRADIEYFSSRGKKRISHQYRVEITIGENEKELLRIYIFDKLFGIRPSVKKGDINA 597
QY 330 --ITDYKKGFSFAFEOLLNYSRANCNKIIMLFTDGGEEAQAEIFNKYNKDKKVRVFRF 387
Db 598 LKITTAKKAVLIQIEELLK-NIESLAPAVLRGF-----PERDATVKNIRS 642
QY 388 SV-----GQHYERGPQIOMACENKGY---YYEIPSGAIGRINTQBYDLVLRPMVLADGK 440
Db 643 TIVVTOGTNNKWKIDIVAKLLSDLGIPYSRYEYKYIENGKELTKHILEITGD----- 695
QY 441 AKQVQWTVNYLDALEGLVITGLPVFNITGQFE-----NKTNLKNOLILGVMGVD 491
Db 696 -----GLILFQTLVGFISSEKNEALEKAEVREMNLKNNFYNLSTPE 739
QY 492 VSLIEDIKRLTPRTFCNPGYFAIDPNGVYLLHPNLOPKNPKSQEPVTLDFDLDAELENDI 551
Db 740 VSSEYKGEVYDLTLEGNPYYFA---NG-LTHNSLYPSIIVTHN-VSPDTLIERE----- 789
```

QY 552 KVEIRNMIDGESGEKTEFTLVKSQDERYIDKGNRTYTTWTPVNGTDYSIALVLPYSFY 611  
 Db 790 -----GCKNYDVAPIVG---YKCKDPPG---F 811  
 QY 612 IKAKLETITQARSKKMKDSETLKPDNFEESGY-----FTIAPRDYCNLDKISD 662  
 Db 812 IPSILGELITMREIKKKMK--ATIDPIEKKMLDYRQRAVKLLANSILPNW---LPIIE 866  
 QY 663 NTEFFLNFEFIDRTPNPNPSNADLNIRVLIDAGFTNELVQYWSKOKNIKGVKAREV 722  
 Db 867 NGEVKFKIGEFIDRYMEQOKVRIVDNTVELEVDNIFAFSLNKESKEIKVKAL-- 924  
 QY 723 VTDGGITRVYPKEAGE 738  
 Db 925 -----IRHKYKGEAYE 935

## RESULT 11

ATX1\_PLAFA STANDARD; PRT: 1956 AA.  
 AC 004956;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Probable cation-transporting ATPase 1 (EC 3.6.3.-).  
 OS Plasmodium falciparum.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=5833;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=T9/96;  
 RA MEDLINE=93132070; PubMed=8421054;  
 RX Krishna S., Cowan G., Meade J.C., Wells R.A., Stringer J.R.,  
 RA Robson K.J.;  
 RT "A family of cation ATPase-like molecules from Plasmodium  
 falciparum";  
 RL J. Cell Biol. 120:385-398(1993).  
 CC -|- CATALYTIC ACTIVITY: ATP + H<sub>2</sub>O = ADP + phosphate.  
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -|- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2,  
 CC ATPASES). SUBFAMILY V.  
 CC  
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 CC  
 CC EMBL; X65738; CAA46646.1; -;  
 CC InterPro; IPR001757; ATPase\_E1-E2.  
 CC Pfam; PF00122; E1-E2\_ATPase; 1.  
 CC PROSITE; PS00154; ATPASE\_E1\_E2; 1.  
 KW Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding.  
 FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 36 58 POTENTIAL.  
 FT DOMAIN 59 61 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 62 80 POTENTIAL.  
 FT DOMAIN 81 407 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 408 427 POTENTIAL.  
 FT DOMAIN 428 440 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 441 462 POTENTIAL.  
 FT DOMAIN 463 1818 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 1819 1837 POTENTIAL.  
 FT DOMAIN 1838 1845 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 1846 1863 POTENTIAL.  
 FT DOMAIN 1864 1881 POTENTIAL.  
 FT TRANSMEM 1882 1905 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 1906 1928 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 1929 1952 POTENTIAL.  
 FT DOMAIN 1953 1956 CYTOPLASMIC (POTENTIAL).

FT MOD\_RES 496 496 PHOSPHORYLATION (BY SIMILARITY).  
 FT METAL 1760 1760 MAGNESIUM (BY SIMILARITY).  
 FT METAL 1764 1764 MAGNESIUM (BY SIMILARITY).  
 FT DOMAIN 246 251 POLY-ASN.  
 FT DOMAIN 252 256 POLY-LYS.  
 FT DOMAIN 937 941 POLY-ASN.  
 FT DOMAIN 1344 1347 POLY-LYS.  
 FT DOMAIN 1363 1372 POLY-ASN.  
 FT DOMAIN 1680 1684 POLY-ASN.  
 SQ SEQUENCE 1956 AA; 230285 MW; AE708AAE99009335 CRC64;  
 Query Match 3.0%; Score 159; DB 1; Length 1956;  
 Best Local Similarity 17.1%; Pred. No. 0.2;  
 Matches 179; Conservative 144; Mismatches 359; Indels 366; Gaps 45;  
 QY 58 VDIYEKYODLYTVEPNNAROLVEIARDEIKLLSNR-----SKALVSLALAEAK 106  
 Db 100 INVY-RYNTSYIISSS-----ELVPGDIYEIKNNMTIPCDTIILSGSVTSEHMLTGES 152  
 QY 107 VQAAHOWREDFASNEVYVYNAKDDLDPEKND-----SEPGSQRIKPVFIEDANFGROIS 160  
 Db 153 V-PIHKERLPFEGNAIINKNKYDSNDEKDDYLRITYNNHASTIMKRNHLLIEETLGKKDR 211  
 QY 161 YQHAAVHIPTDIYEGSTIVLNELNW-TSALDEVFKKREEDPSLLMQVFGSATGLARYYP 219  
 Db 212 EYKSNTH-----DLGSMNKLCYINNTYDDVHMKNKMD----- 244  
 QY 220 ASPWVDNSRTPNKIDLYDVRRRPWTIOGA-ASPKDMLILVDVSGVSLTLKLRTSVSE 278  
 Db 245 ---YNNNNNNKKKKINLN---FVKGYINSNDLLY----- 275  
 QY 279 MLETLSDDDFYNVASFNSNAQDVSCFHLVQANVRNKKVLDKADAVNNITAKGIDYKKKGS 338  
 Db 276 -----DDKIGVNIFF--DDVNNMKH--KFNQNNINYNKDINNLL-----EYNNKHR 317  
 QY 339 FAFEOQLNINYSRANCNKKIIMLFTDGGEEAQAETFNKYNDKKVRFVRSVQGHNYERGP 398  
 Db 318 YIYDCLLKKVEAISQKNKIY-----SNEDINKY----- 346  
 QY 399 IQWACENKGVYVEIPSGAIGAIRNTOEYLDVLRPMVLG-----DKAQOV 444  
 Db 347 ----MLYGGTVLSYLNINKIYNNKKEENRIILG-VIKTGFITTKGIVNNILYHKKKL 401  
 QY 445 QWTVNYLDALGLVITGLPVPFNITGOFENKTLKNOLILG-----V 487  
 Db 402 NLINDSYKFLII-LIIVYALFSVILLIYTLNNEYTNHIIKCLDIITDAIPALPTLT 460  
 QY 488 MGVDVSLIEDIKRLTPRFTLCPNGYFA-----IDPNGYVLLHPNLQ-----PKNPKSQ 535  
 Db 461 VGISIAISRLKKKFSISCLCPHKINIAQINTMVFDTKG-TLTENNLFQIGIITQNKKN 519  
 QY 536 EPVTLDFDLDALENDIKVEIRNKMIDGESGKTFRTLVKSODERYIDKGNRTYTTWTPVNG 595  
 Db 520 NWLS-DFTHIK-----EMWTESIHSKDDNNIINKN----- 549  
 QY 596 TDSIALVLPYSFYIKAKLEETITQARSKKGMKD-----SETLKPDNFEESG 645  
 Db 550 -----SIISEYIKNKMLNLTSSK-KKSTIKERSNPLVQTIKSCLLKQHYIREKK 599  
 QY 646 YTFAPRDYCNLDKISDNN-TEFLIN-----FNEF-IDRKTNNPNSCNADLNIRVLID 696  
 Db 600 KEYVTNNTYCNLDHINDSTCSSYLLNSETKDAYCEYNIIDH-----LCD---INKNMD 650  
 QY 697 AGFTNELVQYWSKOKNIKGVKARFVVDGGITRVYKPEAGENQENPETEYDSFYKRS 756  
 Db 651 INSKNELMGKYSKNELMGKTKNELM-----GKYSKNEL 684  
 QY 757 DNDNYVFTAPYFNKSGPGAYESGINVSKAVEIYIQGLKLPVAVG-----IKIDVNSWI 810  
 Db 685 -----MGKYSKNELMGKYSKNELMGKYSKNELMGKYSKNELMGKYSKNELMGKYSKNEL 737  
 QY 811 ENFTKTSTRD-PCAGPVCDCKRNSDVMDCV-----ILDDGGFLIMANHDDTYNTQIGRE--- 862

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Db 738 MNCNDNYNDYPCD---YNCNNDYHREYHNINKNSFNIPPEKNKSYNNISEHIKI 794
QY 863 -----FGEIDPSLMRLVNSVYAF-----NKSVDYQ 889
Db 795 NYPLLEALACCHTSLKVNKIMGVLEILMFENFCDMLINNNSFIITKEKKKNCSDYFQ 854
QY 890 SVCEPAAKQAGHRSVYVADLIQGWATAAANSILQOFLSLTFPPLLEAVEME 949
Db 855 KI---DCKNIGANDRCHLN---NLVSNILKRF-----884
QY 950 DDFTASLSKQSCITBQTQYFFDNDSKS 977
Db 885 --EFQRLQMSVYKST-YGNNDNN 909

RESULT 12
YFBK_ECOLI
ID YFBK_ECOLI STANDARD; PRT; 575 AA.
AC P76481.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein yfbk.
GN YFBK OR B2270.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OC NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
CC -!- SIMILARITY: TO STNECHOCYSTIS PCC 6803 SLL0103.
CC -!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
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CC -----
DR EMBL; AE000317; AAC75330.1; -
DR EcoGene; EGI4095; yfbk.
DR InterPro; IPR002035; VWFA_A.
DR Pfam; PF00092; vwa; 1.
DR SMART; SM00327; VWFA; 1.
DR PROSITE; PS50234; VWFA; 1.
KW Hypothetical protein; Complete proteome.
FT DOMAIN 216 394 VWFA.
SQ SEQUENCE 575 AA; 63634 MW; 7BB6A1A77A2BE111 CRC64;

Query Match 2.9%; Score 157.5; DB 1; Length 575;
Best Local Similarity 21.6%; Pred. No. 0.042;
Matches 111; Conservative 93; Mismatches 206; Indels 105; Gaps 25;

QY 71 EPNARQLVEIARDEIKLLSNRSKALVSLALEAEKVQAAHQWRDFASNEVYVYNAKDD 130
Db 22 QPENKESQOQFSTPTEQVQVLAQAQAIK---EAEQSAAA---AKALAQEQVQYSDRQA 75
QY 131 LDPEKND-----SEPGSORIKPVFIEDANFGQISYQHA---VHIPTDI 172
Db 76 LQGRLOEAPFAAKAKATHANPCTARYQF---DNPVKVQVQVQVQVQVQVQVQVQV 132
QY 173 YEGSTIVLNE-----LNWTSALDEVFKNREEDPSLLQVFGSATGLARYY 218

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Db 133 YANVERFLNOLLPPPPAVRVEEIVNYPFSDWDI---KDKQSIPASKPIPFAMRYELA--- 187
QY 219 PASPVWDSNRTPNKIDLYDVRRRPWYIQGAASPKDMLILVDSGS-VSGUTLKLRTSVS 277
Db 188 PA-PW-NEQRTLLKVDITLAKDRKSEELPAS-----NLVFLDITSGSMISDRRLPLIQSSLK 241
QY 278 EMLETSLDDDDFVNVSFNSNAQDVSCEQHLVQAVNRNKKVLDKAVNNITAKGITDYKKGF 337
Db 242 LLVKELREQDNIAIVTVAGDSRIA-----LPSTSGSKAEINAAIDSLDAEGSTNGAGL 296
QY 338 SFAPEQLLNTNVSRAKNCNKIIMLTGD-----GEERAQEIFNKNKDKKVRVRFESVGQ 391
Db 297 ELAYQQAATK-GFIKGGINR-ILLATDGFNVGDDPKASIESMVKKQKQESGVTISTFGVN 354
QY 392 HNYERGPIONMACENKGYEYIPEISGAIRINTQBYLDVLRGPMVL--AGDKAKQVQ---- 445
Db 355 SNYNEAMMVRIDVGNVGNYSYIDTLS-----EAKVLNSENMRQLITVAKDVKAQIEFNP 410
QY 446 WTNVYLDALGLVITGTLPVFNITGOFENKTNLKNQILGVMGVD-VSLEDI---KRLT 501
Db 411 WVTET---RQIG-----YE-----KKQLRVEHFNNNDVNDAGDIGAGKHIT 447
QY 502 PRFTLCPNGYFAIDPNGYVLLHPNLQPKNPKSOE 536
Db 448 LFLFELTNGQKASIDKLRYA--PDNKLAKSDKTKE 480

RESULT 13
ITH2_HUMAN
ID ITH2_HUMAN STANDARD; PRT; 946 AA.
AC P19823; Q15484; Q14659;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy
DE chain H2) (Inter-alpha-trypsin inhibitor complex component II)
DE (Serum-derived hyaluronan-associated protein) (SHAP).
DE ITIH2 OR IGHEP2.
GN Homo sapiens (Human).
OS Homo sapiens; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=88152337; PubMed=2450046;
RA Gebhard W., Schreitmüller T., Hochstrasser K., Wachter E.;
RT "Complementary DNA and derived amino acid sequence of the precursor
RT of one of the three protein components of the inter-alpha-trypsin
RT inhibitor complex.";
RL FEBS Lett. 229:63-67(1988).
RN [2]
RP SEQUENCE OF 384-865 FROM N.A.
RX MEDLINE=88068576; PubMed=2446322;
RA Salier J.P., Diarra-Mehrpour M., Sesboue R., Bourguignon J.,
RA Benarous R., Okubo I., Kurachi S., Kurachi K., Martin J.P.;
RT "Isolation and characterization of cDNAs encoding the heavy chain of
RT human inter-alpha-trypsin inhibitor (I alpha II): unambiguous
RT evidence for multipolypeptide chain structure of I alpha II.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:8272-8276(1987).
RN [3]
RP SEQUENCE OF 384-766 FROM N.A.
RX MEDLINE=89076497; PubMed=2462430;
RA Salier J.P., Diarra-Mehrpour M., Sesboue R., Bourguignon J.,
RA Martin J.P.;
RT "Human inter-alpha-trypsin inhibitor. Isolation and characterization
RT of heavy (H) chain cDNA clones coding for a 383 amino-acid sequence
RT of the H chain.";
RL Biol. Chem. Hoppe-Seyler 369:15-18(1988).
RN [4]
RP PARTIAL SEQUENCE FROM N.A.
RX TISSUE=Liver;
RX MEDLINE=88024442; PubMed=3663330;
RA Schreitmüller T., Hochstrasser K., Resinger P.W.M., Wachter E.,

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RA Gebhard W.;  
RT "cDNA cloning of human inter-alpha-trypsin inhibitor discloses three  
RL different proteins.";  
RL Biol. Chem. Hoppe-Seyler 368:963-970(1987).  
RN [5]  
RP SEQUENCE OF 55-74; 116-127; 224-246; 295-307 AND 365-385.  
RX MEDLINE-93380192; PubMed-2476436;  
RA Englund J.J., Thøgersen I.B., Pizzo S.V., Salvesen G.;  
RT "Analysis of inter-alpha-trypsin inhibitor and a novel trypsin  
RL inhibitor, pre-alpha-trypsin inhibitor, from human plasma.  
RL Polypeptide chain stoichiometry and assembly by glycan.";  
RL J. Biol. Chem. 264:15975-15981(1989).  
RN [6]  
RP SEQUENCE OF 55-64.  
RX TISSUE-Plasma;  
RA MEDLINE-93039735; PubMed-1384548;  
RA Malki N., Balduyck M., Maes P., Capon C., Mizon C., Han K.K.,  
RA Tartar A., Fournet B., Mizon J.;  
RT "The heavy chains of human plasma inter-alpha-trypsin inhibitor: their  
RL isolation, their identification by electrophoresis and partial  
RL sequencing. Differential reactivity with concanavalin A.";  
RL Biol. Chem. Hoppe-Seyler 373:1009-1018(1992).  
RN [7]  
RP SEQUENCE OF 55-64 AND 681-702, CROSS-LINK STRUCTURE, AND  
RP CARBOHYDRATE-LINKAGE SITES T-691.  
RX MEDLINE-9332026; PubMed-7682553;  
RA Englund J.J., Salvesen G., Thøgersen I.B., Valnickova Z.,  
RA Pizzo S.V., Hefta S.A.;  
RT "Presence of the protein-glycosaminoglycan-protein covalent cross-link  
RL in the inter-alpha-inhibitor-related proteinase inhibitor heavy chain  
RL 2/bikunin.";  
RL J. Biol. Chem. 268:8711-8716(1993).  
RN [8]  
RP SEQUENCE OF 67-101, AND HYALURONAN BINDING.  
RX TISSUE-Serum;  
RA MEDLINE-94075371; PubMed-7504674;  
RA Huang L., Yoneda M., Kimata K.;  
RT "A serum-derived hyaluronan-associated protein (SHAP) is the heavy  
RL chain of the inter alpha-trypsin inhibitor.";  
RL J. Biol. Chem. 268:26725-26730(1993).  
RN [9]  
RP SEQUENCE OF 699-702, AND COVALENT LINKAGE WITH CHONDROITIN SULFATE.  
RX TISSUE-Plasma;  
RA MEDLINE-94229087; PubMed-7513643;  
RA Morelle W., Capon C., Balduyck M., Sautiere P., Kouach M.,  
RA Michalski C., Fournet B., Mizon J.;  
RT "Chondroitin sulphate covalently cross-links the three polypeptide  
RL chains of inter-alpha-trypsin inhibitor.";  
RL Eur. J. Biochem. 221:881-888(1994).  
RN [10]  
RP CARBOHYDRATE-LINKAGE SITES, AND MASS SPECTROMETRY.  
RX MEDLINE-98343966; PubMed-9677337;  
RA Flahaut C., Capon C., Balduyck M., Ricart G., Sautiere P., Mizon J.;  
RT "Glycosylation pattern of human inter-alpha-inhibitor heavy chains.";  
RL Biochem. J. 333:749-756(1998).  
RN [11]  
RP CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.  
RX MEDLINE-98087700; PubMed-9425062;  
RA Olsen E.H.N., Rahbek-Nielsen H., Thøgersen I.B., Roepstorff P.,  
RA Englund J.J.;  
RT "Posttranslational modifications of human inter-alpha-inhibitor:  
RL identification of glycans and disulfide bridges in heavy chains 1 and  
RL 2.";  
RL Biochemistry 37:408-416(1998).  
CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SRUM OR AS A  
CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,  
CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE  
CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE  
CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES.  
CC -1- SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM  
CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,  
CC BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2  
CC AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND

CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.  
CC -1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN  
CC 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE.  
CC -1- MASS SPECTROMETRY: MW-76508; METHOD-MALDI; RANGE-55-702.  
CC -1- SIMILARITY: BELONGS TO THE ITH FAMILY.  
CC -1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: X071173; CAA30160.1; ALT\_SEQ.  
CC EMBL: M18193; AAA60558.1;  
CC EMBL: M33033; AAAS9195.1;  
CC PIR: S00346; ITHU2.  
CC PIR: B34245; B34245.  
CC GlycoSuiteDB: P19823;  
CC Genew: HGNC:6167; ITH2.  
CC MIM: 146640;  
CC InterPro: IPR002035; VWFA.  
CC Pfam: PF00092; vwa; 1.  
CC SMART: SM00327; VWFA; 1.  
CC PROSITE: P50234; VWFA; 1.  
CC Serine protease inhibitor; Repeat; Signal; Multigene family;  
CC Glycoprotein. 1 18 POTENTIAL.  
CC SIGNAL 19 54 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN  
CC CHAIN 55 702 H2.  
CC  
CC PROPEP 703 946 VWFA.  
CC DOMAIN 308 468  
CC DISULFID 261 264  
CC DISULFID 650 651  
CC CARBOHYD 118 118  
CC CARBOHYD 666 666 N-LINKED (GLCNAC. . .) (COMPLEX).  
CC CARBOHYD 671 671 /FTID-CAR\_000140.  
CC CARBOHYD 673 673 O-LINKED (GALNAC. . .) (PARTIAL).  
CC CARBOHYD 675 675 /FTID-CAR\_000214.  
CC CARBOHYD 691 691 O-LINKED (GLCNAC. . .).  
CC CARBOHYD 691 691 /FTID-CAR\_000215.  
CC CARBOHYD 691 691 O-LINKED (GALNAC. . .).  
CC CARBOHYD 691 691 /FTID-CAR\_000216.  
CC CARBOHYD 691 691 /FTID-CAR\_000217.  
CC MOD\_RES 282 282 CARBOXYLATION.  
CC MOD\_RES 283 283  
CC BINDING 702 702 CHONDROITIN 4-SULFATE, CROSS-LINK SITE.  
CC CONFLICT 374 374 K -> L (IN REF. 5).  
CC CONFLICT 674 674 P -> A (IN REF. 2 AND 3).  
CC CONFLICT 705 705 F -> S (IN REF. 2 AND 3).  
CC CONFLICT 729 729 N -> D (IN REF. 2 AND 3).  
CC CONFLICT 731 731 V -> A (IN REF. 2 AND 3).  
CC SEQUENCE 946 AA; 106436 MW; 1478CF3E8F3BA776 CRC64;  
Query Match 2.9%; Score 154.5; DB 1; Length 946;  
Best Local Similarity 19.9%; Pred. No. 0.13;  
Matches 133; Conservative 106; Mismatches 259; Indels 171; Gaps 29;  
QY 33 IKSVDKMOEDLVLTAKTASGVNQLVDIYKQDLYTVEPNNAQLVIEIARDIEKLISN 92  
DB 26 LSEFVD--YEDLVEL---APGKFQFLVAENRRYQSLPGSEEMEEVDQVTLTKYKQST 80  
QY 93 RSKALVSLALEAEKVQAAHOMRE-----DFASN-----EV 122  
DB 81 ITRSMATMIOSKVVNNSPQPNVVDVQIIPKGFISNFTVDGKTRSSIKETVGRA 140  
QY 123 VYNAK-----DDLDPKNDSE-----PGSQRTKPVFIEDANFGROISQVH---- 163  
DB 141 LYAQAARAKGKTAGLVRRSSALDMPNFRTEVNVLPKAGQFELHYQFVKRWKLGSEHYRIYL 200





138	KTROGNNWYKTSINPSVIITG---- <pre>PRENIIDPETSTFKLTNNNTFAAQBGFGALSIIS</pre>	192
158	-----QISYQHAHVHTPTDIYEGS----- <pre>TIVLNELNWTSALDEVFK---KNRE</pre>	198
193	ISPREMLTYSNAT-----NDVGGRFSKFCMDPTLILMHELN----- <pre>HAMHNLYGTAIPNDQ</pre>	246
199	EDPSLQWQVGSATGLARYYP----- <pre>ASPWDNSRTPKNKIDLYDVRRRPWTIQGAASPKD</pre>	253
247	TISSVTSNIFYSQYNNVKLEYAEIYAFGGPTID-- <pre>LIPKSARKYFEKALDYIYRSIAKRLN</pre>	304
254	MLILVDVSG-----SVSLGTLTKLR----- <pre>TSVSEMLETISDDDFVNVASFNSNAQDVSCF</pre>	304
305	SITTANPSSFNKYIGYKOKLRKYFVYVESSEGV-- <pre>TJNRNKFEVL---YNELTQIFTEF</pre>	360
305	QHLVQANVRNKV--LKDAVNNTAK----- <pre>GIPDYKKGFSFAFEQL---LNNYYSR----</pre>	351
361	NYAKIYNVQNRKIYLSNVYTPVTANILDDNVYDIQNGENI <pre>PKSNLNVLFMGNLRSNPAL</pre>	420
352	--ANCHNKIIMLFT----- <pre>DGGEERAQEIFNK-----YNKD-----</pre>	386
421	RKVNPENMLYLFTKFCHKAIDG----- <pre>RSLYNKTLDCRELLVKNKTDLPFGIDSDVKTI</pre>	475
387	FSVGQHNHYBRGPTQWMACENKGYEIPSGAIGARI-- <pre>NTOEY--LDVL-----</pre>	430
476	FLRKDINEETEYV----- <pre>YYPDNVSDQVILSKNTSEHQJLDLLYPSIDSESEILP</pre>	526
431	GRPMVLAGDKAKOVQWTN-- <pre>VYLDALDELGLVITGTLVPENITGQPENKTN-----</pre>	478
527	GENQFYDNTQNVYLSYYILESOKL----- <pre>SDNVEDFTFRSIEEALDNSAKVYTYFP</pre>	582
479	-LKNQLILGYMG----- <pre>VDSLESDIKRLTPRTLCPNGYFTAIDPNQYVLLHHPNLOPK</pre>	530
583	TLANKVNAGYOGGGLFMWANDVVEDFTNILRKDTLDKISDVSALIP----- <pre>YIGPALNIS</pre>	638
531	NPKSQEPVTLDF----- <pre>LDLAELENDI-----KVEIRNMKIDGESGETFRTL</pre>	572
639	NSVRGRGTFEAFVGTGVTILLEAFPEFTIPALGAFVIYSKVQERNEII----- <pre>KTIDNC</pre>	692
573	VKSODERYIDKGNRTYTW----- <pre>TPVNGTDYSLALVPTYSFYIYKAKLEETITQ</pre>	622
693	LEQRIKRWKD----- <pre>SYMGMGTWLSRIITQFNNISYQMYDSL--NYQAGAKAKID-----</pre>	742
623	ARSKKKKKMOSETLKP--DNFESGYTFIAPROYCNDKLKISDNNTFELNFPNEFI----- <pre>YNAEVESE</pre>	894
743	LEYKKGSGSOKENIKSOVENLKNS----- <pre>LDVKIS-----BAMNNIKFIRECSV</pre>	787
676	----- <pre>DRKTPNPNFCNADLINRVLLDA-----</pre>	697
788	TYLPKNMLPKVIDELNEFDRT----- <pre>KAKLIN--LIIDSHNILLVGEVDKLLKAKVNNSF</pre>	839
698	-----GFTN----- <pre>ELVQYVW-----SKOKNIKGVKAREPVVTDGGITRYVPKEAGE</pre>	738
840	QNTIPNIFSYTNNLSLLKDIINEYFNINISDKILSLQNRKNTLVDTSG----- <pre>YNAEVESE</pre>	894
739	--NMQENPTEYDSFYKRSLDNDNVYTABYFNKSGPGAYESIMYSKAVEIYIOGKLK <pre>796</pre>	
895	EGDVQLNP----- <pre>IP--PFDPKLAGSSGEDRGKVLVTQENENIYVNSMYE</pre>	935
797	PAVGIKIDVNSWIENFTKTSIRDPACPVCDCKRNSDVMDCVILDDGGFLMANHD---- <pre>853</pre>	
936	SFSISFWIRIIRKNSVNLPGYTIID----- <pre>SVKNNSGWSIGIISNLFVFTLKQNEDESG</pre>	988
854	-----DYTNQIGR----- <pre>FFGEIDPSLMRHLVNIISVYAFNKSVDYQSVCE</pre>	893
998	STNRSYQJLSNADGCKWKEFFVTYVNNMNG----- <pre>NMKIYINGKLIDTJKVKL1035</pre>	

RESULT 15

RESULT 15		
Y103_SYNY3	Y103_SYNY3	Y103_SYNY3
ID	Y103_SYNY3	STANDARD;
AC	AC 05874;	
DT	01-NOV-1997	(Rel. 35, Created)
DT	01-NOV-1997	(Rel. 35, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)  
Hypothetical protein sl10103.  
SL10103.  
OS Synechocystis sp. (strain PCC 6803).  
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.  
NCBI\_Taxid=1148;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=96127529; PubMed=8590279;  
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,  
RA Sugihara M., Tabata S.,  
RT "Sequence analysis of the genome of the unicellular cyanobacterium  
RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 MD  
RT region from map positions 64% to 92% of the genome.";  
RL DNA Res. 2:153-166(1995).  
CC -!- SIMILARITY: TO E.COLI YEFBK.  
CC -!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.  
-----  
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Search completed: February 10, 2003, 14:19:39  
Job time : 15.3394 secs



GenCore version 5.1.1.3  
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OM protein - protein search, using sw model

Run on: February 10, 2003, 14:13:54 ; Search time 19.3759 seconds  
(without alignments)  
5050.861 Million cell updates/sec

Title: US-10-090-827-13

Perfect score: 5346

Sequence: 1 MAAGCLLALTTLFQSLIG.....TNLIIFVESKGTCPDTRL 1018

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_73.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5346	100.0	1091	2 JH0565	calcium channel al
2	5145	96.2	1091	2 A44147	calcium channel pr
3	5132.5	96.0	1106	1 CHRBA2	calcium channel al
4	1085	20.3	1091	2 T30256	CS0C3.11 protein -
5	607	11.4	734	2 S44617	probable calcium c
6	569.5	10.7	1148	2 T18770	hypothetical prote
7	198	3.7	1450	2 C96880	inter-alpha-trypsi
8	194.5	3.6	886	2 S54355	inter-alpha-trypsi
9	185	3.5	885	2 S30350	uncharacterized pr
10	175.5	3.3	1819	2 D97033	inter-alpha-trypsi
11	164.5	3.1	889	2 J05576	variant-specific s
12	161	3.0	2706	2 T28155	p-type cation tran
13	159	3.0	1984	2 A44396	hypothetical prote
14	157.5	2.9	575	2 D64998	lipoprotein [impor
15	156.5	2.9	918	2 E90542	membrane associate
16	155.5	2.9	680	2 A97331	RAD2 endonuclease
17	155	2.9	1516	2 E71619	cytotoxin L - C105
18	155	2.9	2364	2 I40884	inter-alpha-trypsi
19	154.5	2.9	946	1 IVH02	fibrinogen-binding
20	154.5	2.9	1315	2 T28679	inter-alpha-inhibi
21	153	2.9	932	2 J05953	botulinum neurotox
22	152	2.8	1291	2 S46431	botulinum neurotox
23	152	2.8	1291	2 A49777	hypothetical prote
24	151.5	2.8	420	2 S76691	hypothetical prote
25	151.5	2.8	1426	2 A99580	inter-alpha-trypsi
26	150.5	2.8	921	2 J04625	hypothetical prote
27	150.5	2.8	1385	2 D89824	hypothetical prote
28	150	2.8	654	2 A69656	ATP-binding protei
29	150	2.8	1027	2 B90527	

#### ALIGNMENTS

RESULT 1

JH0565

calcium channel alpha-2b chain precursor - human

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 20-Aug-1999

C:Accession: JH0565

R:Williams, M.E.; Feldman, D.H.; McCue, A.F.; Brenner, R.; Velicelebi, G.; Ellis, S.B

Neuron 8, 71-84, 1992

A:Title: Structure and functional expression of alpha1, alpha2, and beta subunits of

A:Reference number: JH0564; MUID:92110010; PMID:1309651

A:Accession: JH0565

A:Molecule type: mRNA

A:Residues: 1-1091 <WIL>

A:Cross-references: GB:M76559; NID:gl79761; PIDN:AAA51903.1; PID:gl79762

A:Experimental source: basal ganglia

A:Note: Several conflicts are found between GenBank submission, authors' translation and is derived by analysis of the total score distribution.

C:Comment: This protein is a subunit of the voltage dependent calcium channel.

C:Superfamily: calcium channel alpha-2 chain

C:Keywords: glycoprotein; phosphoprotein

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-1067/Product: calcium channel alpha-2b chain #status predicted <CAL>

F:32,268,326,539,635,1087/Binding site: phosphate (Thr) (covalent) (by protein kinase

F:91,142,320,625,817/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #

F:92,136,184,324,348,468,475,585,594,663,682,769,812,876,883,973,986/Binding site: ca

F:501/Binding site: phosphate (Thr) (covalent) #status predicted

F:833/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status pre

Query Match 100.0%; Score 5346; DB 2; Length 1091;

Best Local Similarity 100.0%; Pred. No. 1.7e-313;

Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAAGCLLALTTLFQSLIGPSSEPPPSAVTTSWYDKMQEDLVTLAKTASGVNQLVDI 60

Db 1 MAAGCLLALTTLFQSLIGPSSEPPPSAVTTSWYDKMQEDLVTLAKTASGVNQLVDI 60

Qy 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVOAAHQRDFASN 120

Db 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVOAAHQRDFASN 120

Qy 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFTEDANFGRIQISYQHAHVHPTDIYEGSTIVL 180

Db 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFTEDANFGRIQISYQHAHVHPTDIYEGSTIVL 180

Qy 181 NELNWTLSALDEVFVKNEEDPSLLQVFGSATGLIARYYPASPWVDSNRTPNKIDLYDVR 240

Db 181 NELNWTLSALDEVFVKNEEDPSLLQVFGSATGLIARYYPASPWVDSNRTPNKIDLYDVR 240

Qy 241 RPWTIOGAASPKDMLILVDVSGSVGLTLKLRITSVSEMLETISDDDFVAVFNSNAQD 300

Db 241 RPWTIOGAASPKDMLILVDVSGSVGLTLKLRITSVSEMLETISDDDFVAVFNSNAQD 300

Qy 301 VSCFQHLVQAVNRKVKLVKDAVNNITAKGITDYKKGSFAFEQLLNYSRANCKIIML 360

Db 301 VSCFQHLVQAVNRKVKLVKDAVNNITAKGITDYKKGSFAFEQLLNYSRANCKIIML 360

Qy 360 VSCFQHLVQAVNRKVKLVKDAVNNITAKGITDYKKGSFAFEQLLNYSRANCKIIML 360

Db 360 VSCFQHLVQAVNRKVKLVKDAVNNITAKGITDYKKGSFAFEQLLNYSRANCKIIML 360

Qy 360 VSCFQHLVQAVNRKVKLVKDAVNNITAKGITDYKKGSFAFEQLLNYSRANCKIIML 360

Db 360 VSCFQHLVQAVNRKVKLVKDAVNNITAKGITDYKKGSFAFEQLLNYSRANCKIIML 360

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Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNNVSRANCKIIML 360
QY 361 FTDGGEERAQEIIFNKYNKDKKVRFRFSVGOHNYERGPQIOWMACENKGYIYEIPSGAIR 420
Db 361 FTDGGEERAQEIIFNKYNKDKKVRFRFSVGOHNYERGPQIOWMACENKGYIYEIPSGAIR 420
QY 421 INTQEYLDVLGRPMVLAGDKAKQVQWNTNYLDALGLVITGTLVPFNITGQFENKTNLK 480
Db 421 INTQEYLDVLGRPMVLAGDKAKQVQWNTNYLDALGLVITGTLVPFNITGQFENKTNLK 480
QY 481 NQLILGVMGVDVSLIEDIKRLTPFTLCPNGYIFAIDPNGYVLLHPNLQPNKPSQEPVTL 540
Db 481 NQLILGVMGVDVSLIEDIKRLTPFTLCPNGYIFAIDPNGYVLLHPNLQPNKPSQEPVTL 540
QY 541 DFLDAELNDIKVEIRNKMIDGESGKFTFTLVKSODERYIDKGNRTYTWTPVNGTDYSL 600
Db 541 DFLDAELNDIKVEIRNKMIDGESGKFTFTLVKSODERYIDKGNRTYTWTPVNGTDYSL 600
QY 601 ALVLPTYSFYIYKAKLEETITQARSKKGMKDSSETLKPONFESGYTFIAPRDYCNLKI 660
Db 601 ALVLPTYSFYIYKAKLEETITQARSKKGMKDSSETLKPONFESGYTFIAPRDYCNLKI 660
QY 661 SDNTEFLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYWSKQNIKGAKR 720
Db 661 SDNTEFLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYWSKQNIKGAKR 720
QY 721 FVVTGGITRVYPKEAGENQENPETEYDSFYKRSIDNDNYVFTAPYFNKSGPGAYESGI 780
Db 721 FVVTGGITRVYPKEAGENQENPETEYDSFYKRSIDNDNYVFTAPYFNKSGPGAYESGI 780
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTKTSIRDPKAGVPCDCKRNSDVMDCVI 840
Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTKTSIRDPKAGVPCDCKRNSDVMDCVI 840
QY 841 LDGGLMANHDDYTNQIGRFFGEIDPSLMRHLNIVSYAFNKSIDYQSVCEPGAAPKQ 900
Db 841 LDGGLMANHDDYTNQIGRFFGEIDPSLMRHLNIVSYAFNKSIDYQSVCEPGAAPKQ 900
QY 901 GAGHSAYVPSVADILQIGWATAAASWILQOFLSLFPRLLEAVEMEDDDFTASLSKQ 960
Db 901 GAGHSAYVPSVADILQIGWATAAASWILQOFLSLFPRLLEAVEMEDDDFTASLSKQ 960
QY 961 SCITEQTOYFFNDKSKFSGLDGCNCSRIHFHGEKLMNTNLIIFINVESKGCPCDTRL 1018
Db 961 SCITEQTOYFFNDKSKFSGLDGCNCSRIHFHGEKLMNTNLIIFINVESKGCPCDTRL 1018

```

## RESULT 2

A44147  
 N:Alternate names: dihydropyridine-2 chain precursor - rat  
 N:Contains: calcium channel alpha-2 chain  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 20-Aug-1999  
 C:Accession: A44147  
 R:Kim, H.L.; Kim, H.; Lee, P.; King, R.G.; Chin, H.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 3251-3255, 1992  
 A:Title: Rat brain expresses an alternatively spliced form of the dihydropyridine-sensitive  
 A:Reference number: A44147; MUID:92228762; PMID:1314383  
 A:Accession: A44147  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-1091 <KIM>  
 A:Cross-references: GB:W66621; NID:g203954; PIDN:AAA41088.1; PID:g203955  
 C:Superfamily: calcium channel alpha-2 chain  
 C:Keywords: calcium; glycoprotein; ion channel; transmembrane protein

Query Match 96.2%; Score 5145; DB 2; Length 1091;  
 Best Local Similarity 95.8%; Pred. No. 2,1e-301;  
 Matches 976; Conservative 22; Mismatches 19; Indels 2; Gaps 2;

QY 1 MAAGCLLALTTLTFLQSLIGPSSPEPFPSTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

```

Db 1 MAAGCLLALTTLTFLQSLIGPSSPEPFPSTIKSWDKMQEDLVTLAKTASGVNQLADI 60
QY 61 YEKYQDLYTVFNNARQLVEIAARDIEKLSNRSKALVSLALEAKVQAAHQWREDFASN 120
Db 61 YEKYQDLYTVFNNARQLVEIAARDIEKLSNRSKALVSLALEAKVQAAHQWREDFASN 120
QY 121 EVVYNNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROISYQHAHVHTPTDIYEGSTIVL 180
Db 121 EVVYNNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROISYQHAHVHTPTDIYEGSTIVL 180
QY 181 NELNWTALDEVFYKKNREEDPSLLMQVFGSGLTLKLI RTSVSMLETLSDDDFVNVASNSNAOD 240
Db 181 NELNWTALDEVFYKKNREEDPSLLMQVFGSGLTLKLI RTSVSMLETLSDDDFVNVASNSNAOD 240
QY 241 RPWYIQAASPKDMLILVDVSGVSGGLTKLIRTSVSEMLETLSDDDFVNVASNSNAOD 300
Db 241 RPWYIQAASPKDMLILVDVSGVSGGLTKLIRTSVSEMLETLSDDDFVNVASNSNAOD 300
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNNVSRANCKIIML 360
Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNNVSRANCKIIML 360
QY 361 FTDGGEERAQEIIFNKYNKDKKVRFRFSVGOHNYERGPQIOWMACENKGYIYEIPSGAIR 420
Db 361 FTDGGEERAQEIIFNKYNKDKKVRFRFSVGOHNYERGPQIOWMACENKGYIYEIPSGAIR 420
QY 421 INTQEYLDVLGRPMVLAGDKAKQVQWNTNYLDALGLVITGTLVPFNITGQFENKTNLK 480
Db 421 INTQEYLDVLGRPMVLAGDKAKQVQWNTNYLDALGLVITGTLVPFNITGQFENKTNLK 480
QY 481 NQLILGVMGVDVSLIEDIKRLTPFTLCPNGYIFAIDPNGYVLLHPNLQPNKPSQEPVTL 540
Db 481 NQLILGVMGVDVSLIEDIKRLTPFTLCPNGYIFAIDPNGYVLLHPNLQPNKPSQEPVTL 540
QY 541 DFLDAELNDIKVEIRNKMIDGESGKFTFTLVKSODERYIDKGNRTYTWTPVNGTDYSL 599
Db 541 DFLDAELNDIKVEIRNKMIDGESGKFTFTLVKSODERYIDKGNRTYTWTPVNGTDYSL 599
QY 600 LALVPTYSFYIYKAKLEETITQARSKKGMKDSSETLKPONFESGYTFIAPRDYCNLKI 659
Db 600 LALVPTYSFYIYKAKLEETITQARSKKGMKDSSETLKPONFESGYTFIAPRDYCNLKI 659
QY 660 ISDNTEFLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYWSKQNIKGAKR 719
Db 660 ISDNTEFLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYWSKQNIKGAKR 719
QY 720 FVVTGGITRVYPKEAGENQENPETEYDSFYKRSIDNDNYVFTAPYFNKSGPGAYESG 779
Db 720 FVVTGGITRVYPKEAGENQENPETEYDSFYKRSIDNDNYVFTAPYFNKSGPGAYESG 779
QY 780 IMYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTKTSIRDPKAGVPCDCKRNSDVMDCV 839
Db 780 IMYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTKTSIRDPKAGVPCDCKRNSDVMDCV 839
QY 840 ILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLNIVSYAFNKSIDYQSVCEPGAAPK 899
Db 840 ILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLNIVSYAFNKSIDYQSVCEPGAAPK 899
QY 900 QGAGHSAYVPSVADILQIGWATAAASWILQOFLSLFPRLLEAVEMEDDDFTASLSK 959
Db 900 QGAGHSAYVPSVADILQIGWATAAASWILQOFLSLFPRLLEAVEMEDDDFTASLSK 959
QY 960 QSCITEQTOYFFNDKSKFSGLDGCNCSRIHFHGEKLMNTNLIIFINVESKGCPCDTRL 1018
Db 960 QSCITEQTOYFFNDKSKFSGLDGCNCSRIHFHGEKLMNTNLIIFINVESKGCPCDTRL 1018

```

## RESULT 3

CHRB2  
 N:Alternate names: dihydropyridine-binding protein, 140K  
 C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 22-Jun-1999  
C;Accession: S10579; A39518; A33409  
R;Ellis, S.B.; Williams, M.E.; Ways, N.R.; Brenner, R.; Sharp, A.H.; Leung, A.T.; Campbell  
Science 241, 1661-1664, 1988  
A;Title: Sequence and expression of mRNAs encoding the alpha(1) and alpha(2) subunits of  
A;Reference number: S10579; MUID:88336904; PMID:2458626  
A;Accession: S10579  
A;Molecule type: mRNA  
A;Residues: 1-1106 <ELL>  
A;Cross-references: EMBL:M21948; NID:g164762; PIDN:AAA81562.1; PID:g164763  
A;Note: 57-Asn, 106-Lys, and deletion of 620-Ser were also found  
R;Jay, S.D.; Sharp, A.H.; Kahl, S.D.; Vedvick, T.S.; Harpold, M.M.; Campbell, K.P.  
J. Biol. Chem. 266, 3287-3293, 1991  
A;Title: Structural characterization of the dihydropyridine-sensitive calcium channel al  
A;Reference number: A39518; MUID:91131638; PMID:1847144  
A;Accession: A39518  
A;Molecule type: protein  
A;Residues: 961-973 <JAY>  
A;Note: This sequence represents the amino end of a glycosylated peptide that appears at  
e at the amino end and identical molecular weights (17K) following deglycosylation  
R;Hamilton, S.L.; Hawkes, M.J.; Brush, K.; Cook, R.  
Biochemistry 28, 7820-7828, 1989  
A;Title: Subunit composition of the purified dihydropyridine binding protein from skelet  
A;Reference number: A33409; MUID:90122765; PMID:2558713  
A;Accession: A33409  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 27-44, S', 46-47 <HAM>  
C;Superfamily: calcium channel alpha-2 chain  
C;Keywords: calcium; disulfide bond; glycoprotein; ion channel; membrane protein; phosph  
F:1-26/Domain: signal sequence #status Predicted <SIG>  
F:27-1106/Product: calcium channel alpha-2 chain #status  
F:94,138,186,326,350,470,477,606,615,678,697,784,827,891,898,988,1001,1081/Binding site:  
Query Match 96.08; Score 5132.5; DB 1; Length 1106;  
Best Local Similarity 94.78; Pred. No. 1.2e-300;  
Matches 985; Conservative 14; Mismatches 12; Indels 29; Gaps 4;

QY 1 MAAGCLLALTTLFOS--LLIGPSSEEPFSAVTIKSWDKMQEDLVTLAKTASGVNQLV 58  
Db 1 MAAGRPLATLTLQAWLILIGPSSEEPFSAVTIKSWDKMQEDLVTLAKTASGVHQLV 60  
QY 59 DIYEKYQDLYTVEPNARQLVEIARDAIEKLLSNRSKALVSLALEAEKVAQAAHQWREDA 118  
Db 61 DIYEKYQDLYTVEPNARQLVEIARDAIEKLLSNRSKALVSLALEAEKVAQAAHQWREDA 120  
QY 119 SNEVYVYNAKDDLPKNDSEPGSQRIKPVFTEDANFGROIYSOHAAVHIPTDIYEGSTI 178  
Db 121 SNEVYVYNAKDDLPKNDSEPGSQRIKPVFTEDANFRQVSYQHAAVHIPTDIYEGSTI 180  
QY 179 VLNELNWTLSALDEVFKKNEEDPSLLQVFGSATGLARYYPASVPWVDSNRTPNKIDLYDV 238  
Db 181 VLNELNWTLSALDDVFKKNEEDPSLLQVFGSATGLARYYPASVPWVDSNRTPNKIDLYDV 240  
QY 239 RRRPWYIOGAASPKDMLILVDVSGVSGLTUKLRTSVSEMLETLSDDDDFNVASFNSNA 298  
Db 241 RRRPWYIOGAASPKDMLILVDVSGVSGLTUKLRTSVSEMLETLSDDDDFNVASFNSNA 300  
QY 299 QDVSCFOHLVQANRNKKVLDKAVNNITAKGITDYKKGFSFAFEOLLNYSRANCNKII 358  
Db 301 QDVSCFOHLVQANRNKKVLDKAVNNITAKGITDYKKGFSFAFEOLLNYSRANCNKII 360  
QY 359 MLFTDGEERAQEIFNKNKDKKVRFRFSVGOHNYERGPQIOWMACENKGYIYETPSIGA 418  
Db 361 MLFTDGEERAQEIFAKYNNKDKKVRFTFSVGOHNYDRGPQIOWMACENKGYIYETPSIGA 420  
QY 419 IRTNTOEYLDVLRPMVLADGAKAQVQWNTNYDLALGLVLTGTPLPNTIGQFENKTN 478  
Db 421 IRTNTOEYLDVLRPMVLADGAKAQVQWNTNYDLALGLVLTGTPLPNTIGQFENKTN 480  
QY 479 LKNOLLTGVGVDVSLIEDIKRLTPRTLCPCNGYYFAIDPNGVLLHPNLQPK----- 530  
Db 481 LKNOLLTGVGVDVSLIEDIKRLTPRTLCPCNGYYFAIDPNGVLLHPNLQPKIGVGIPT 540

QY 531 -----NPKSQEPVTLDFLDAELNDIKVEIRNMIDGESGEKTFRTLVKSQDER 579  
Db 541 INLRKRRPNVQPKSQEPVTLDFLDAELNDIKVEIRNMIDGESGEKTFRTLVKSQDER 600  
QY 580 YIDKGNRTYTTPVNGTDY-SIALVLPTYSFYIYAKLEETITQARSKKGKKMKDSETLKP 638  
Db 601 YIDKGNRTYTTPVNGTDYSSIALVLPTYSFYIYAKLEETITQARY-----SETLKP 653  
QY 639 DNFEESGYTFIAPRYCNDLKISDNNTEFLNFEFIDRKTNNPNSCNADLINRVLLDAG 698  
Db 654 DNFEESGYTFIAPRYCNDLKISDNNTEFLNFEFIDRKTNNPNSCNADLINRVLLDAG 713  
QY 699 FTNELVQNTWSKQKNIKGVKARFVVDGDTTRYYPKEAGENWOENPETVEDSFYKRSND 758  
Db 714 FTNELVQNTWSKQKNIKGVKARFVVDGDTTRYYPKEAGENWOENPETVEDSFYKRSND 773  
QY 759 DNYVFTAPYFNKSGPAYESGIMVSKAVEIYOGKLLKPAVVGIIKIDVNSWIENFTKTSI 818  
Db 774 DNYVFTAPYFNKSGPAYESGIMVSKAVEIYOGKLLKPAVVGIIKIDVNSWIENFTKTSI 833  
QY 819 RDCAGPVCDCRNSDMDCVILDDGGFLLMANHDDYTQIGRFFGEIDPSLMRHLVNIS 878  
Db 834 RDCAGPVCDCRNSDMDCVILDDGGFLLMANHDDYTQIGRFFGEIDPSLMRHLVNIS 893  
QY 879 VYAFNKSYDYQSVCEPGAAPKQAGHRSYVPSVADILQIGWMTAAASVILQOFLLSLT 938  
Db 894 VYAFNKSYDYQSVCEPGAAPKQAGHRSYVPSVADILQIGWMTAAASVILQOFLLSLT 953  
QY 939 FPRLLAEVEMEDDDFASLSKQSCITEQTYFPDNDKSKFSVGLDCGNSRIFPHGKLMN 998  
Db 954 FPRLLAEVEMEDDDFASLSKQSCITEQTYFPDNDKSKFSVGLDCGNSRIFPHGKLMN 1013  
QY 999 TNLIFIMVESKGTCPDTRL 1018  
Db 1014 TNLIFIMVESKGTCPDTRL 1033

RESULT 4  
T30256  
calcium channel alpha-2-delta-C chain - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 20-Jun-2000  
C;Accession: T30256  
R;Klugbauer, N.; Lacinova, L.; Marais, E.; Hobom, M.; Hofmann, F.  
J. Neurosci. 19, 648-691, 1999  
A;Title: Molecular diversity of the calcium channel alpha2delta subunit.  
A;Reference number: Z20794  
A;Accession: T30256  
A;Status: preliminary; translated from CB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-1091 <KLU>  
A;Cross-references: EMBL:AJ010949; PIDN:CAA09423.1  
A;Experimental source: brain  
C;Superfamily: calcium channel alpha-2 chain  
Query Match 20.3%; Score 1085; DB 2; Length 1091;  
Best Local Similarity 28.7%; Pred. No. 4.4e-57;  
Matches 309; Conservative 22; Mismatches 416; Indels 128; Gaps 40;

QY 3 AGCLLALTTLFOSLIGPSSEEPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDIYE 62  
Db 14 ASALLA-TALLYAALGDVVRSEQQIPLSV-VKLWASAFGEIKSIAAKYSGSOLLQKKYK 71  
QY 63 KYQDLYTVEPNARQLVEIARDAIEKLLSNRSKALVSLALEAEKVAQAAHQWREDAFASNEV 122  
Db 72 EYKDVATEEIDGLQVKKLAKIMEEMFHKKSEAVRRLVEAAEBAHLKHEFDADL---QY 128  
QY 123 VYNAK--DDLDPEKNSEPGSQRIKPVFTEDANFGR-QISYQHAAYHIPTDIYEGSTIV 179  
Db 129 EYFNAVLINERDKGNLELGEKEFI---LAPNDHFNLPLPNVISLSLDYQVPTNMYNKDPAI 185  
QY 180 LNELNWTLSALDEVFKKNEEDPSLLQVFGSATGLARYYPASVPWVDSNRTPNKIDLYDVR 239

Db 186 VNGVWSESLNKFVDFNDFRPSLWYFGSAGKFFRQYFGIKWEPDE---NGVIAFDCR 242  
Qy 240 RRPVYIOGAASPDKMLILVDVSGSVGLTKLRTSVSEMLETSDDFVNVASFNSNAQ 299  
Db 243 NRKWTIOGAASPDKVILVDVSGSMKGLRTIAKQTVSSILDTIGDDDFNIIITYNEELH 302  
Qy 300 DVS-CFO-HLVQANVRNKKVADAVNNITAKGTDYKKGFSFAFEQOLLNVNVRAN-CN 355  
Db 303 YVEPLNGTLVQADRTNKEHREHLDKLFAKGLMDIALNEAFNLSDFNHTGQSGSICS 362  
Qy 356 KIIMFTDGEERAQETFNKYN-KDKKRVRFVSQGHNYERPIQWMAKNGKYYEYIP 414  
Db 363 QAIMLITDGAVIDYTIKAYNNPDRKVRTFTYLIGREAAFAADNLKMAKNGKFFQISL 422  
Qy 415 SIGAIRNTOEYLDVLRPMVLADRAKQVQWNTVYLD-----ALELGLVI--TGT 463  
Db 423 TLADVQENVWEYLVHLSRPKVI--DOEHVWVTEAVIDSTLPOAKLADDOGLVMTTVA 480  
Qy 464 LPVFNITGPFENKTNLKNQILGVMGVDSLEDIKRLTFRFTLCPNGYFAIDPNCYVLL 523  
Db 481 MPVFS-----KONETRSKG-ILLGVGTDVPVKELLKTIKYLKLGHYAFATNNGYILT 535  
Qy 524 HPNLQP---KNPKSQEP--VTLDLDALENDIKVIRKMKIDGESGKTFRTLKVSQDE 578  
Db 536 HPELRPLIEGKKRRKPNYSVSDLSSEVEDRDDV-LRNAMVNRKTKG--FSMEYK---- 588  
Qy 579 RYIDKGNRT-----YTWPVNGTDSLALVLT-YSFYIYIAKLEETITQARSKKGKMK 631  
Db 589 KTVDKKRVLVNDYYIDIKGTPSGLVALSRHGKRYFF-----RGNTV 634  
Qy 632 DSTLKPDPFESGYFTIAPRYCN-DLKISDNTEFFLNFNEFIDRKTNPNNPCNADLI 690  
Db 635 IEELG--HDLHPDVSLEADSEWYCNCTDLHPEHRLSLEAIAKLYLKKEP-LLQCDKELI 691  
Qy 691 NRVLIDAGFTNELVQNYWS-----KQNKIKGVKARFVVDGGITRVYP----- 733  
Db 692 QEVLEDA-VVSAPIEAYWTSALNKSENKSGKVEAFVLTGRLSRLNLFVGAELTNOQ 750  
Qy 734 -KEAGENMOENPETEDSFYKRSLDN--DNYVFTAPY----FNKSGPAYESGIMVSKAV 786  
Db 751 FLKAGDKENIFENADHPLWYRAAQIAGSFVYSIPFTGTGVNKS-----NVVTASTSI 804  
Qy 787 EYIYIOCKLLKPAVGIKIDVNSWIEFNFTKTSIRDPACGPVDCCKRNSDVMDCVILDDGGF 846  
Db 805 QLLDERKSPVAAVGIOMKLEFFQKFTWASQASLDGKGSICDDDETVCYLIDNNGF 864  
Qy 847 LLMANHDYTNQIGRFFGIDPSLMRHLVNSVYAFNKSXYQSVCEPAGAPKAGHRS 906  
Db 865 ILVS--EDYT-QTGDFFGEVGAUNKLLTMGSPKRTILYDQAWCR---ANKESDSDAH 918  
Qy 907 AYVPSVADILQIGWATAAASIIQQFLLSLTFPRLLAEVEMEDDDFTASLSK-----QS 961  
Db 919 GLLDYPYKAFI-----SAAKWLMTLVLFLVEF-----NLCSSWHSMDTAKAQLKQLEP 968  
Qy 962 CITEQTYFFDNDKSFSGVLDCNCSRIHFGEKLMNTNLIIFIMVESKGTCPCDT 1016  
Db 969 CDTEPAFVSERTIKETGTNACDCSKSFVIOQIPSSNLFVWVYDS--SCLCES 1021

## RESULT 5

S44617

C50C3.11 protein - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 30-Jun-2001

C:Accession: S44617

R:Favell, A.D.

submitted to the EMBL Data Library, May 1993

A:Description: Sequence of the C. elegans cosmid C50C3.

A:Reference number: S44617

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-734 <FAV>  
A:Cross-references: EMBL:IL14433; NID:g289649; PID:g289650  
C:Genetics:  
A:Introns: 24/2; 87/3; 175/1; 259/1; 290/3; 346/3; 460/3; 538/3

Query Match 11.4%; Score 607; DB 2; Length 734;  
Best Local Similarity 26.6%; Pred. No. 1.4e-28;  
Matches 180; Conservative 127; Mismatches 25; Indels 112; Gaps 20;

Qy 47 LAKTAGVNLQVLDIYKQYODLYTVPENARQLVETAAARDIEKLLSNRS-----KALVSLAL 102  
Db 36 MKETESKISHETILKQNYEKLVEEQDFPRAELKSKKHRIEDYLKVRSQFAYKAKIS--L 93  
Qy 103 EAEKQAAHQHREDPASNEVVYNAKDDLDPEK-NDSEPGSQRIKP-----VFIEDANF 155  
Db 94 EARSVRNDSTVNDPQSKSFIRMSAKQNDGTTIYESNHLKRLKVNKTKSFNITQANF 153  
Qy 156 -GRQISYQHAHVHTDIYEGSTIVLNELNWTLSALDEVFKKKNREEDPSLLMQVFGSATGL 214  
Db 154 YTLPTSSVSSAVHIPTPLYDRNEDLLRKIDW-SDIDAVYRTNREETKDLAFQLFCSEAGY 212  
Qy 215 ARYTPASPVW-DNSRTPNKIDLYDVRPPWYIOGAASPKMDLILVDVSGSVGLTKLIR 273  
Db 213 MRYTPAASWFDNQ--DEHLDLDFCRNTEWYINSATSKNVILMLDMSGMLGQRYEVAK 270  
Qy 274 TSVSEMLETISDDDFVNVASFNSNA---QDVSCFOHLVQANVRNKKVLDKAVNNITAKGI 330  
Db 271 QTTEAILTSHNDYFNIMTFKNTFLDDGCGNGTNGLLQATMRNKKALRRKMDTYQSEK 330  
Qy 331 TDYKKGFSFAFEQLLNYN-----VSRANCKKIIMLFTDGEERAQETFNKYNKDKKRVF 385  
Db 331 AEYKALPLAFSVLLDINNGGDNNGACENVIMLITDGAPNAYKKIFDMYNADKKRVF 390  
Qy 386 RFSVGHNYERGPQIOMACENKGYIYEPSIGAIRINTQEVL---DYLGRPMVLADGKA 441  
Db 391 TELVGEAIDFNEVREMACNRRGYVHVANMADVDEKIHYYIRMSKVRGHRHYKESGOLS 450  
Qy 442 KQWQWNYIDALELGL--VITGLPVFNITGQFENKTN-----AELENDIKVEIRNMID 478  
Db 451 ---WWTGVYERLYLPRPEIFAEPVPTITGSAFVNMKMSRRKIRLQKSEARSEMEVTVV 507  
Qy 479 ---LKNOLLIGVMGVDSLEDIKRLTFRFTLCPNGYFAIDPNCYVLLHPNLOPNP-- 532  
Db 508 SYPVYNTEPMGVAANVPILEVAQKSHPANIGSKSYFFMLDQNGFVMTHPQLRPIDPT 567  
Qy 533 --KSQEPVTLDFLD-----AELENDIKVEIRNMID 561  
Db 568 KYHKQNYNNMDLLELVGQONVRSQKSOAVSDLYCESGANYAECVDLLKRAVRKMIID 627  
Qy 562 GESSEKTRTLVKSQDERY----IDK---GNRTYTPVNGTIDYSLALVLPITYSYIYKA 614  
Db 628 CDNSD-----VOOLDVLYATELLDRVYPQTNTIYAEACINHANFVLGLAVAKGDDYRVVK 681  
Qy 615 KLEETITQARSKKGKMK 631  
Db 682 K-----QKKYDFGRVK 692

## RESULT 6

T18770

probable calcium channel protein - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 29-Oct-1999

C:Accession: T18770; T25249

R:Suiston, J.

submitted to the EMBL Data Library, June 1995

A:Reference number: Z19019

A:Accession: T18770

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1148 &lt;WIL&gt;

A:Cross-references: EMBL:Z49907; PIDN:CAA90091.1; GSPDB:GN00020; CESP:T24F1.6

A:Experimental source: clone B0491

R;Chui, C.  
submitted to the EMBL Data Library, June 1995

A:Reference number: Z20004

A:Accession: T25249

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1148 <W12>

A:Cross-references: EMBL:Z49912; PIDN:CAA90141.1; GSPDB:GN00020; CBSP:T24F1.6

A:Experimental source: clone T24F1

C:Genetics:

A:Gene: CBSP:T24F1.6

A:Map position: 2

A:Introns: 91/2; 131/3; 170/3; 283/1; 322/2; 410/3; 487/1; 563/1; 602/3; 654/3; 683/3;

Query Match 10.7%; Score 569.5; DB 2; Length 1148;

Best Local Similarity 21.5%; Pred. No. 5e-26;

Matches 234; Conservative 216; Mismatches 406; Indels 233; Gaps 42;

Qy 37 VDKMQEDLVTLA-----KTAGVNLQVLDIYKQDYVPEPNNARQLVEIAARDI 86

Db 99 VDTIEEPASIAQFSANILRDFETQSRFSLVQEEFEKLPDIKSKEDAAEKLRAVEHL 158

Qy 87 EKLNSRKSALVSLALEAEKVOAAHQWREDFASNEVYVYNNAKDLDPEKNDSEPGSOR-- 144

Db 159 DRLVTNRVDALKKLASSAASAAVF-----DEYDQAYAVPQADKRCE 201

Qy 145 --IKPFTEDANFGROIYQH---AAVHIPTDIYEGSTIVLNLNWTSA--LDEVFKNR 197

Db 202 AYMKKNESDMHFVSNM-VEHNSKSGIHTIVESQCDPRVWRDFDTGTHLEKTSMDNK 260

Qy 198 BEDPSLLMQVFGSATGLARYPASPVNDNSRTPNKIDLYVRRPWPYIOGAASPKMLIL 257

Db 261 EKAPEMGHQYIGTSGLTRMYPRRHW-KVEPTITIDLPFRPFPVNAESVPKDIVFL 319

Qy 258 VDVSGSVGLKILRTSVSEMLTSLDDEDFVNVASNAQD-VSCFQH-LVQANVRN 315

Db 320 LDYSGVSGPMTLHKITWYLSLSPNDYFFGVYNNHNPNIISCANRTFMPATTSNK 379

Qy 316 KVLDAVNNAITAKGIDTKKGFSAFEOL---LNNYVS-----RANCNKIIMLFTDGEE 367

Db 380 KYFPEELGMEKQQAHPATPLKFSLDVLRGNLDSNQLFADYRSEGHKLLIIFTDGVE 439

Qy 368 RAOEIFN---KYNKDKVVRFSVQGHYERGIOWMACENKGYEIEISGAIRNTQ 424

Db 440 WPHQIDLEEFOTRNSILIRIFGSMGYGTSLLPLQOYNACKSHGYSIDSMVDKPSR 499

Qy 425 EYLDVLRPMVLGAK-----QVQWTVNYLDALGLVITGTLPVFNITQGFENKT 477

Db 500 TIONVLSQ---VRGDELAKTNAEKREPSWTQLYMETQGTGPVILSLPILT-----SEQR 551

Qy 478 NLKNQILILGVMGVDSLEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHPNLQ-PKNPK--- 533

Db 552 IWRQKLAGVVAIDISIKFTKHLPL--TSSEQMYGIYVNDNGMLIYHPQLQIPKTEVHCV 609

Qy 534 -----SQEPV-----TLDFLDAELNDIKVEIRN 557

Db 610 RRSACYDAQVQKQKAGSLRVHYGFSDEVRVRLVGLIDSIPFLDMYDEGSDAIRLRR 669

Qy 558 KMIDGESKEFTRLVLKQSDERYIDKGNKRTWTVPNGTDSLALV--LPTYSFYIKAK 615

Db 670 -----RITTKCYEAIKDNSEKHCYHSHIKSDPFTLVNNIQLKTYYYDDSV 717

Qy 616 LREETITQ-----ARSKKMKMDSETLKPDPNFEEGYTFIAPRDYQ--NDLKISDNNT 665

Db 718 QELGLTDNKLVTFFYPDRVCQKLDYAAHDFRV--WSDISEKEICAQDDMLPRAFT 775

Qy 666 EFLNPFNFIKRTPNNSCHADLINRVLLDAGFTNELVQYNSKQKIKGVKARFVVD 725

Db 776 KGLGSWTQSWPKSDIEHTTC-----LLAQYPENASVPHYVNS-----FVHTR 817

Qy 726 GGITRVYKPEAGENQENPETEYDSFKRSILDNDNYVFTAPYFNKSGPGAYESGIMYSKA 785

Db 818 SKLTAFYPTCSSHDMKANVKAFDEEI--KLTDNDNFV-----QFSWR-----SESLIYRT 866

Qy 786 VEYIQGKLLKPAVGVIKIDVN---SWIENFTKTSIRDPCAGPVCDCKRNSD-----VMD 837

Db 867 IADYDNRL--AVVGTQWKNEFFDQYDFNFT-----RQNPDKICKRQE 908

Qy 838 CVILDDGGFLLMANHDDYTNQIGRPFGEIDPSLMRHLNLSVYAFNKSVDYQSVCE-PGA 896

Db 909 CSTITRNGHVIASSAHRAPAHLAKF---DPQLFESLVKVNLSVNSTNSWTEVQSECKAKRV 964

Qy 897 AKQOGAGHRS-----YVPSVADILQIGWATAAASIILOQFLL-----SLTFP 940

Db 965 APWSSAAPGSSSILRYFVVISIKLAKTSFWR-----NLLESALTLDVDAQPSMTGTCTCFQ 1019

Qy 941 RL--LEAVEMEDDDFTASLSKOSCIETQYFFDNDKSKFSFGLDCGNCGRIFHGEKLMN 998

Db 1020 KIKPFCECFMKPFHYMTLN---ITKQLQ-----LTGMSTCSRVAKLY---PVPH 1063

Qy 999 TNLIFIMVE 1007

Db 1064 TTLSLIAD 1072

#### RESULT 7

C86880

hypothetical protein yvcC [imported] - Lactococcus lactis subsp. lactis (strain IL140)  
C:Species: Lactococcus lactis subsp. lactis

C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001

C:Accession: C86880

R:Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Eh

Genome Res. 11, 731-753, 2001

A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis

A:Reference number: A86625; MUID:21235186; PMID:11337471

A:Accession: C86880

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1450 <STO>

A:Cross-references: GB:AE005176; PID:g12725093; PIDN:AAK06141.1; GSPDB:GN00146

A:Experimental source: strain IL1403

C:Genetics:

A:Gene: yvcC

Query Match 3.7%; Score 198; DB 2; Length 1450;

Best Local Similarity 21.0%; Pred. No. 0.0017;

Matches 242; Conservative 149; Mismatches 439; Indels 322; Gaps 56;

Qy 37 VDKMQEDLVTLAKTAGVNLQVLDIYKQDYVPEPNNARQLVEIAARDIEK-----L 89

Db 69 INKTENDKELKLPFSGNQPIEBE--NESWTLKEKNT-----IISDFEKENECKIVL 120

Qy 90 LSNRSKALVSLALEAEKVOAAHQW---EDFA-----SNEVYVYNA 127

Db 121 RANNSISLLNLEIQADAKLIENDQEVISEDILAKKESTIFSLYIPENKADSKKONKNT 180

Qy 128 KDDLDPKNDSEPCSORIKP---VFIEDANFGHQSIVQAAHV-----167

Db 181 EEVLNNESSQEEVVSQKDKSQLAFSPNFGKAFSNDLAQNYENISPYRODETGISP 240

Qy 168 ----IPTDIYEGSTIVLNLNWTLSALDEVFKKREEDPSLLMQVFGSATGLARYYPASPW 223

Db 241 NHSWIPT---GNTTVVNHGWSNF-----SSQWDGVNSWN--GEATNLENSIYEAG 287

Qy 224 VDN-----SRTPNKKIDLY-DVRRRPWYIOGAASPKDMLILVDVSGVSGITLK 270

Db 288 VNNPVDPALRKYAKETETPLGLYVYLVNVRGN---VQNPVKPVDIVLVIDMSGMOGAKET 344

Qy 271 LIRTSVSEMLETLSDO---DFVNV--ASPNNAQDYSCFQHLVQANVRNKKVLKD----A 321

Db 345 AVROGVSDFLSTQNTAYAYVNVGVISPPGNYVTGASGYITVPI---DKVSESHKVS 402

Qy 322 VNNITA---KGITDYKKGFSAFEQLNLYNVSRANCKIIMLFTDGDGEERAQIFNKYK 378

Db 403 INQALAPQFSGGIFTQLGRKGTML---BQDSSDNQKMMILMTDG-----VPTFSYKVS 455

```

QY 379 DKVR--VFRFSGQHNVERG---PIQ---WMACENKGYEYI-----PSICAIRINTQE 425
Db 456 ASKDVNIYQSGFAESRDEPGNTSIQSPYVYKIDNGSNIERTDWTATLGEAEISKQE 515
QY 426 YLDVLGRPMVLADG-----KAKQVQWTVNYLDALGLGLVITGTLFVENVITGOF 474
Db 516 ISEIHTLGIQNGDSYLSQAEVKSRTSLIATGLYQDANSAN-----DITDYLK 565
QY 475 NKTN-----LKNQLILGVNGVDVSLIEDIKRLTPRFTLCPNGYIFAIDPNGYVLLHPN 526
Db 566 NQANVLSRFNTITNGLILDPLGAQFEYKDKT-----FEITSVG----- 604
QY 527 LQPKPKSQEPVTLDFDAELNDIKVIRKMKIDGESGKTFRTLVKSQDERYDKGNR 586
Db 605 -----EDSIDNLTPTGINKEGLEISNLNI--GKNQEVQIHYQVRLNTDITDFKTY 653
QY 587 TY-----TWTVPNGT--DYSIALVLPITYFYIYKAKLE-----ETITQARSKK 627
Db 654 WYQMGNEITLP--NGSNDPNKVNFCVPSAKSSGNLTLEKOWLANSENIENVELLIGRR 712
QY 628 GKMKDSE-----TLKPDNFESSGYTFIAPRYCNDLKISDNNTFLNFNEDIDRKTNN 682
Db 713 SAQISSDWTKVTLKEDDEWRSOLENLPKYSILGEEFYIYKDEIVLN--SEIYDWTITGE 771
QY 683 PSCNADLINRVLLD---AGFTNELVQNYWSKQKNIKCVKARFVVTGGITRVYPKEAGE 738
Db 772 DKTITANIEKFLQLIKTSNHDNEPLSEVEFVLKNSQGEEDKAVTN-----EKGE 822
QY 739 --NQWENPTYEDSFYKRSLDNDNTVFTAPYFNKSGPGAYESGIMVSK-----AVEIYIQ 791
Db 823 ILFDKTRNLNGEYQLEHIEIKSPGHSLEGPKWIKT--EFENGQPIIKVDGEQIALDHYN 879
QY 792 GKLLKPAVVGKIDVNSHIEFNFTKTSIRDCAGPVCDCKRNSVDMCVILD-----DG-- 844
Db 880 KEMIS---LNTINDIN--VEEF-----RNSVTIDKRAVDSEKLDGAV 917
QY 845 -GFLLMANHHDDYTQIGRFCEIDPFLMRHLNIVSYAFNKSVDYQSVCPGAPKOGAG 903
Db 918 FNLQIESVDDELQKPL--EITNNLLPGL-----YALQESVNGFYRDEV 964
QY 904 H--RSAYVPSVADILQIGWATAAAMSTLOQFL-----LSLTF-- 939
Db 965 HFRYKNGSIVAIGSEG-----IDPFLDENESGNGLVNLNEENGDLHLTLIFY 1015
QY 940 ---PRLEAVEMEDDDPTASLSKQSC--ITEQTQYFFDNDS-----KSFSGVLDCGNCRI 990
Db 1016 NQAVPPLQLEVDKIDDDFTSLPAGVSELTPLKGRKSTDSVVKRINSFDRILKTFN--NE 1073-
QY 991 FHGEKL--MNTNL 1001
Db 1074 FTGETIALKSNL 1085

```

## RESULT 8

S54355

inter-alpha-trypsin inhibitor heavy chain 3 precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 04-Feb-2000

C:Accession: S54355

R:Chan, P.; Risler, J.L.; Raguenez, G.; Salier, J.P.

Biochem. J. 306, 505-512, 1995

A:Title: The three heavy-chain precursors for the inter-alpha-inhibitor family in mouse:

A:Reference number: S54353; MUID:95194326; PMID:7534067

A:Accession: S54355

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-886 &lt;CHA&gt;

A:Cross-references: EMBL:X70393; NID:g695635; PIDN:CAA49843.1; PID:g695636

C:Superfamily: inter-alpha-trypsin inhibitor complex component II

Query Match

Best Local Similarity 3.6%; Score 194.5; DB 2; Length 886;

Matches 185; Conservative 138; Mismatches 347; Indels 261; Gaps 44;

## RESULT 9

S30350

inter-alpha-trypsin inhibitor heavy chain 3 precursor - human

N:Alternate names: HC3; inter-alpha-trypsin inhibitor chain H3; pre-alpha-inhibitor h

C:Species: Homo sapiens (man)

C:Date: 03-May-1994 #sequence\_revision 20-Feb-1995 #text\_change 04-Feb-2000

C:Accession: S30350; S34123; S02141; D34245; A39079; S50133; B53642; A59167



R; Bourguignon, J.; Diarra-Mehrpour, M.; Thiberville, L.; Bost, F.; Sesbouee, R.; Martin, Eur. J. Biochem. 212, 771-776, 1993  
 A; Title: Human pre-alpha-trypsin inhibitor-precursor heavy chain cDNA and deduced amino-acid sequence  
 A; Reference number: S30350; MUID: 93215656; PMID: 7681778  
 A; Accession: S30350  
 A; Molecule type: mRNA  
 A; Residues: 1-885 <BOU1>  
 A; Cross-references: EMBL: X67055; NID: g288562  
 R; Bourguignon, J.  
 submitted to the EMBL Data Library, June 1992  
 A; Reference number: S34123  
 A; Accession: S34123  
 A; Molecule type: mRNA  
 A; Residues: 1-310, 'K', 312-343, 'R', 345-885 <BOU2>  
 A; Cross-references: EMBL: X67055; NID: g288562; PIDN: CAA47439.1; PID: g35465  
 R; Diarra-Mehrpour, M.; Bourguignon, J.; Sesbouee, R.; Mattel, M.G.; Passage, E.; Salier, Eur. J. Biochem. 179, 147-154, 1989  
 A; Title: Human plasma inter-alpha-trypsin inhibitor is encoded by four genes on three chromosomes  
 A; Reference number: S02141; MUID: 89137072; PMID: 2465147  
 A; Accession: S02141  
 A; Status: not compared with conceptual translation  
 A; Molecule type: protein  
 A; Residues: 341-356, 'G', 358-845, 'H', 847-885 <DIAL>  
 A; Cross-references: EMBL: X14690; NID: g35464; PIDN: CAA32821.1; PID: g35465  
 R; Englund, J.J.; Thøgersen, I.B.; Pizzo, S.V.; Salvesen, G.  
 J. Biol. Chem. 264, 15975-15981, 1989  
 A; Title: Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-alpha-trypsin inhibitor  
 A; Reference number: A92736; MUID: 89380192; PMID: 2476436  
 A; Accession: D34245  
 A; Molecule type: protein  
 A; Residues: 30-49 <ENGL>  
 R; Englund, J.J.; Salvesen, G.; Hefta, S.A.; Thøgersen, I.B.; Rutherford, S.; Pizzo, S.V.  
 J. Biol. Chem. 266, 747-751, 1991  
 A; Title: Chondroitin 4-sulfate covalently cross-links the chains of the human blood proteinase inhibitor  
 A; Reference number: A39079; MUID: 91093267; PMID: 1898736  
 A; Accession: A39079  
 A; Molecule type: protein  
 A; Residues: 631-647 <ENG2>  
 R; Diarra-Mehrpour, M.; Bourguignon, J.; Sarafan, N.; Bost, F.; Sesbouee, R.; Muschio-Boncompagni, A.  
 Biochim. Biophys. Acta 1219, 551-554, 1994  
 A; Title: Tandem orientation of the inter-alpha-trypsin inhibitor heavy chain H1 and H3 genes  
 A; Reference number: S50132; MUID: 95002176; PMID: 7522574  
 A; Accession: S50133  
 A; Status: preliminary  
 A; Molecule type: DNA  
 A; Residues: 1-27 <DIA2>  
 A; Cross-references: EMBL: X75318  
 R; Wisniewski, H.G.; Burgess, W.H.; Oppenheim, J.D.; Vilcek, J.  
 Biochemistry 33, 7423-7429, 1994  
 A; Title: TSG-6, an arthritis-associated hyaluronan binding protein, forms a stable complex with hyaluronan  
 A; Reference number: A53642; MUID: 94271799; PMID: 7516184  
 A; Accession: B53642  
 A; Molecule type: protein  
 A; Residues: 30-34, 'X' <WIS>  
 R; Jensen, T.E.; Faarvang, K.L.; Ploug, M.  
 FEBS Lett. 230, 195-200, 1988  
 A; Title: Carbohydrate as covalent crosslink in human inter-alpha-trypsin inhibitor: a novel crosslink  
 A; Reference number: S02431; MUID: 88167187; PMID: 2450785  
 A; Accession: A59167  
 A; Molecule type: protein  
 A; Residues: 30-32, GEREQAVDT' <JES>  
 C; Comment: As pre-alpha-inhibitor, this protein is covalently cross-linked by chondroitin-6-sulfate  
 C; Genetics:  
 A; Gene: GDB: 120109; OMIM: 146650  
 A; Cross-references: GDB: 120109; OMIM: 146650  
 A; Map position: 3p13-3p12  
 C; Superfamily: inter-alpha-trypsin inhibitor complex component II  
 C; Keywords: chondroitin sulfate proteoglycan; glycoprotein; heterodimer; proteinase inhibitor  
 F; 1-19/Domain: signal sequence #status predicted <STG>  
 F; 20-29/Domain: propeptide #status predicted <PRO>  
 F; 30-647/Product: inter-alpha-trypsin inhibitor heavy chain 3 #status experimental <NAT>  
 F; 648-885/Domain: carboxyl-terminal propeptide #status predicted <CNP>  
 F; 87, 576/Binding site: carbohydrate (Asn) (covalent) #status predicted

F: 647/Modified site: chondroitin sulfate ester carboxyl end (Asp) (in mature form) #s  
 Query Match 3.5%; Score 185; DB 2; Length 885;  
 Best Local Similarity 20.4%; Pred. No. 0.0046;  
 Matches 133; Conservative 106; Mismatches 243; Indels 170; Gaps 33;  
 QY 27 FPSAVTIKSWDKMOEDLVLTAKTAGSVNQLVDIYEKYQDLTVPEPNARQLVEIAARDI 86  
 DB 97 YPCNVKEKEVAKQYKAVSQGTAG-----LVKASGRKL 131  
 QY 87 EKLLSNRSKAL---VSLALEAEKVAQAHOQWREDFASNEVVYVYNAKDDLDPEKKNREDPSL 203  
 DB 132 EKFTSVNVAAGSKVTFELTYELLKRHKGK-----YEMYLKVPQPK-----Q 173  
 QY 144 RIKPVFIEDANFGRQISQYHAAVHIPTDIYEGSTIVLNEINWTSALDEYFKKNREDPSL 203  
 DB 174 LVKHFRIE-----VDIFPQGISMLDAEASFITNDLL-----GSA 208  
 QY 204 LMOVEGSAATGLARYPASPWVDSRT--PNKID-----LYDVRRRP-----WY 244  
 DB 209 LTKSFGSKGKHVSFKFS---LDQORSCPTCTDSLLNGDFTIYDVNRESGPNVQVINGYF 265  
 QY 245 I-----QG-AASPKDMLILVDVSGVSGLTCLKLIRTSVSEMLETSLDDDDFVNVASPNNA 298  
 DB 266 VHFAPQGLPVVPKNVAFVVIDISSMAGRKLEOTKEALLRILEDMQEDYLNIFLFSG-- 323  
 QY 299 QDVSCF--OHLVQANVRNKKVKDAVNNTAKGTDYKKGFSFAFEQLLNYSR----- 351  
 DB 324 -DVSTWKEHLVQATPENLOEATFKVSKMEDKGMTINDGLLRIGISML---NKAREHRIP 379  
 QY 352 ANCKIIMLFTDG---GEERAOEIFKNYK---DKRVRFVFSVGOHNYERGPIONMACE 405  
 DB 380 ERSTSVIMLTGDDANVGESRPEKIQENVRNATGGKFLPNLGF--NLLNYNLENMALE 438  
 QY 406 NKGYVEIPSIGAIRINTQSYDLVGLRPMVLGADKAKQVQWTVNYDLAE-----L 456  
 DB 439 NHGFARRIEDSDADLQGLFYEEVANPL-LTGVEMEYEP--NAILDLTQNTYOHFYDGS 495  
 QY 457 GLVITGTLVPNTGQFENTNLK-----NQLILGVMGVDVSLIEDIKRLTPRTLCNGY 511  
 DB 496 EIVVAGRL-VDEDMNSF--KADVKGHGATNDL---TFTEEDMKMEK-----ALQERY 544  
 QY 512 YFAIDPN-----GYVLLHPNLOPK---NFKSOEPVTLDFLDAELENDIKVEIRKNMIDG 562  
 DB 545 IFG---NYIERLWAYLIEQLLEKKNHGEKENLTARALDLSLKHVFTPLTSWVTK 601  
 QY 563 ESSEKTEFTLVKSQDERYI--DKGNRTYTTPVN--GTDYSLALVLPYTSFYI 612  
 DB 602 PE-----DNEDEAIAKPCGDAEATPVSPAMSYLTSYQPQNPYYV 644  
 RESULT 10  
 D97033  
 uncharacterized protein, probably surface-located [imported] - Clostridium acetobutyli  
 C; Species: Clostridium acetobutylicum  
 C; Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001  
 C; Accession: D97033  
 R; Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L  
 J. Bacteriol. 183, 4823-4838, 2001  
 A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium  
 A; Reference number: A96900; MUID: 21359325; PMID: 21359325  
 A; Accession: D97033  
 A; Status: preliminary  
 A; Molecule type: DNA  
 A; Residues: 1-1819 <KUR>  
 A; Cross-references: GB: AE001437; PIDN: AAK79055.1; PID: g15023996; GSPDB: GN00168  
 A; Experimental source: Clostridium acetobutylicum ATCC824  
 C; Genetics:  
 A; Gene: CAC1081  
 Query Match 3.3%; Score 175.5; DB 2; Length 1819;  
 Best Local Similarity 18.8%; Pred. No. 0.053;

Matches 193; Conservative 154; Mismatches 342; Indels 335; Gaps 51;

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QY 24 BEPPSAVTIKSWDKMQEDL-VTLAKTAGVNLVD-----IYEKYODLYTVBPNNNA 75
DQ 133 EQQIKNARTSKG-ADLTFKDGTITIASTDSIKGIFDMTKGTAIVSDYQFLLITQVNSN 191
QY 76 RQLVEIARDIEKLLNRSKALYSIALE-----AEKVOAHQWREFPASFNEVYYNA 127
DQ 192 N-----LQDINSWLTGKRYALSKILSTVDKITTAVSNINNAHDESDFTALQI--YV 243
QY 128 KDDLPKND-----SEPGSRIKPVF-----IEDANFGR-QISYOH--A 164
DQ 244 QEDLVPLNENISAAKNKSGDLSSEINVTVKDSLKQLDALERINLQGLDDYHFTG 303
QY 165 AVHPTPIYEGSTIVLNELNWTALDEVPKKNR--BEDPSLLMQV--FGSATGLARYPA 220
DQ 304 AANDENNEDVNGWANGKW-----FERNNAIEINSIVEPLSRINSGDSTAADYA 356
QY 221 --SPWVDSNRTN-----KIDLYDVRPRPWYIQA 248
DQ 357 IQVDGVDNNDNIDKSVIAEKKOLKGNLNIABIKSAVEEYKTVLDFYDLIKK---GT 411
QY 249 ASPKD--MLILVDVS--GSVSGL-----TLKLIRTSVSEMLFTLSD-----DD 287
DQ 412 AKVSDYNAIGLTGVTEDNVTMNEELLKNDIKTLNKLQDNINSIISKLNINAGTDPD 471
QY 288 FVNVASFNSNAQDVSCF-----QHLVQANVR--NKKVLKDVANNITAK----- 328
DQ 472 YTML-NISSVTQDNIFIRDDIKTAKQANGSLNKGKIQDSVNSNLSKLRSAMDRI 530
QY 329 GITDYK-----KGFSAFAEQLLANYSRANCKIIMLFTDGGPERAQELFNKYNK----- 378
DQ 531 ALDDYNLIGIEGVTSDNLTFVNNQVKSCKTIDELKTKVSD--ALKLYDSNKVNNNGDA 588
QY 379 --DKKVRV--FRSVGQHNTYERGIOWMACENKGY--YEIPISG--AIRN----- 422
DQ 589 TYDDYKIGIKGIEEVTYING-----VFKGNYETLEELKVGINIAVRISTENIKNG 643
QY 423 -----TOEYLDVLRPMVLGDKAKOV-----QWTVNVL 451
DQ 644 VGSVEDFTIAGTYGVTEENIKYINKVIEGGDASPEASNIITEVNVIEIQSLKRWSSQV 703
QY 452 ---DALELGL-VITGLPVNITGOFENKTNLKNLILGVMGVDVSLDEDIKRLTPREFLC 507
DQ 704 TAEDVKSLSIVTEENISYIMDRVVKNTYYYSKVELLEAVEAIIKEKEIYERINLQATV 763
QY 508 PNGYIFAI-----DPNGYVLLHPNLQPNKPSQEPVILDFDLDALENDIKVE----- 554
DQ 764 ADYEYIKVTGVTSMITSINDV-----KSNLTTREELQAKI--DVVIEQTO 810
QY 555 -----IRNMIDGSGSEKTFE-----TLVKSODERYIDKGNRTYTWTPVNGTDYSLALVL 604
DQ 811 VAHTDWIGRVNLGRANISDFEFGITVNVSNFYQVDDHLKDDKYITIDAIKAAVTYV 870
QY 605 PYSFYIYAKALEEITQARSKKKMKKQSETLKPDPFEESGYTFIAPRDYCNLKDSDNN 664
DQ 871 GQSYIY-----EBIN-----KGTATL-----DIYNSLIGITCVT 898
QY 665 TFFLNEFEIDRKTPNPNPCNADLIRVLLDAGTNNELVNYNSKQNKIKGVKARFVVT 724
DQ 899 TENIYINLNKESYFNAS---DIQTKV-----NALISVGYEIEINKGEATVDVYT 948
QY 725 DGGITRVYPKEAGENWQENPETEYDSFYKRSLLDNVYFTAPYFNKSPGAYESGIMVSK 784
DQ 949 SLGITGV-----TKENIIFNTYIKE---COYFOLTSILKS 980
QY 785 AVEI-----YIQ---GKLLKPAVVGKIDVNSWIENTFTKTSIRDPACGVCDCKRNSD 834
DQ 981 SVEVLEEKYEAYVKITSGK-----AVVG-----DYTKVGIKDVTENIYINLNI 1026
QY 835 VMDK 838
DQ 1027 LQNC 1030
```

## RESULT 11

JC5576

inter-alpha-trypsin inhibitor heavy chain 3 - golden hamster  
C:Species: Mesocricetus auratus (golden hamster)

C>Date: 23-Sep-1997 #sequence\_revision 23-Sep-1997 #text\_change 17-Mar-1999

C:Accession: JC5576; PC4486

R:Nakatani, T.; Suzuki, Y.; Yamamoto, T.; Sinohara, H.

J. Biochem. 122, 71-82, 1997  
A:Title: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precursors  
in inhibitor heavy chain family.

A:Reference number: JC5574; MUID:97420688; PMID:9276673

A:Accession: JC5576

A:Molecule type: mRNA

A:Residues: 1-889 <NAK>

A:Cross-references: DDBJ:D89287

A:Experimental source: liver

A:Accession: PC4486

A:Molecule type: protein

A:Residues: 34-53; 449-475; 509-526 <NA2>

C:Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3  
that the complexes play important role for pancreatic cancer.

C:Superfamily: inter-alpha-trypsin inhibitor complex component II

F:236-239, 664-865/Disulfide bonds: #status predicted

## Query Match

3.1%; Score 164.5; DB 2; Length 889;

Best Local Similarity 23.2%; Pred. No. 0.079;

Matches 66; Conservative 56; Mismatches 112; Indels 51; Gaps 11;

QY 202 SLLNQVFGSATGLARYYPASPWDNSRT-PNKID-----LYDVRNR-PWYIQA-- 248

DQ 211 SALTKSFSGKGVHSPKPS---LDQQRSCPTCTDSSLNGDFTIVDVNRESPGNVQVNG 267

QY 249 -----ASPKDMLILVDVSGSVGLTKLIRTSVSEMLFTLSDDDFVNVASFNS 296

DQ 268 YFVUFPAPQPLVPPVNFVIDISGSMAGRKIQOTVALLKILDDMKQDDYLFST 327

QY 297 NAQDVSCFQHLVQANVRNKKVLKDAVNNTAKGTYDKKGFSAFEOLN-----YVNSRA 352

DQ 328 GV---TTWKDSLQVATPANLEARTFVRSISDQGMTNINDGLRGIRMLTDARQHVPER 385

QY 353 NCNKIIMLFTDG---GEERAQELFNKYNKDKKVRVFRFSVG-OHNYERGIOWMACENK 407

DQ 386 STSIIML--TDGDANTGESPEKIQENVRKAIDGREFPLYNLGFCNNLNVFLETMALENH 444

QY 408 GYTYEIPSGAIRINTQYLDVLRPMVLGDKAKQVQWTVNVL 452

DQ 445 GVARRIVEDSDANLQOGFEEVANPLL-----TNVEVE 478

## RESULT 12

T28155

variant-specific surface protein 1 - malaria parasite (Plasmodium falciparum) (fragme  
N:Alternate names: erythrocyte membrane binding protein 1 (EMPI)

C:Species: Plasmodium falciparum

C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 20-Jun-2000

C:Accession: T28155

R:Rowe, J.A.; Moulds, J.M.; Newbold, C.I.; Miller, L.H.

Nature 388, 292-295, 1997

A:Title: Plasmodium falciparum rosetting is mediated by PfEMP1 and requires complemen  
A:Reference number: Z20477; MUID:97373957; PMID:9230440

A:Accession: T28155

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-2706 <ROW>

A:Cross-references: EMBL:Y13402; PIDN:CAA73831.1

A:Experimental source: strain IT 4/25/5

C:Genetics: 2493/3

A:Note: R29R+var1

## Query Match

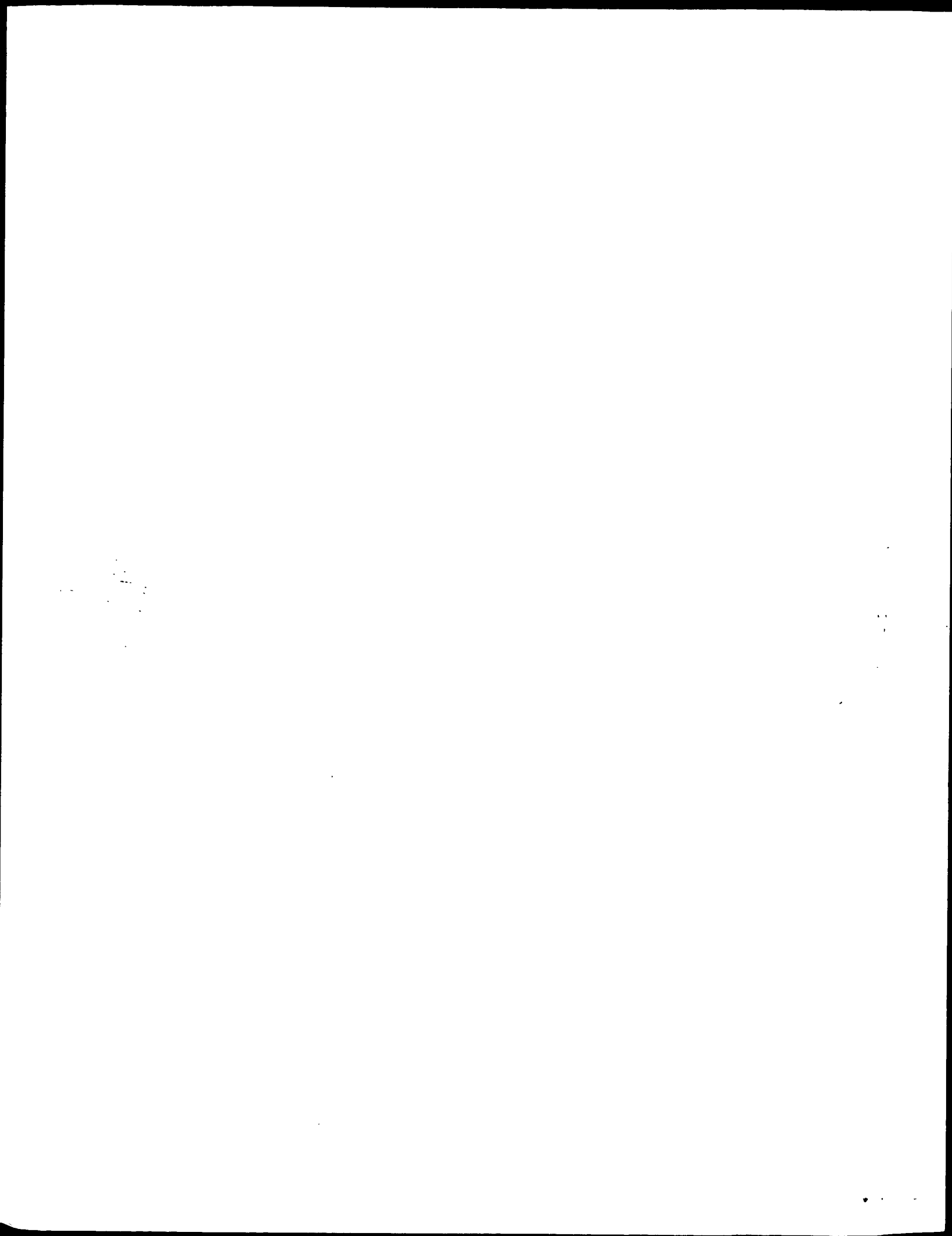
3.0%; Score 161; DB 2; Length 2706;



A:Plattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, D.L.; Rasmussen, L.B.; Karpman, A.J.; Osofsky, J.S.; White, O.; Salzberg, S.L.; Aronson, A.D.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A:title: The complete genome sequence of *Escherichia coli* K-12.  
A:Reference number: A6720; PMID:97426617; PMID:9278503  
A:Accession: D64998  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-575 <BLAT>  
A:Cross-references: GB:AE000317; GB:U000096; NID:g1788605; PIDN:AAC75330.1; PID:g1788606;  
A:Experimental source: strain K-12, substrain MG1655

Query Match					
Best Local Similarity 2.9%; Score 156.5; DB 2; Length 918;					
Matches 122; Conservative 99; Mismatches 229; Indels 161; Gaps 29;					
QY	305	QHLVQANVRNKKV----	LKDAVNITAKGITDYKKGFSAFEOQLLNYNVSRANCNKIIML	360	
Db	91	KRLPSNVNENIDFNLSKLITKDNTLIGEKNTPKNYTAFSDPN--SVENASADN----	145		
QY	361	FTDGGEEAAQIEFNKNKDKKV---	RVPFSVGQHNRGPIOWMACENKNGYYEIPSIG	417	
Db	146	-TDG-----SMNIIVSLKKONGVLEKVKIT-----	GLLSELEYIS	181	
QY	418	AIRINTQEYLDVLGRPMVLAGKAKOVQWNTNYDLAELGLVITGTP-----	VF	467	
Db	182	DQNLK-----VDVPNKENILASSIVEEQITNE-----	KISLTQGKVPSTFLTLYDTSF	232	
QY	468	NITGQFENKTINKNOILVMG-----	VDVSLIEDIKR--LTPRETL-CPNGYFFAIDPN	518	
Db	233	HVLSHDEKGSLKIRVSLSAKSSTKSKDFYIEGGFKQSFLDRISLKAKQGVNKTADE-	291		
QY	519	GIVLLHPNPQNPKRSQEPVTYLDFAELENDIKVBIRNMIDGESGEKTFRTLVSQDE	578		
Db	292	--IIKSLQLLPSSASED--KLNVLSAYSIDSVPDGLKFNFVSFEAKQGTf-----	338		
QY	579	RYIDGNRTYTPTPVNGTDSYALVLPTYFYIIKAKLEETIQARBSKGMKDSETLK-	637		
Db	339	---DKGVLTYELTQINGTRTERTEVKLDIOTFNIIKYRLDETILKIDSV--VLIKENSUKN	393		
QY	638	--PDNFESGYTFIAPRDYCNDLKISDNNTPELLNFNEF-IDRKTPNNPSCNADLINRVL	694		
Db	394	SLPSELVENKEI-----ENNQNEIELDSSKAKINVKNEFOVSVSTSANPEYN-----	L	442	
QY	695	LDAGTNE-----LVQNYWSKQKNICKVKARF--VVTDGGITRVYP--KEAGENHQE	742		
Db	443	IDGSUNVEVRIISRGDIVQKVRKLSGLTKLDANLFDVAKANYSNQLPGNLKAKDTNFKF	502		
QY	743	NPETEY-DSF-----YKRSLDN-----DNVFTAPY--FNKSGPCAYESG	779		
Db	503	GKTESTDSEFLKFPKNAKENNSILNLYKLSLENVKLNKFGQVSFDVFKTRGTCCKEKEN	562		
QY	780	INVSKAVEIYIQGKLL-----	KPAVVGIKIDVNSWIENFTKTSIRDPCAG	824	
Db	563	VVISKKTNFKQVLDFFDDQRYRYFDENDHFHKAIALTTKMTRNEFIK-----	610		
QY	825	PVCDCRKNSDV	835		
Db	611	-TVDAEFNDOL	620		

Search completed: February 10, 2003, 14:22:18  
Job time : 27.3759 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 10, 2003, 14:13:50 ; Search time 33.0366 Seconds  
(without alignments)  
4106.031 Million cell updates/sec

Title: US-10-090-827-6

Perfect score: 5349

Sequence: 1 MAACLLALTLTLFQSLIG.....TNLIFINVESKGTCPDTRL 1018

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_101002.\*

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- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*
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- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5349	100.0	1018	22	AAU01028
2	5349	100.0	1018	22	AAU01028
3	5349	100.0	1036	22	AAU01029
4	5349	100.0	1036	22	AAU01030
5	5349	100.0	1063	22	AAU01030
6	5349	100.0	1063	22	AAU01030
7	5349	100.0	1069	22	AAU01031
8	5349	100.0	1069	22	AAU01031
9	5349	100.0	1091	22	AAU01027
10	5349	100.0	1091	22	AAU01027

11	5288	98.9	1018	22	AAU01032	Human secreted sol
12	5288	98.9	1018	22	AAU01032	Porcine calcium ch
13	5288	98.9	1036	22	AAU01033	Human secreted sol
14	5288	98.9	1036	22	AAU01034	Porcine calcium ch
15	5288	98.9	1063	22	AAU01034	Human secreted sol
16	5288	98.9	1063	22	AAU01034	Porcine calcium ch
17	5288	98.9	1091	16	AAU01011	Human neuronal cal
18	5288	98.9	1091	16	AAU01011	Human calcium chan
19	5288	98.9	1091	21	AAU010576	Human calcium chan
20	5288	98.9	1091	22	AAU01035	Human secreted sol
21	5288	98.9	1091	22	AAU01035	Porcine calcium ch
22	5288	98.9	1091	22	AAU01035	Human calcium chan
23	5288	98.9	1091	14	AAU01035	Sequence of the al
24	5288	98.9	1110	19	AAU01035	Human calcium chan
25	5288	98.9	1110	19	AAU01035	Human neuronal cal
26	5288	98.9	1110	19	AAU01035	Human calcium chan
27	5288	98.9	1110	19	AAU01035	Human neuronal cal
28	5288	98.9	1110	19	AAU01035	Human calcium chan
29	5288	98.9	1110	19	AAU01035	Human neuronal cal
30	5288	98.9	1110	19	AAU01035	Human calcium chan
31	5288	98.9	1110	19	AAU01035	Human neuronal cal
32	5288	98.9	1110	19	AAU01035	Human calcium chan
33	5288	98.9	1110	19	AAU01035	Human neuronal cal
34	5288	98.9	1110	19	AAU01035	Human calcium chan
35	5288	98.9	1110	19	AAU01035	Human neuronal cal
36	5288	98.9	1110	19	AAU01035	Human calcium chan
37	5288	98.9	1110	19	AAU01035	Human neuronal cal
38	5288	98.9	1110	19	AAU01035	Human calcium chan
39	5288	98.9	1110	19	AAU01035	Human neuronal cal
40	5288	98.9	1110	19	AAU01035	Human calcium chan
41	5288	98.9	1110	19	AAU01035	Human neuronal cal
42	5288	98.9	1110	19	AAU01035	Human calcium chan
43	5288	98.9	1110	19	AAU01035	Human neuronal cal
44	5288	98.9	1110	19	AAU01035	Human calcium chan
45	5288	98.9	1110	19	AAU01035	Human neuronal cal

# ALIGNMENTS

RESULT 1  
AAU01028  
ID AAU01028 standard; Protein; 1018 AA.

XX AAU01028;

DT 04-JUL-2001 (first entry)

DE Pig secreted soluble alpha2delta calcium channel subunit #2 protein.

XX Pig; secreted calcium channel alpha2delta subunit; alpha2delta-2;

KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;

KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;

KW filter binding assay; wheat germ lectin flashplate assay; porcine.

XX Sus scrofa.

OS Sus scrofa.

PN WO200119870-A2.

XX 22-MAR-2001.

XX 18-SEP-2000; 2000WO-EP09137.

XX 16-SEP-1999; 99US-0397550.

XX (WARN ) WARNER LAMBERT CO.

PI Brown JP, Bertelli F;

XX WPI; 2001-235262/24.

XX N-PSDB; AAS01420.

PT Calcium channel alpha2delta subunits, useful in e.g. SPA assays,

Flashplate assays, Nickel Flashplate assays, Filter binding assays or Wheat Germ Lectin Flashplate assays -  
 Claim 31; Page 113-117; 160pp; English.

The present sequence represents pig secreted calcium channel alpha2delta subunit #2 which is soluble and retains the functional characteristics of the full length or wild type alpha2delta subunit from which it is derived. The invention relates to truncated alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins which retain their affinity for radioactively labelled gabapentin. The alpha2delta subunit is 1 of the components of the heteromultimeric voltage-dependent calcium channel (VDCC) complexes present in neuronal and non-neuronal tissues including heart and skeletal muscle. Numerous soluble forms of the human calcium channel alpha2delta subunits (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the porcine calcium channel alpha2delta subunits (AAU01027-AAU01031) are described. The secreted soluble alpha2delta subunit may be used in assays e.g. scintillation proximity assay (SPA), flashplate, nickel flashplate, filter binding or wheat germ lectin flashplate assays to detect or measure the binding or interaction of a ligand (e.g. gabapentin, L-Norleucine, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Isoleucine, L-Valine, Spermine and/or L-Phenylalanine) of a calcium channel alpha2delta subunit.

Sequence 1018 AA;

Query Match 100.0%; Score 5349; DB 22; Length 1018;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALITLQSLIGPSSQEPSPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
 DB 1 MAAGCLLALITLQSLIGPSSQEPSPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
 QY 61 YEKYQDLTYVEPNARQLVEIAARDIEKLLSNRSKALVRLALEAEKVQAAHQWREDFASN 120  
 DB 61 YEKYQDLTYVEPNARQLVEIAARDIEKLLSNRSKALVRLALEAEKVQAAHQWREDFASN 120  
 QY 121 EYVYNAKDDLDPKNDSEPGSQRIKPVFIDANFGRQISYQHAHVHIPTDIYEGSTIVL 180  
 DB 121 EYVYNAKDDLDPKNDSEPGSQRIKPVFIDANFGRQISYQHAHVHIPTDIYEGSTIVL 180  
 QY 181 NELNWTSALEDFVKKNREEDSLQWVFGSATGLARYPASPWDNSRTPNKIDLYDVR 240  
 DB 181 NELNWTSALEDFVKKNREEDSLQWVFGSATGLARYPASPWDNSRTPNKIDLYDVR 240  
 QY 241 RPWYIQAASPKDMLILDVSSVSGSLTKLIRTSVSEMLETTLSDDDFVNVSFNSNAQD 300  
 DB 241 RPWYIQAASPKDMLILDVSSVSGSLTKLIRTSVSEMLETTLSDDDFVNVSFNSNAQD 300  
 QY 301 VSCFOHLVQANVRNKKVLKDVANNITAKGITYDKGFSFAFEQLLNVSRANCKNIIML 360  
 DB 301 VSCFOHLVQANVRNKKVLKDVANNITAKGITYDKGFSFAFEQLLNVSRANCKNIIML 360  
 QY 361 FTDGGEERAQELFAKYNKKVRFTFSVGOHNDRGPQIWMACENKGYEIPISGAIR 420  
 DB 361 FTDGGEERAQELFAKYNKKVRFTFSVGOHNDRGPQIWMACENKGYEIPISGAIR 420  
 QY 421 INTQYLDVLGRPMVLADKAKOVQWTVNYLDALGLVITGTLVPFNITQGNENKTNLK 480  
 DB 421 INTQYLDVLGRPMVLADKAKOVQWTVNYLDALGLVITGTLVPFNITQGNENKTNLK 480  
 QY 481 NQLILGVMGVDVSLDIKRLTPRTLCPNGYFFAIDPNGYVLLHPNLPKNPKSQEPVTL 540  
 DB 481 NQLILGVMGVDVSLDIKRLTPRTLCPNGYFFAIDPNGYVLLHPNLPKNPKSQEPVTL 540  
 QY 541 DFLDALENDIKVEIRNKMIDSEKTRFLVKSQDERYIDKGNRYTWTTPVNGTDYSL 600  
 DB 541 DFLDALENDIKVEIRNKMIDSEKTRFLVKSQDERYIDKGNRYTWTTPVNGTDYSL 600  
 QY 601 ALVLPYTFYFKAKIETITQARSKGKMDSETLKPDPNFEEGYTFIAPRDCNDLKI 660  
 DB 601 ALVLPYTFYFKAKIETITQARSKGKMDSETLKPDPNFEEGYTFIAPRDCNDLKI 660

QY 661 SDNTEFLNFEFTDRKTPNPNPSCNTDLINRVLLDAGFTNELVQNYWSKQNIKGVKAR 720  
 DB 661 SDNTEFLNFEFTDRKTPNPNPSCNTDLINRVLLDAGFTNELVQNYWSKQNIKGVKAR 720  
 QY 721 FVVTGGITRVYPKRAGENQWQENPETEYDSFYKRSILDNDNVFTAPYFNKSGPGAYESGI 780  
 DB 721 FVVTGGITRVYPKRAGENQWQENPETEYDSFYKRSILDNDNVFTAPYFNKSGPGAYESGI 780  
 QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWENFTKTSIRDPCAGPVCDCKRNSDVMDCVI 840  
 DB 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWENFTKTSIRDPCAGPVCDCKRNSDVMDCVI 840  
 QY 841 LDGGFLLMANHDDTYNQIGRFFGEIDPSLMRHLNIVSYAFNKSIDYQSVCEPAAAPKQ 900  
 DB 841 LDGGFLLMANHDDTYNQIGRFFGEIDPSLMRHLNIVSYAFNKSIDYQSVCEPAAAPKQ 900  
 QY 901 GAGHSAYVPSIADILHIGWATAAAWSILOQFLLSLTFPPRLLEAVEMEDDDFTASLSKQ 960  
 DB 901 GAGHSAYVPSIADILHIGWATAAAWSILOQFLLSLTFPPRLLEAVEMEDDDFTASLSKQ 960  
 QY 961 SCITEQTYFFDNDKSFSGVLDGNCNCRIFHVEKLMNTNLIFIMVESKGTGCPDTRL 1018  
 DB 961 SCITEQTYFFDNDKSFSGVLDGNCNCRIFHVEKLMNTNLIFIMVESKGTGCPDTRL 1018

RESULT 2  
 AAB62252

ID AAB62252 standard; Protein; 1018 AA.

XX AAB62252;

DT 11-JUN-2001 (first entry)

XX Porcine calcium channel subunit alpha2delta-2.

XX Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;  
 nervous system disorder; pain; epilepsy; anxiety; pig.

XX Sus scrofa.

XX WO200120336-A2.

XX 22-MAR-2001.

PF 18-SEP-2000; 2000WO-EP09136.

PR 16-SEP-1999; 99US-0397549.

XX (WARN ) WARNER LAMBERT CO.

XX Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;

XX WPI; 2001-257902/26.

DR N-PSDB; AAF57557.

XX Competitive binding assay for screening ligands which bind a cerebral  
 cortical voltage-dependent calcium channel alpha2delta-1 subunit,  
 where the ligands identified are useful for treating disorders of the  
 nervous system, including pain -

XX Claim 8; Page 112-116; 158pp; English.

XX The invention relates to a new method for screening ligands which bind a  
 cerebral cortical voltage-dependent calcium channel alpha2delta subunit,  
 preferably alpha2delta-1 subunit. The method comprises contacting a  
 secreted soluble recombinant alpha2delta-1 subunit with a ligand of  
 interest and a labelled compound which binds the subunit, followed by  
 measuring the level of binding of the labelled compound to alpha2delta-1  
 subunit. The method is useful for screening ligands, preferably  
 biologically active products that modulate a nervous system function,  
 which bind a cerebral cortical voltage-dependent calcium channel  
 alpha2delta-1 subunit. The ligands identified by the method are useful



CC for treating disorders of the nervous system, including pain, epilepsy  
CC and anxiety. The present sequence represents a porcine calcium channel  
CC subunit alpha2delta-2.

XX  
SQ Sequence 1018 AA;  
Query Match 100.0%; Score 5349; DB 22; Length 1018;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAAGCLLALTLFOSLLIGPSSQPPFSAVTIKSWDKMQEDLVTLAKTAGVGNQLVDI 60  
DB 1 MAAGCLLALTLFOSLLIGPSSQPPFSAVTIKSWDKMQEDLVTLAKTAGVGNQLVDI 60  
QY 61 YEKYQDLYTVEPNARQLVEIARDIEKLLSNRSLVRLALEAEKVAQAHHQWREDFASN 120  
DB 61 YEKYQDLYTVEPNARQLVEIARDIEKLLSNRSLVRLALEAEKVAQAHHQWREDFASN 120  
QY 121 EVVYNAKDDLPKNDSEPGSQRIPKPFIDANFGRQISYQHAHVHPTDIYEGSTIVL 180  
DB 121 EVVYNAKDDLPKNDSEPGSQRIPKPFIDANFGRQISYQHAHVHPTDIYEGSTIVL 180  
QY 181 NELNWTSSALDEYFKKNREDDPSLLQWVGSATGLARYYPASPWVDSNRTPNKIDLYDYRR 240  
DB 181 NELNWTSSALDEYFKKNREDDPSLLQWVGSATGLARYYPASPWVDSNRTPNKIDLYDYRR 240  
QY 241 RPWYIQAASPKDMLILVDVSGSVSLTLKLI RTSVSEMLETSLDDDFVNVASFNSNAQD 300  
DB 241 RPWYIQAASPKDMLILVDVSGSVSLTLKLI RTSVSEMLETSLDDDFVNVASFNSNAQD 300  
QY 301 VSCFQHLVQANRKNKYLKDAVNNITAKGITDYKKGFSFAFEQLLNYSRANCNKIIML 360  
DB 301 VSCFQHLVQANRKNKYLKDAVNNITAKGITDYKKGFSFAFEQLLNYSRANCNKIIML 360  
QY 361 FTDGGEARAEIYAKYKDKKRVFTFSVGOHNYDRGPQIOWMACENKGYEYIPEISGAIR 420  
DB 361 FTDGGEARAEIYAKYKDKKRVFTFSVGOHNYDRGPQIOWMACENKGYEYIPEISGAIR 420  
QY 421 INTQEYLDVLRPMVLGAKAKOVQWNTVYLDALDELGLVITGTLVPVFNITQONENKTNL 480  
DB 421 INTQEYLDVLRPMVLGAKAKOVQWNTVYLDALDELGLVITGTLVPVFNITQONENKTNL 480  
QY 481 NQILIGVMGVDSLEDIKRLTPRFLPCPNNGYFFAIDPNGYVLLHLPNLPKPKSQEPVTL 540  
DB 481 NQILIGVMGVDSLEDIKRLTPRFLPCPNNGYFFAIDPNGYVLLHLPNLPKPKSQEPVTL 540  
QY 541 DFLDAELENDIKVEIRNKMIDGESKEKTRTLVKSQDERYIDKGNRTYTWTPVNGTDSL 600  
DB 541 DFLDAELENDIKVEIRNKMIDGESKEKTRTLVKSQDERYIDKGNRTYTWTPVNGTDSL 600  
QY 601 ALVLPITYSFYIIKAKIETITQARSKKGMKDSSETLKPDNFEESGYTFIAPRDYCNDLKI 660  
DB 601 ALVLPITYSFYIIKAKIETITQARSKKGMKDSSETLKPDNFEESGYTFIAPRDYCNDLKI 660  
QY 661 SDNNTFELNFEFTDRKTPNPNPCNTDLINRVLLDAGFTNELVQYNSKOKNKGVAR 720  
DB 661 SDNNTFELNFEFTDRKTPNPNPCNTDLINRVLLDAGFTNELVQYNSKOKNKGVAR 720  
QY 721 FVVTGGITRVYPKAGENWQENPETYEDSFYKRSLDNDNVFTAPYFNKSGPGAYESSI 780  
DB 721 FVVTGGITRVYPKAGENWQENPETYEDSFYKRSLDNDNVFTAPYFNKSGPGAYESSI 780  
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDCRNSVDVDCVI 840  
DB 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDCRNSVDVDCVI 840  
QY 841 LDDGGFLLMANHDDYTNQIGREFGEIDPSLMRHLVNI SVYAFNKSYDYQSCEPGAAPKQ 900  
DB 841 LDDGGFLLMANHDDYTNQIGREFGEIDPSLMRHLVNI SVYAFNKSYDYQSCEPGAAPKQ 900  
QY 901 GAGHSAYVPSTADILHIGWATAAAWSTLQOFLSLFLPRLLEAVEDEDDFTASLSKQ 960  
DB 901 GAGHSAYVPSTADILHIGWATAAAWSTLQOFLSLFLPRLLEAVEDEDDFTASLSKQ 960

QY 961 SCITEQTYFFDNDKSKFSGLDCGNCGRIFHVEKLMNTNLIFIMVSKGTCPCDTRL 1018  
DB 961 SCITEQTYFFDNDKSKFSGLDCGNCGRIFHVEKLMNTNLIFIMVSKGTCPCDTRL 1018

RESULT 3  
AAU01029  
ID AAU01029 standard; Protein; 1036 AA.

XX AAU01029;

DT 04-JUL-2001 (first entry)

XX Pig secreted soluble alpha2delta calcium channel subunit #3 protein.

XX Pig; secreted calcium channel alpha2delta subunit; alpha2delta-2;  
KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;  
KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;  
KW filter binding assay; wheat germ lectin flashplate assay; porcine.

OS Sus scrofa.

XX WO200119870-A2.

XX 22-MAR-2001.

XX 18-SEP-2000; 2000WO-EP09137.

XX 16-SEP-1999; 99US-0397550.

XX (WARN ) WARNER LAMBERT CO.

XX Brown JP, Bertelli F;

XX WPI; 2001-235262/24.

XX N-PSDB; AAS01421.

XX Calcium channel alpha2delta subunits, useful in e.g. SPA assays,  
PT Flashplate assays, Nickel Flashplate assays, Filter binding assays or  
PT Wheat Germ Lectin Flashplate assays -

XX Claim 31; Page 117-120; 160pp; English.

XX The present sequence represents pig secreted calcium channel alpha2delta  
CC subunit #3 which is soluble and retains the functional characteristics  
CC of the full length or wild type alpha2delta subunit from which it is  
CC derived. The invention relates to truncated alpha2delta-2, alpha2delta-3  
CC or alpha2delta-4 subunit soluble proteins which retain their affinity for  
CC radioactively labelled gabapentin. The alpha2delta subunit is 1 of the  
CC components of the heteromultimeric voltage-dependent calcium channel  
CC (VDCC) complexes present in neuronal and non-neuronal tissues including  
CC heart and skeletal muscle. Numerous soluble forms of the human calcium  
CC channel alpha2delta subunits (AAU01014-AAU01024 and AAU01032-AAU01038)  
CC and 5 soluble forms of the porcine calcium channel alpha2delta subunits  
CC (AAU01027-AAU01031) are described. The secreted soluble alpha2delta  
CC subunit may be used in assays e.g. scintillation proximity assay (SPA),  
CC flashplate, nickel flashplate, filter binding or wheat germ lectin  
CC flashplate assays to detect or measure the binding or interaction of a  
CC ligand (e.g. gabapentin, L-Norleucine, L-Allo-Isoleucine, L-methionine,  
CC L-leucine, L-Isoleucine, L-Valine, Spermine and/or L-Phenylalanine) of  
CC a calcium channel alpha2delta subunit.

XX Sequence 1036 AA;

! Query Match 100.0%; Score 5349; DB 22; Length 1036;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLFOSLLIGPSSQPPFSAVTIKSWDKMQEDLVTLAKTAGVGNQLVDI 60  
DB 1 MAAGCLLALTLFOSLLIGPSSQPPFSAVTIKSWDKMQEDLVTLAKTAGVGNQLVDI 60

QY 61 YEKYODLYTVEPNAROLVETAAARDIEKLLSNRSKALVRLALEAEKVQAAAHQWREDFASN 120  
 Db 61 YEKYODLYTVEPNAROLVETAAARDIEKLLSNRSKALVRLALEAEKVQAAAHQWREDFASN 120  
 QY 121 EVVYNAKDDLDPEKNDSPEGSQRIKPVFIDDAFNGRQISYQHAHVHIPTDIYEGSTIVL 180  
 Db 121 EVVYNAKDDLDPEKNDSPEGSQRIKPVFIDDAFNGRQISYQHAHVHIPTDIYEGSTIVL 180  
 QY 181 NELNWTSSALDEVFYKKNREEDPSLLWQVFGSATGLARYYPASPPWVDSNRTPNKIDLYDVR 240  
 Db 181 NELNWTSSALDEVFYKKNREEDPSLLWQVFGSATGLARYYPASPPWVDSNRTPNKIDLYDVR 240  
 QY 241 RPWYIQAASPKDMLILVDVSGVSGLTLLKIRTSVSEMLETLSDDDFVNVASFNSNAQD 300  
 Db 241 RPWYIQAASPKDMLILVDVSGVSGLTLLKIRTSVSEMLETLSDDDFVNVASFNSNAQD 300  
 QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDTYKKGFSFAFEQLLNNVSRANCKIIML 360  
 Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDTYKKGFSFAFEQLLNNVSRANCKIIML 360  
 QY 361 FTGDEGEERAQEIFAKYKNDKKVRVFTSVGQHNHYDRGPIQWMACENKGYIYEIPSIGAIR 420  
 Db 361 FTGDEGEERAQEIFAKYKNDKKVRVFTSVGQHNHYDRGPIQWMACENKGYIYEIPSIGAIR 420  
 QY 421 INTQFYLDVLGRPMVLAGDKAKQVQWNTNVLDALELGLVITGTLVFNITGQENKTNLK 480  
 Db 421 INTQFYLDVLGRPMVLAGDKAKQVQWNTNVLDALELGLVITGTLVFNITGQENKTNLK 480  
 QY 481 NQLILGVMGVDVSLDKRLTPRTCLPNGYFFAIDPNGYVLLHPNLPKNPKSQEPVTL 540  
 Db 481 NQLILGVMGVDVSLDKRLTPRTCLPNGYFFAIDPNGYVLLHPNLPKNPKSQEPVTL 540  
 QY 541 DFLDALENDIKVEIRKMKIDGEGEFTFTLVKSQDERVIDKGNRTYTTPVNGTDYSL 600  
 Db 541 DFLDALENDIKVEIRKMKIDGEGEFTFTLVKSQDERVIDKGNRTYTTPVNGTDYSL 600  
 QY 601 ALVLPYTSFYIYKAKIETITQARKSKGKMKDSETLAPDNFEEGTYFFIAPROYCNDLKI 660  
 Db 601 ALVLPYTSFYIYKAKIETITQARKSKGKMKDSETLAPDNFEEGTYFFIAPROYCNDLKI 660  
 QY 661 SDNTEFLNFPNEFIDRKTNPNSCNTDLINRVLLDAGFTNELVQVYWSQKNIKGVYKAR 720  
 Db 661 SDNTEFLNFPNEFIDRKTNPNSCNTDLINRVLLDAGFTNELVQVYWSQKNIKGVYKAR 720  
 QY 721 FVWTDGGITRVYPKEAGENQWENPETEDSFYKRSNDNDNYVFTAPYFNKSGGAYESGI 780  
 Db 721 FVWTDGGITRVYPKEAGENQWENPETEDSFYKRSNDNDNYVFTAPYFNKSGGAYESGI 780  
 QY 781 MVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPGAGPVCDCRNSDVMDCVI 840  
 Db 781 MVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPGAGPVCDCRNSDVMDCVI 840  
 QY 841 LDDGGFLMANHDDYTQIGRFFGEIDPSLMRHLVNI SVYAFNKSXDYQSVCEPGAAPKQ 900  
 Db 841 LDDGGFLMANHDDYTQIGRFFGEIDPSLMRHLVNI SVYAFNKSXDYQSVCEPGAAPKQ 900  
 QY 901 GAGHSAYVPSIADILHIGWATAAASIIQQFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
 Db 901 GAGHSAYVPSIADILHIGWATAAASIIQQFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
 QY 961 SCITEQTYQFFDNDKSFSGVLDGCNCSRIFFHVEKLMNTNLIIFTWESKGTGCPDTRL 1018  
 Db 961 SCITEQTYQFFDNDKSFSGVLDGCNCSRIFFHVEKLMNTNLIIFTWESKGTGCPDTRL 1018

## RESULT 4

ID AAB62253  
 ID AAB62253 standard; Protein; 1036 AA.

AC AAB62253;  
 AC AAB62253;

DT 11-JUN-2001 (first entry)

XX

DE Porcine calcium channel subunit alpha2delta-3.  
 XX Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;  
 KW nervous system disorder; pain; epilepsy; anxiety; pig.  
 XX OS Sus scrofa.  
 XX PN WO200120336-A2.  
 XX PD 22-MAR-2001.  
 XX PF 18-SEP-2000; 2000WO-EP09136.  
 XX PR 16-SEP-1999; 99US-0397549.  
 XX PA (WARN ) WARNER LAMBERT CO.  
 XX PI Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;  
 XX DR WPI; 2001-257902/26.  
 XX DR N-PSDB; AAF57558.  
 XX PT Competitive binding assay for screening ligands which bind a cerebral  
 PT cortical voltage-dependent calcium channel alpha2delta-1 subunit,  
 PT where the ligands identified are useful for treating disorders of the  
 PT nervous system, including pain -  
 XX Claim 8; Page 116-119; 158pp; English.  
 XX The invention relates to a new method for screening ligands which bind a  
 CC cerebral cortical voltage-dependent calcium channel alpha2delta subunit,  
 CC preferably alpha2delta-1 subunit. The method comprises contacting a  
 CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of  
 CC interest and a labelled compound which binds the subunit, followed by  
 CC measuring the level of binding of the labelled compound to alpha2delta-1  
 CC subunit. The method is useful for screening ligands, preferably  
 CC biologically active products that modulate a nervous system function,  
 CC which bind a cerebral cortical voltage-dependent calcium channel  
 CC alpha2delta-1 subunit. The ligands identified by the method are useful  
 CC for treating disorders of the nervous system, including pain, epilepsy  
 CC and anxiety. The present sequence represents a porcine calcium channel  
 CC subunit alpha2delta-3.  
 XX SQ Sequence 1036 AA;

Query Match 100.0%; Score 5349; DB 22; Length 1036;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLLFQSLIGPSSQEPFSAVTKSWDKMQEDLVTLAKTAGVNLVDI 60  
 Db 1 MAAGCLLALTLLFQSLIGPSSQEPFSAVTKSWDKMQEDLVTLAKTAGVNLVDI 60  
 QY 61 YEKYODLYTVEPNAROLVETAAARDIEKLLSNRSKALVRLALEAEKVQAAAHQWREDFASN 120  
 Db 61 YEKYODLYTVEPNAROLVETAAARDIEKLLSNRSKALVRLALEAEKVQAAAHQWREDFASN 120  
 QY 121 EVVYNAKDDLDPEKNDSPEGSQRIKPVFIDDAFNGRQISYQHAHVHIPTDIYEGSTIVL 180  
 Db 121 EVVYNAKDDLDPEKNDSPEGSQRIKPVFIDDAFNGRQISYQHAHVHIPTDIYEGSTIVL 180  
 QY 181 NELNWTSSALDEVFYKKNREEDPSLLWQVFGSATGLARYYPASPPWVDSNRTPNKIDLYDVR 240  
 Db 181 NELNWTSSALDEVFYKKNREEDPSLLWQVFGSATGLARYYPASPPWVDSNRTPNKIDLYDVR 240  
 QY 241 RPWYIQAASPKDMLILVDVSGVSGLTLLKIRTSVSEMLETLSDDDFVNVASFNSNAQD 300  
 Db 241 RPWYIQAASPKDMLILVDVSGVSGLTLLKIRTSVSEMLETLSDDDFVNVASFNSNAQD 300  
 QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDTYKKGFSFAFEQLLNNVSRANCKIIML 360  
 Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDTYKKGFSFAFEQLLNNVSRANCKIIML 360

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Qy 361 FTDGGEERAQEIFAKYKNDKVRVTFVSGQHNVDGRPIQWMAKNGKGYEIPISGAI 420
Db 361 FTDGGEERAQEIFAKYKNDKVRVTFVSGQHNVDGRPIQWMAKNGKGYEIPISGAI 420
Qy 421 INTQYLDVLRPMVLAGDRAKQVQWTVNYLDALGLVITGTLPVFNITGQENKTNLK 480
Db 421 INTQYLDVLRPMVLAGDRAKQVQWTVNYLDALGLVITGTLPVFNITGQENKTNLK 480
Qy 481 NQLILGVMGVDVSLIEDIKRLTPRTCLPNGYIFADPNGYVLLHPNLPKNPSQEPVTL 540
Db 481 NQLILGVMGVDVSLIEDIKRLTPRTCLPNGYIFADPNGYVLLHPNLPKNPSQEPVTL 540
Qy 541 DFLDAELNDIKVIRKMDIGSGEKTFTLVKSQDERIDKGNRTYTWTPVNGTDYSL 600
Db 541 DFLDAELNDIKVIRKMDIGSGEKTFTLVKSQDERIDKGNRTYTWTPVNGTDYSL 600
Qy 601 ALVLPTYSFYIKAKIETITQARSKKGMKDSKTLKPDNPFESGYTFIAPROYCNDLKI 660
Db 601 ALVLPTYSFYIKAKIETITQARSKKGMKDSKTLKPDNPFESGYTFIAPROYCNDLKI 660
Qy 661 SDNTEFLNENFIDRKTPNPNPCNTDLINRVLLDAGFTNELVONYSKQKNIKGVYKAR 720
Db 661 SDNTEFLNENFIDRKTPNPNPCNTDLINRVLLDAGFTNELVONYSKQKNIKGVYKAR 720
Qy 721 FVVTDDGGITRYYPKEAGENQWENPETEYDSFYKRSKSLDNNDYVFTAPYFNKSGPGAYESGI 780
Db 721 FVVTDDGGITRYYPKEAGENQWENPETEYDSFYKRSKSLDNNDYVFTAPYFNKSGPGAYESGI 780
Qy 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWENFTKTSIRDPKAGPVCDCRNSDVMDCVI 840
Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWENFTKTSIRDPKAGPVCDCRNSDVMDCVI 840
Qy 841 LDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVTAFNKSVDYQSVCEPGAAPKQ 900
Db 841 LDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVTAFNKSVDYQSVCEPGAAPKQ 900
Qy 901 GAGHRSAYVPSTADILHIGWATAAAMSILQOFLLSLTFPRLLBAVEMEDDDFTASLSKQ 960
Db 901 GAGHRSAYVPSTADILHIGWATAAAMSILQOFLLSLTFPRLLBAVEMEDDDFTASLSKQ 960
Qy 961 SCITEQTOYFNDNSKSFVLDGNCGRIFHVEKLMNTNLI FTWVSKGTCPCDTRL 1018
Db 961 SCITEQTOYFNDNSKSFVLDGNCGRIFHVEKLMNTNLI FTWVSKGTCPCDTRL 1018

RESULT 5
AAU01030
ID AAU01030 standard; Protein; 1063 AA.
XX AC AAU01030;
XX DT
XX DE
DE pig secreted soluble alpha2delta calcium channel subunit #4 protein.
XX KW pig; secreted calcium channel alpha2delta subunit; alpha2delta-2;
KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;
KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;
KW filter binding assay; wheat germ lectin flashplate assay; porcine.
XX OS
OS Sus scrofa.
XX PN
PN WO200119870-A2.
XX PD
PD 22-MAR-2001.
XX PF 18-SEP-2000; 2000WO-EP09137.
XX PR 16-SEP-1999; 99US-0397550.
XX PA (WARN ) WARNER LAMBERT CO.
XX PI Brown JP, Bertelli F;

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XX WPI: 2001-235262/24.
DR N-PSDB; AAS01422.
XX
PT Calcium channel alpha2delta subunits, useful in e.g. SPA assays,
PT Flashplate assays, Nickel Flashplate assays, Filter binding assays or
PT Wheat Germ Lectin Flashplate assays -
XX
PS Claim 31; Page 120-124; 160pp; English.
XX
CC The present sequence represents pig secreted calcium channel alpha2delta
CC subunit #4 which is soluble and retains the functional characteristics
CC of the full length or wild type alpha2delta subunit from which it is
CC derived. The invention relates to truncated alpha2delta-2, alpha2delta-3
CC or alpha2delta-4 subunit soluble proteins which retain their affinity for
CC radioactively labelled gabapentin. The alpha2delta subunit is 1 of the
CC components of the heteromultimeric voltage-dependent calcium channel
CC (VDCC) complexes present in neuronal and non-neuronal tissues including
CC heart and skeletal muscle. Numerous soluble forms of the human calcium
CC channel alpha2delta subunits (AAU01014-AAU01024 and AAU01032-AAU01038)
CC and 5 soluble forms of the porcine calcium channel alpha2delta subunits
CC (AAU01027-AAU01031) are described. The secreted soluble alpha2delta
CC subunit may be used in assays e.g. scintillation proximity assay (SPA),
CC flashplate, nickel flashplate, filter binding or wheat germ lectin
CC flashplate assays to detect or measure the binding or interaction of a
CC ligand (e.g. gabapentin, L-Norleucine, L-Allo-Isoleucine, L-methionine,
CC L-Leucine, L-Isoleucine, L-Valine, Spermine and/or L-Phenylalanine) of
CC a calcium channel alpha2delta subunit.
XX
SQ Sequence 1063 AA;
Query Match 100.0%; Score 5349; DB 22; Length 1063;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAAGCLLALTLTFLQSLLIGPSSQEPFPPSAVTIKSWDKMOEDLVTLAKTASGVNOLVDI 60
Db 1 MAAGCLLALTLTFLQSLLIGPSSQEPFPPSAVTIKSWDKMOEDLVTLAKTASGVNOLVDI 60
Qy 61 YEKYQDLYTVEPNARQVLAARDIEKLSNRKALVRLALEAEKVQAAHQRWDFASN 120
Db 61 YEKYQDLYTVEPNARQVLAARDIEKLSNRKALVRLALEAEKVQAAHQRWDFASN 120
Qy 121 EVVYNAKDDLDPEKNDSEPGSORIKPVFIDDFANFGQISYQHAHVHPIFDIYEGSTIVL 180
Db 121 EVVYNAKDDLDPEKNDSEPGSORIKPVFIDDFANFGQISYQHAHVHPIFDIYEGSTIVL 180
Qy 181 NELNWTSALEVPKKNREDEPSLLWQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVR 240
Db 181 NELNWTSALEVPKKNREDEPSLLWQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVR 240
Qy 241 RPWYIOGAASPDKMLILVDVSGSVSGTLKLIRTSVSEMLETSDDDFVNVASFNSNAQD 300
Db 241 RPWYIOGAASPDKMLILVDVSGSVSGTLKLIRTSVSEMLETSDDDFVNVASFNSNAQD 300
Qy 301 VSCFQHLVQANVRNKKVLDVANNITAKGTIDYKKGFSFAFEOLLNYSRANCNKITML 360
Db 301 VSCFQHLVQANVRNKKVLDVANNITAKGTIDYKKGFSFAFEOLLNYSRANCNKITML 360
Qy 361 FTDGGEERAQEIFAKYKNDKVRVTFVSGQHNVDGRPIQWMAKNGKGYEIPISGAI 420
Db 361 FTDGGEERAQEIFAKYKNDKVRVTFVSGQHNVDGRPIQWMAKNGKGYEIPISGAI 420
Qy 421 INTQYLDVLRPMVLAGDRAKQVQWTVNYLDALGLVITGTLPVFNITGQENKTNLK 480
Db 421 INTQYLDVLRPMVLAGDRAKQVQWTVNYLDALGLVITGTLPVFNITGQENKTNLK 480
Qy 481 NQLILGVMGVDVSLIEDIKRLTPRTCLPNGYIFADPNGYVLLHPNLPKNPSQEPVTL 540
Db 481 NQLILGVMGVDVSLIEDIKRLTPRTCLPNGYIFADPNGYVLLHPNLPKNPSQEPVTL 540
Qy 541 DFLDAELNDIKVIRKMDIGSGEKTFTLVKSQDERIDKGNRTYTWTPVNGTDYSL 600
Db 541 DFLDAELNDIKVIRKMDIGSGEKTFTLVKSQDERIDKGNRTYTWTPVNGTDYSL 600

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Db 541 DFLDAELNDIKVEIRNKMIDGESGKFTFLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
 QY 601 ALVLPYTFYIIKAKIETITQARSKKGMKDSKSETLKPDPNFESGVTFTIAPRDYCNLDKI 660  
 Db 601 ALVLPYTFYIIKAKIETITQARSKKGMKDSKSETLKPDPNFESGVTFTIAPRDYCNLDKI 660  
 QY 661 SDNTEFLNFEIDRKTNNPSCNTDLINRVLLDAGFTNVLQVYWSKQKNIKGVKAR 720  
 Db 661 SDNTEFLNFEIDRKTNNPSCNTDLINRVLLDAGFTNVLQVYWSKQKNIKGVKAR 720  
 QY 721 FVVTGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSPGAYESGI 780  
 Db 721 FVVTGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSPGAYESGI 780  
 QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDCKRNSDVMDCVI 840  
 Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDCKRNSDVMDCVI 840  
 QY 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLNYSVYAFNKSVDYQSCVCEGAPKQ 900  
 Db 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLNYSVYAFNKSVDYQSCVCEGAPKQ 900  
 QY 901 GAGHSAYVPSIADILHIGWATAAAWSILOQFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
 Db 901 GAGHSAYVPSIADILHIGWATAAAWSILOQFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
 QY 961 SCITQOTQFFDNDKSGFSGVLDGNCNKRIFHVEKLMNTNLFIMVESKGTCPDTRL 1018  
 Db 961 SCITQOTQFFDNDKSGFSGVLDGNCNKRIFHVEKLMNTNLFIMVESKGTCPDTRL 1018

RESULT 6  
 AAB62254  
 ID AAB62254 standard; Protein; 1063 AA.  
 AC AAB62254;  
 XX  
 DT 11-JUN-2001 (first entry)  
 XX  
 DE Porcine calcium channel subunit alpha2delta-4.  
 KW Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;  
 EW nervous system disorder; pain; epilepsy; anxiety; pig.  
 XX  
 OS Sus scrofa.  
 XX  
 PN WO200120336-A2.  
 XX  
 PD 22-MAR-2001.  
 XX  
 PF 18-SEP-2000; 2000WO-EP09136.  
 XX  
 PR 16-SEP-1999; 99US-0397549.  
 XX  
 PA (WARN ) WARNER LAMBERT CO.  
 XX  
 PI Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;  
 XX  
 DR WPI; 2001-257902/26.  
 DR N-PSDB; AAF57559.  
 XX  
 PT Competitive binding assay for screening ligands which bind a cerebral  
 PT cortical voltage-dependent calcium channel alpha2delta-1 subunit,  
 PT where the ligands identified are useful for treating disorders of the  
 PT nervous system, including pain -  
 XX  
 PS Claim 8; Page 119-122; 158pp; English.  
 XX  
 CC The invention relates to a new method for screening ligands which bind a  
 CC cerebral cortical voltage-dependent calcium channel alpha2delta subunit,  
 CC preferably alpha2delta-1 subunit. The method comprises contacting a  
 CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of  
 CC interest and a labelled compound which binds the subunit, followed by

CC measuring the level of binding of the labelled compound to alpha2delta-1  
 CC subunit. The method is useful for screening ligands, preferably  
 CC biologically active products that modulate a nervous system function,  
 CC which bind a cerebral cortical voltage-dependent calcium channel  
 CC alpha2delta-1 subunit. The ligands identified by the method are useful  
 CC for treating disorders of the nervous system, including pain, epilepsy  
 CC and anxiety. The present sequence represents a porcine calcium channel  
 CC subunit alpha2delta-4.  
 XX  
 SQ Sequence 1063 AA;

Query Match 100.0%; Score 5349; DB 22; Length 1063;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALVTLFQSLIGPSSQEPFPPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60  
 Db 1 MAAGCLLALVTLFQSLIGPSSQEPFPPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60  
 QY 61 YEKYQDLTYVEPNNAQOLVEIAARDIEKLLSNRSKALVRLALEAEKVOAAHQRDFASN 120  
 Db 61 YEKYQDLTYVEPNNAQOLVEIAARDIEKLLSNRSKALVRLALEAEKVOAAHQRDFASN 120  
 QY 121 EYVYNAKDDLDEKNDSEPGSQRIKPVFIDDAFNGRQISYQHAAYHIPTDIYEGSTIVL 180  
 Db 121 EYVYNAKDDLDEKNDSEPGSQRIKPVFIDDAFNGRQISYQHAAYHIPTDIYEGSTIVL 180  
 QY 181 NELNWTLSALDEVKPKNREDEPSLLQWFGSATGLARYYPASPWDNSRTPNKIDLDVRR 240  
 Db 181 NELNWTLSALDEVKPKNREDEPSLLQWFGSATGLARYYPASPWDNSRTPNKIDLDVRR 240  
 QY 241 RPWYIOGAASPKDMLILVDVSGSVGLTLKIRTSVSEMLETSLSDDDFVNFASFNSNAOD 300  
 Db 241 RPWYIOGAASPKDMLILVDVSGSVGLTLKIRTSVSEMLETSLSDDDFVNFASFNSNAOD 300  
 QY 301 VSCFOHLVQANVKNKKVLDKAVNNITAKITDYKKGFSFAFOLLNYSRANCNKIIML 360  
 Db 301 VSCFOHLVQANVKNKKVLDKAVNNITAKITDYKKGFSFAFOLLNYSRANCNKIIML 360  
 QY 361 FTDGEERAQEIFAKYNDKKKRVVFTFSVGOHNYDRGPIQWACENKGYIETPSTGAIR 420  
 Db 361 FTDGEERAQEIFAKYNDKKKRVVFTFSVGOHNYDRGPIQWACENKGYIETPSTGAIR 420  
 QY 421 INTQEYLDVLGRPMVLGAKAKQVQWNTNYLDALGLVITGLPVFNITQONKNTLK 480  
 Db 421 INTQEYLDVLGRPMVLGAKAKQVQWNTNYLDALGLVITGLPVFNITQONKNTLK 480  
 QY 481 NQILGVMGVDVSLIEDIKRLTPRFTLCPNGYFAIDPNGYVLLHNPKNPKSQEPVTL 540  
 Db 481 NQILGVMGVDVSLIEDIKRLTPRFTLCPNGYFAIDPNGYVLLHNPKNPKSQEPVTL 540  
 QY 541 DFLDAELNDIKVEIRNKMIDGESGKFTFLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
 Db 541 DFLDAELNDIKVEIRNKMIDGESGKFTFLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
 QY 601 ALVLPYTFYIIKAKIETITQARSKKGMKDSKSETLKPDPNFESGVTFTIAPRDYCNLDKI 660  
 Db 601 ALVLPYTFYIIKAKIETITQARSKKGMKDSKSETLKPDPNFESGVTFTIAPRDYCNLDKI 660  
 QY 661 SDNTEFLNFEIDRKTNNPSCNTDLINRVLLDAGFTNVLQVYWSKQKNIKGVKAR 720  
 Db 661 SDNTEFLNFEIDRKTNNPSCNTDLINRVLLDAGFTNVLQVYWSKQKNIKGVKAR 720  
 QY 721 FVVTGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSPGAYESGI 780  
 Db 721 FVVTGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSPGAYESGI 780  
 QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDCKRNSDVMDCVI 840  
 Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDCKRNSDVMDCVI 840  
 QY 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLNYSVYAFNKSVDYQSCVCEGAPKQ 900  
 Db 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLNYSVYAFNKSVDYQSCVCEGAPKQ 900

Db 841 LDDGGFLMANHDDYTQIGRFFGEIDPSLMRHLVNI SVAFNKSVDYQSVCEFGAAPKQ 900  
 QY 901 GAGHSAYVPSIADILHGWATAAASIILOQFLSLTFPRLLAEVMEDEDDFTASLSKQ 960  
 Db 901 GAGHSAYVPSIADILHGWATAAASIILOQFLSLTFPRLLAEVMEDEDDFTASLSKQ 960  
 QY 961 SCITEQTYFFDNDKSFSGVLDGCGNSRIFHVEKLMNTNLIIFIMVESKGTCPDTRL 1018  
 Db 961 SCITEQTYFFDNDKSFSGVLDGCGNSRIFHVEKLMNTNLIIFIMVESKGTCPDTRL 1018

RESULT 7  
 AAU01031  
 ID AAU01031 standard; Protein; 1069 AA.  
 XX  
 AC AAU01031;  
 DT 04-JUL-2001 (first entry)  
 XX

Pig secreted soluble alpha2delta calcium channel subunit #5 protein.  
 DE  
 XX  
 KW Pig; secreted calcium channel alpha2delta subunit; alpha2delta-2;  
 KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;  
 KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;  
 KW filter binding assay; wheat germ lectin flashplate assay; porcine.  
 OS  
 XX Sus scrofa.  
 XX  
 PN WO200119870-A2.  
 XX  
 PD 22-MAR-2001.  
 XX  
 PF 18-SEP-2000; 2000WO-EP09137.  
 XX  
 PR 16-SEP-1999; 99US-0397550.  
 XX  
 XX (WARN ) WARNER LAMBERT CO.  
 PA Brown JP, Bertelli F;  
 PI WPI; 2001-235262/24.  
 XX  
 XX Calcium channel alpha2delta subunits, useful in e.g. SPA assays,  
 PT Flashplate assays, Nickel Flashplate assays, Filter binding assays or  
 PT Wheat Germ Lectin Flashplate assays -  
 XX  
 PS Disclosure; Page 124-127; 160pp; English.  
 XX

The present sequence represents pig secreted calcium channel alpha2delta subunit #5 which is soluble and retains the functional characteristics of the full length or wild type alpha2delta subunit from which it is derived. The invention relates to truncated alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins which retain their affinity for radioactively labelled gabapentin. The alpha2delta subunit is 1 of the components of the heteromultimeric voltage-dependent calcium channel (VDCC) complexes present in neuronal and non-neuronal tissues including heart and skeletal muscle. Numerous soluble forms of the human calcium channel alpha2delta subunits (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the porcine calcium channel alpha2delta subunits (AAU01027-AAU01031) are described. The secreted soluble alpha2delta subunit may be used in assays e.g. scintillation proximity assay (SPA), flashplate, nickel flashplate, filter binding or wheat germ lectin flashplate assays to detect or measure the binding or interaction of a ligand (e.g. gabapentin, L-Norleucine, L-Allo-Isoleucine, L-methionine, L-leucine, L-Isoleucine, L-Valine, Spermine and/or L-Phenylalanine) of a calcium channel alpha2delta subunit.

XX Sequence 1069 AA;  
 Query Match 100.0%; Score 5349; DB 22; Length 1069;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCILLALTLTLFQSLILGPSQEPFPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
 Db 1 MAAGCILLALTLTLFQSLILGPSQEPFPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
 QY 61 YEKYQDLYTEPNARQOLVEIAARDIEKLLSNRSKALVRLALEAEKVAQAAHWRDFASN 120  
 Db 61 YEKYQDLYTEPNARQOLVEIAARDIEKLLSNRSKALVRLALEAEKVAQAAHWRDFASN 120  
 QY 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFIDDFANFRQISYQHAHVHIPTDIYEGSTIVL 180  
 Db 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFIDDFANFRQISYQHAHVHIPTDIYEGSTIVL 180  
 QY 181 NELNWTALDEVPFKKNREEDPSLLWQVFSATGLARYYPASPWVDSRPNKIDLDYDVR 240  
 Db 181 NELNWTALDEVPFKKNREEDPSLLWQVFSATGLARYYPASPWVDSRPNKIDLDYDVR 240  
 QY 241 RPWYIOGAASPKDMLILVDVSGSVGLTLKLRISYSEMLETLSDDDFNVNVSFNSNAQD 300  
 Db 241 RPWYIOGAASPKDMLILVDVSGSVGLTLKLRISYSEMLETLSDDDFNVNVSFNSNAQD 300  
 QY 301 VSCFQHLVQANVRNKKVLDVANNITAKGITDYKGFSAFEQLLNYSRANCNKIIML 360  
 Db 301 VSCFQHLVQANVRNKKVLDVANNITAKGITDYKGFSAFEQLLNYSRANCNKIIML 360  
 QY 361 FTDGGERAQEIIFAKYNNKKKVVFTFSVCOHNDYDRGPIQWMACENKGYIYIPIPSIGAIR 420  
 Db 361 FTDGGERAQEIIFAKYNNKKKVVFTFSVGOHNDYDRGPIQWMACENKGYIYIPIPSIGAIR 420  
 QY 421 INTQEYLDVLGRPMVLADGKAKOVQNTVNYLDALGLVITGTLPVFNITQGENKTNLK 480  
 Db 421 INTQEYLDVLGRPMVLADGKAKOVQNTVNYLDALGLVITGTLPVFNITQGENKTNLK 480  
 QY 481 NQLILVGMGVDSVLEDIKRLTPRFTLCPNGYIFAIDPNGYVLLHPLNLPKNPKSQEPVTL 540  
 Db 481 NQLILVGMGVDSVLEDIKRLTPRFTLCPNGYIFAIDPNGYVLLHPLNLPKNPKSQEPVTL 540  
 QY 541 DFLDAELENDIKVEIRNKMIDGESGEKTFRTLKVSQDERYIDKGNRTYTWTPVNGTDYSL 600  
 Db 541 DFLDAELENDIKVEIRNKMIDGESGEKTFRTLKVSQDERYIDKGNRTYTWTPVNGTDYSL 600  
 QY 601 ALVLTYSFYIRAKIETITQARSKKGMKDSSETLPDNFESGYTFIAPRYCNDLKI 660  
 Db 601 ALVLTYSFYIRAKIETITQARSKKGMKDSSETLPDNFESGYTFIAPRYCNDLKI 660  
 QY 661 SDNTEFLNFEIDRKTNNPNSCNTDLINRVLLDAGFTNELVQNYWSKQNKIKGVKAR 720  
 Db 661 SDNTEFLNFEIDRKTNNPNSCNTDLINRVLLDAGFTNELVQNYWSKQNKIKGVKAR 720  
 QY 721 FVVTDDGGITRVYPKEAGENQENPETVEDSFYKBSLNDNMYVETAPYFNKSGPGAYESGI 780  
 Db 721 FVVTDDGGITRVYPKEAGENQENPETVEDSFYKBSLNDNMYVETAPYFNKSGPGAYESGI 780  
 QY 781 MYSKAVEIYIQGLLKPAVVGVIKIDVNSWIENFTKTSIRDPGAGPVCDCKRNSDVMDCVI 840  
 Db 781 MYSKAVEIYIQGLLKPAVVGVIKIDVNSWIENFTKTSIRDPGAGPVCDCKRNSDVMDCVI 840  
 QY 841 LDDGGFLMANHDDYTQIGRFFGEIDPSLMRHLVNI SVAFNKSVDYQSVCEFGAAPKQ 900  
 Db 841 LDDGGFLMANHDDYTQIGRFFGEIDPSLMRHLVNI SVAFNKSVDYQSVCEFGAAPKQ 900  
 QY 901 GAGHSAYVPSIADILHGWATAAASIILOQFLSLTFPRLLAEVMEDEDDFTASLSKQ 960  
 Db 901 GAGHSAYVPSIADILHGWATAAASIILOQFLSLTFPRLLAEVMEDEDDFTASLSKQ 960  
 QY 961 SCITEQTYFFDNDKSFSGVLDGCGNSRIFHVEKLMNTNLIIFIMVESKGTCPDTRL 1018  
 Db 961 SCITEQTYFFDNDKSFSGVLDGCGNSRIFHVEKLMNTNLIIFIMVESKGTCPDTRL 1018

RESULT 8  
 AAB62255  
 ID AAB62255 standard; Protein; 1069 AA.  
 XX

AC AAB62255;  
 XX 11-JUN-2001 (first entry)  
 XX Porcine calcium channel subunit alpha2delta-1 deletion mutant.  
 XX  
 DE Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;  
 XX nervous system disorder; pain; epilepsy; anxiety; pig; mutant.  
 KW  
 KW Sus scrofa.  
 XX  
 OS WO200120336-A2.  
 XX  
 PN 22-MAR-2001.  
 XX  
 PD 18-SEP-2000; 2000WO-EP09136.  
 XX  
 PF 16-SEP-1999; 99US-0397549.  
 XX  
 PR (WARN ) WARNER LAMBERT CO.  
 XX  
 PA Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;  
 XX WPI; 2001-257902/26.  
 XX  
 PT Competitive binding assay for screening ligands which bind a cerebral  
 PT cortical voltage-dependent calcium channel alpha2delta-1 subunit,  
 PT where the ligands identified are useful for treating disorders of the  
 PT nervous system, including pain -  
 XX  
 XX Claim 8; Page 122-126; 158pp; English.  
 XX  
 CC The invention relates to a new method for screening ligands which bind a  
 CC cerebral cortical voltage-dependent calcium channel alpha2delta subunit,  
 CC preferably alpha2delta-1 subunit. The method comprises contacting a  
 CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of  
 CC interest and a labelled compound which binds the subunit, followed by  
 CC measuring the level of binding of the labelled compound to alpha2delta-1  
 CC subunit. The method is useful for screening ligands, preferably  
 CC biologically active products that modulate a nervous system function,  
 CC which bind a cerebral cortical voltage-dependent calcium channel  
 CC alpha2delta-1 subunit. The ligands identified by the method are useful  
 CC for treating disorders of the nervous system, including pain, epilepsy  
 CC and anxiety. The present sequence represents a porcine calcium channel  
 CC subunit alpha2delta-1 deletion mutant.  
 XX  
 XX Sequence 1069 AA;  
 SQ

Query Match 100.0%; Score 5349; DB 22; Length 1069;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAAGCLLALTTLFQSLIGPSSQEPFPPSAVTIKSWVDKMQEDLVTLAKTAGVGNQLVDI 60  
 DB 1 MAAGCLLALTTLFQSLIGPSSQEPFPPSAVTIKSWVDKMQEDLVTLAKTAGVGNQLVDI 60  
 QY 61 YEKYQDLYTVENPNARQVLAARQIEKLLSNRSKALVRLALEAEKVOAAHQWREDFASN 120  
 DB 61 YEKYQDLYTVENPNARQVLAARQIEKLLSNRSKALVRLALEAEKVOAAHQWREDFASN 120  
 QY 121 EYVYNNAKDDLDPKENDSEPGSQRIKPVFIDANFGROIYSQHAHVHPDPTDIYEGSTIVL 180  
 DB 121 EYVYNNAKDDLDPKENDSEPGSQRIKPVFIDANFGROIYSQHAHVHPDPTDIYEGSTIVL 180  
 QY 181 NELNWTSSALDEVFKKNREEDPSLLQWFGSATGLARYYPASPWWVDSNRTPNKIDLYDVR 240  
 DB 181 NELNWTSSALDEVFKKNREEDPSLLQWFGSATGLARYYPASPWWVDSNRTPNKIDLYDVR 240  
 QY 241 RPWYIQGAASPKDMLILVDVSGVSGLTLLKIRTSVSEMLETISDDDFVNVASFNSNAQD 300  
 DB 241 RPWYIQGAASPKDMLILVDVSGVSGLTLLKIRTSVSEMLETISDDDFVNVASFNSNAQD 300  
 QY 301 VSCFQHLVQANVRNKKVLKAVNNITAKGITDYKKGFSFAFQQLNLYNVRANCNKIIML 360

DB 301 VSCFQHLVQANVRNKKVLKAVNNITAKGITDYKKGFSFAFQQLNLYNVRANCNKIIML 360  
 QY 361 FTDGGEERAQELFAKYNKDKKVRVFTESVGOHNYDRGPLOMACENKGYEYFISGAIR 420  
 DB 361 FTDGGEERAQELFAKYNKDKKVRVFTESVGOHNYDRGPLOMACENKGYEYFISGAIR 420  
 QY 421 INTQBYLDVLGRPMVLGADKAKOVQWNTVYLDALDELGLVITGTLVPFNITQONENKTNLK 480  
 DB 421 INTQBYLDVLGRPMVLGADKAKOVQWNTVYLDALDELGLVITGTLVPFNITQONENKTNLK 480  
 QY 481 NOLILGVNMGVDVSLIEDIKRLTPRFTLCPNGYFFAIDPNNGYVLLHPNLPKPKSQEPVTL 540  
 DB 481 NOLILGVNMGVDVSLIEDIKRLTPRFTLCPNGYFFAIDPNNGYVLLHPNLPKPKSQEPVTL 540  
 QY 541 DFLDAELENDIKVEIRNKMIDGESCEKTFRTLVKSQDERYIDKGNRTYTTPVNGTDSL 600  
 DB 541 DFLDAELENDIKVEIRNKMIDGESCEKTFRTLVKSQDERYIDKGNRTYTTPVNGTDSL 600  
 QY 601 ALVLPYTSFYIYKAKIETITQARSKKGMKDSSETLKPDPNFEESSGYTFIAPRDYCNDLKI 660  
 DB 601 ALVLPYTSFYIYKAKIETITQARSKKGMKDSSETLKPDPNFEESSGYTFIAPRDYCNDLKI 660  
 QY 661 SDNTEFLNENEFIDRKTPNPNPCNTDNLNRVLLDAGFTNELVQNTWSKQNKIKGVYKAR 720  
 DB 661 SDNTEFLNENEFIDRKTPNPNPCNTDNLNRVLLDAGFTNELVQNTWSKQNKIKGVYKAR 720  
 QY 721 FVWTDGGITRVYPKEAGENQENPETYEDSFYKSLDNDNVTFTAPYFNKSGGCAYESGI 780  
 DB 721 FVWTDGGITRVYPKEAGENQENPETYEDSFYKSLDNDNVTFTAPYFNKSGGCAYESGI 780  
 QY 781 MYSKAVEIYIGKLLKPAVVGKIDVNSWIENTFTKTSIRDCAGPVCDCRNSDVMDCVI 840  
 DB 781 MYSKAVEIYIGKLLKPAVVGKIDVNSWIENTFTKTSIRDCAGPVCDCRNSDVMDCVI 840  
 QY 841 LDDGGFLLMANHDDYTNOIGRFGEIDPMSLRHLVNIYSVAFNKSVDYQSVCEPGAAPKQ 900  
 DB 841 LDDGGFLLMANHDDYTNOIGRFGEIDPMSLRHLVNIYSVAFNKSVDYQSVCEPGAAPKQ 900  
 QY 901 GAGHSAYVPSIADILHIGWATAAASILQQFLLSLTPRLLLEAVEMEDDDFTASLSKQ 960  
 DB 901 GAGHSAYVPSIADILHIGWATAAASILQQFLLSLTPRLLLEAVEMEDDDFTASLSKQ 960  
 QY 961 SCITEQYQYFFDNDKSFSGVLDGNCSTRFHVEKLMNTNLIIFIMVESKGTCPDTRL 1018  
 DB 961 SCITEQYQYFFDNDKSFSGVLDGNCSTRFHVEKLMNTNLIIFIMVESKGTCPDTRL 1018  
 RESULT 9  
 AAU01027  
 ID AAU01027 standard; Protein; 1091 AA.  
 XX  
 AC AAU01027;  
 XX  
 DT 04-JUL-2001 (first entry)  
 XX  
 DE Pig secreted soluble alpha2delta calcium channel subunit #1 protein.  
 XX  
 KW Pig; secreted calcium channel alpha2delta subunit; alpha2delta-2;  
 KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;  
 KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;  
 KW filter binding assay; wheat germ lectin flashplate assay; porcine.  
 XX  
 OS Sus scrofa.  
 XX  
 PN WO200119870-A2.  
 XX  
 PD 22-MAR-2001.  
 XX  
 PF 18-SEP-2000; 2000WO-EP09137.  
 XX  
 PR 16-SEP-1999; 99US-0397550.  
 XX

(WARN ) WARNER LAMBERT CO.

Brown JP, Bertelli F;

WPI; 2001-235262/24.

N-PSDB; AAS01419.

Calcium channel alpha2delta subunits, useful in e.g. SPA assays, Flashplate assays, Nickel Flashplate assays, Filter binding assays or Wheat Germ Lectin Flashplate assays -

Claim 30; Page 110-113; 160pp; English.

The present sequence represents pig secreted calcium channel alpha2delta subunit #1 which is soluble and retains the functional characteristics of the full length or wild type alpha2delta subunit from which it is derived. The invention relates to truncated alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins which retain their affinity for radioactively labelled gabapentin. The alpha2delta subunit is 1 of the components of the heteromultimeric voltage-dependent calcium channel (VDCC) complexes present in neuronal and non-neuronal tissues including heart and skeletal muscle. Numerous soluble forms of the human calcium channel alpha2delta subunits (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the porcine calcium channel alpha2delta subunits (AAU01027-AAU01031) are described. The secreted soluble alpha2delta subunit may be used in assays e.g. scintillation proximity assay (SPA), flashplate, nickel flashplate, filter binding or wheat germ lectin flashplate assays to detect or measure the binding or interaction of a ligand (e.g. gabapentin, L-Norleucine, L-Allo-Isoleucine, L-methionine, L-leucine, L-isoleucine, L-Valine, Spermine and/or L-Phenylalanine) of a calcium channel alpha2delta subunit.

Sequence 1091 AA;

Query Match 100.0%; Score 5349; DB 22; Length 1091;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PA	541	DFDLAELENDIKVEIRNKMIDGESGEKTRTLVKSDERYIDKGNRTYTWTVPNGTDYSL	600
XX			
PI	541	DFDLAELENDIKVEIRNKMIDGESGEKTRTLVKSDERYIDKGNRTYTWTVPNGTDYSL	600
XX			
DR			
DR	601	ALVLPYSEYIKAKTEETITQARSKKGMKDSKSELTLPDNFEESGYTFTAPRDYCNLDKI	660
XX			
DR	601	ALVLPYSEYIKAKTEETITQARSKKGMKDSKSELTLPDNFEESGYTFTAPRDYCNLDKI	660
XX			
PT	661	SDNNTFELNFEFIDRKTTPNPNPSCNTDLINRVLLDAGFTNVLQVYNSKQKNIKGVKAR	720
PT			
PT	661	SDNNTFELNFEFIDRKTTPNPNPSCNTDLINRVLLDAGFTNVLQVYNSKQKNIKGVKAR	720
XX			
PS	721	FVYDGGITRVYKKEAGNENQENPETEYDSFYKRSIDNDNYVFTAPYFNKSGPGAYESGI	780
XX			
CC	721	FVYDGGITRVYKKEAGNENQENPETEYDSFYKRSIDNDNYVFTAPYFNKSGPGAYESGI	780
CC			
CC	781	MYSKAVEIYIQGKLLKPAVVGKIDVNSWIENTTTSIRDPKAGPVCCDKRNSDMDCVI	840
CC			
CC	781	MYSKAVEIYIQGKLLKPAVVGKIDVNSWIENTTTSIRDPKAGPVCCDKRNSDMDCVI	840
CC			
CC	841	LDDGGFLLMANHDDYTNQIGRFFGEIDPSIMRHLVNIISVYAFNKSVDYQSVCEPGAAPKQ	900
CC			
CC	841	LDDGGFLLMANHDDYTNQIGRFFGEIDPSIMRHLVNIISVYAFNKSVDYQSVCEPGAAPKQ	900
CC			
CC	901	GAGHRSAYVPSIADIHIGWATAAAWSILQOFLSLTPRLLLEAVEMEDDDFTASLSKQ	960
CC			
CC	901	GAGHRSAYVPSIADIHIGWATAAAWSILQOFLSLTPRLLLEAVEMEDDDFTASLSKQ	960
CC			
CC	961	SCITEQTQVFFDNDKSKFSQVLDGCGNCSRFHFVHEKLMNTNLIIFIMVESKGTCPCDTRL	1018
CC			
CC	961	SCITEQTQVFFDNDKSKFSQVLDGCGNCSRFHFVHEKLMNTNLIIFIMVESKGTCPCDTRL	1018
XX			

RESULT 10  
 AAB62251  
 ID AAB62251 standard; Protein; 1091 AA.  
 XX  
 AC AAB62251;  
 XX  
 DT 11-JUN-2001 (first entry)  
 XX  
 DE Porcine calcium channel subunit alpha2delta-1.  
 XX  
 KW Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;  
 KW nervous system disorder; pain; epilepsy; anxiety; pig.  
 XX  
 OS Sus scrofa.  
 XX  
 PN WC200120336-A2.  
 XX  
 PD 22-MAR-2001.  
 XX  
 PF 18-SEP-2000; 2000WO-EP09136.  
 XX  
 PR 16-SEP-1999; 99US-0397549.  
 XX  
 PA (WARN ) WARNER LAMBERT CO.  
 XX  
 PI Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;  
 XX  
 DR WPI; 2001-257902/26.  
 DR N-PSDB; AAF57556.  
 XX  
 PT Competitive binding assay for screening ligands which bind a cerebral  
 PT cortical voltage-dependent calcium channel alpha2delta-1 subunit,  
 PT where the ligands identified are useful for treating disorders of the  
 PT nervous system, including pain -  
 XX  
 PS Claim 7; Page 109-112; 158pp; English.  
 CC  
 CC The invention relates to a new method for screening ligands which bind a  
 CC cerebral cortical voltage-dependent calcium channel alpha2delta subunit,



CC preferably alpha2delta-1 subunit. The method comprises contacting a  
 CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of  
 CC interest and a labelled compound which binds the subunit, followed by  
 CC measuring the level of binding of the labelled compound to alpha2delta-1  
 CC subunit. The method is useful for screening ligands, preferably  
 CC biologically active products that modulate a nervous system function,  
 CC which bind a cerebral cortical voltage-dependent calcium channel  
 CC alpha2delta-1 subunit. The ligands identified by the method are useful  
 CC for treating disorders of the nervous system, including pain, epilepsy  
 CC and anxiety. The present sequence represents a porcine calcium channel  
 CC subunit alpha2delta-1.  
 CC  
 XX Sequence 1091 AA;  
 SQ

Query Match 100.0%; Score 5349; DB 22; Length 1091;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLFOSLLIGSPSPFPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
 Db 1 MAAGCLLALTLFOSLLIGSPSPFPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

QY 61 YEKYQDLTYVEPNNAQQLVEAARDEIKLLSNRSKALVRLALEAEKVQAAHQRWEDFASN 120  
 Db 61 YEKYQDLTYVEPNNAQQLVEAARDEIKLLSNRSKALVRLALEAEKVQAAHQRWEDFASN 120

QY 121 EYVYNAKDDLPKNDSEPSQRIKPVFIDANFGROISYOHAAVHIPTDIYEGSTIVL 180  
 Db 121 EYVYNAKDDLPKNDSEPSQRIKPVFIDANFGROISYOHAAVHIPTDIYEGSTIVL 180

QY 181 NELNWTSSALDEYFKKRNREDPSLLQVFGSGATGLARYYPASPWVDSNTPKNIIDLYDVR 240  
 Db 181 NELNWTSSALDEYFKKRNREDPSLLQVFGSGATGLARYYPASPWVDSNTPKNIIDLYDVR 240

QY 241 RPWYIOGAASPKDMLILVDVSSVGLFLKIRTSVSEMLETLSDDDFVNVSFNSNAQD 300  
 Db 241 RPWYIOGAASPKDMLILVDVSSVGLFLKIRTSVSEMLETLSDDDFVNVSFNSNAQD 300

QY 301 VSCFOHLVQANVRNKKVILKDVANNITAKGIDTDYKGFSAFEQLLNYNVSRANCKIIML 360  
 Db 301 VSCFOHLVQANVRNKKVILKDVANNITAKGIDTDYKGFSAFEQLLNYNVSRANCKIIML 360

QY 361 FTDGGEERAQEIFAKYNNKDKVRVFTSVSGOHNYDRGPIONMACENKGYIETPSIGAIR 420  
 Db 361 FTDGGEERAQEIFAKYNNKDKVRVFTSVSGOHNYDRGPIONMACENKGYIETPSIGAIR 420

QY 421 INTQBYLDVLGRPMVLAGDKAKQVQWNTNVLDALELGLVITGTLVPVNIITQONENKTNLK 480  
 Db 421 INTQBYLDVLGRPMVLAGDKAKQVQWNTNVLDALELGLVITGTLVPVNIITQONENKTNLK 480

QY 481 NOLLILGVMGVDVSLIEDIKRLTPRTLCPPNGYFFAIDPNGYVLLHPNLQPNKPSQEPVTL 540  
 Db 481 NOLLILGVMGVDVSLIEDIKRLTPRTLCPPNGYFFAIDPNGYVLLHPNLQPNKPSQEPVTL 540

QY 541 DFLDAELNDIKVEIRNKMIDGSEGETFTFLVKSQDERYIDKGNRTYTTPVNGTDYSL 600  
 Db 541 DFLDAELNDIKVEIRNKMIDGSEGETFTFLVKSQDERYIDKGNRTYTTPVNGTDYSL 600

QY 601 ALVLPYTSFYIYKAKIETITQARSKGKMKDSETLKPDPNFESGYTFFIAPRDCYNDLKI 660  
 Db 601 ALVLPYTSFYIYKAKIETITQARSKGKMKDSETLKPDPNFESGYTFFIAPRDCYNDLKI 660

QY 661 SDNTEFLNNEFIDRKTPNPNPCNTDLNVRLLDAGFTNELVQYWSKQKIKGVKAR 720  
 Db 661 SDNTEFLNNEFIDRKTPNPNPCNTDLNVRLLDAGFTNELVQYWSKQKIKGVKAR 720

QY 721 FVVTDDGITRYPKEAGENQENPETEYDSFYKRSKLDNDNYVTAPVFNKSGPCAVESGI 780  
 Db 721 FVVTDDGITRYPKEAGENQENPETEYDSFYKRSKLDNDNYVTAPVFNKSGPCAVESGI 780

QY 781 MYSKAVIYIYOGKLLKPAVVGKIDVNSWIENTTKTSIRDPACGPDCKRNSDVMDCVI 840  
 Db 781 MYSKAVIYIYOGKLLKPAVVGKIDVNSWIENTTKTSIRDPACGPDCKRNSDVMDCVI 840

QY 841 LDGGFLLMANHDDYTNOIGRFGETIDPSLMRHLVNLISVYAFNKSVDYQSVCEGPAAPKQ 900  
 Db 841 LDGGFLLMANHDDYTNOIGRFGETIDPSLMRHLVNLISVYAFNKSVDYQSVCEGPAAPKQ 900

QY 901 GAGHRSAYVPSIADILHIGWATAAAWSIIQQFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960  
 Db 901 GAGHRSAYVPSIADILHIGWATAAAWSIIQQFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960

QY 961 SCITEQTYEFDNDKSFSGVLDCGNCGRIFPHVEKLMNTNLIIFIMVESKGTCTCDTRL 1018  
 Db 961 SCITEQTYEFDNDKSFSGVLDCGNCGRIFPHVEKLMNTNLIIFIMVESKGTCTCDTRL 1018

## RESULT 11

AAU01032  
 ID AAU01032 standard; Protein; 1018 AA.  
 XX  
 AC AAU01032;  
 XX  
 DT 04-JUL-2001 (first entry)  
 XX  
 DE Human secreted soluble alpha2delta calcium channel subunit #12 protein.  
 XX  
 KW Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;  
 KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;  
 KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;  
 KW filter binding assay; wheat germ lectin flashplate assay.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200119870-A2.  
 XX  
 PD 22-MAR-2001.  
 XX  
 PF 18-SEP-2000; 2000WO-BP09137.  
 XX  
 PR 16-SEP-1999; 99US-0397550.  
 XX  
 PA (WARN ) WARNER LAMBERT CO.  
 XX  
 PI Brown JP, Bertelli F;  
 XX  
 DR WPI; 2001-235262/24.  
 XX  
 DR N-PSDB; AAS01423.  
 XX  
 PT Calcium channel alpha2delta subunits, useful in e.g. SPA assays,  
 PT Flashplate assays, Nickel Flashplate assays, Filter binding assays or  
 PT Wheat Germ Lectin Flashplate assays -  
 XX  
 PS Claim 31; Page 130-133; 160pp; English.  
 XX  
 CC The present sequence represents human secreted calcium channel  
 CC alpha2delta subunit #12 which is soluble and retains the functional  
 CC characteristics of the full length or wild type alpha2delta subunit  
 CC (AAU01025) from which it is derived. The invention relates to truncated  
 CC alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins  
 CC which retain their affinity for radioactively labelled gabapentin. The  
 CC alpha2delta subunit is 1 of the components of the heteromultimeric  
 CC voltage-dependent calcium channel (VDCC) complexes present in neuronal  
 CC and non-neuronal tissues including heart and skeletal muscle. Numerous  
 CC soluble forms of the human calcium channel alpha2delta subunits  
 CC (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the  
 CC porcine calcium channel alpha2delta subunits (AAU01027-AAU01031) are  
 CC described. The secreted soluble alpha2delta subunit may be used in assays  
 CC e.g. scintillation proximity assay (SPA), flashplate, nickel flashplate,  
 CC filter binding or wheat germ lectin flashplate assays to detect or  
 CC measure the binding or interaction of a ligand (e.g. gabapentin,  
 CC L-Norleucine, L-Allo-isoleucine, L-methionine, L-Leucine, L-Isoleucine,  
 CC L-Valine, Spermine and/or L-Phenylalanine) of a calcium channel  
 CC alpha2delta subunit.  
 XX  
 SQ Sequence 1018 AA;



Query Match 98.9%; Score 5288; DB 22; Length 1018;  
Best Local Similarity 98.8%; Pred. No. 0;  
Matches 1006; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLTQSLILGPSSQEPFSAVITKSWDKMQEDLVTLAKTASGVNQLVDI 60  
DB 1 MAAGCLLALTTLTQSLILGPSSQEPFSAVITKSWDKMQEDLVTLAKTASGVNQLVDI 60

QY 61 YEKYQDLYTVEPNARQLVEIAARDIEKLISNRKALVRLALEAEKVQAAHQRDEFASN 120  
DB 61 YEKYQDLYTVEPNARQLVEIAARDIEKLISNRKALVRLALEAEKVQAAHQRDEFASN 120

QY 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFIIDANFGRQISYQHAHVHPTDIYEGSTIVL 180  
DB 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFIIDANFGRQISYQHAHVHPTDIYEGSTIVL 180

QY 181 NELNWTSAIDVEFKKNEEDPSLLWQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240  
DB 181 NELNWTSAIDVEFKKNEEDPSLLWQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240

QY 241 RPWYIOGAASPKDMLILVDVSGVSLTLKLIIRTSVSEMLETLSDDDFVNVASFNSNAQD 300  
DB 241 RPWYIOGAASPKDMLILVDVSGVSLTLKLIIRTSVSEMLETLSDDDFVNVASFNSNAQD 300

QY 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGIDYKKGFSFAFQOLLNINVSANCKIIML 360  
DB 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGIDYKKGFSFAFQOLLNINVSANCKIIML 360

QY 361 FTDGGERAQEIFAKYKDKKRYVTFVSGOHNYDRGPLOWACENKGYVYIPIGAI 420  
DB 361 FTDGGERAQEIFAKYKDKKRYVTFVSGOHNYDRGPLOWACENKGYVYIPIGAI 420

QY 421 INTQEYLDVLGRPMVLGAKQOVQNTVYLDALGLVITGTLVFNITGQENKTNLK 480  
DB 421 INTQEYLDVLGRPMVLGAKQOVQNTVYLDALGLVITGTLVFNITGQENKTNLK 480

QY 481 NQILILGVMDVSLDIEKILTRFTLCPNGYFAIDPNGYVLLHNPQKNPKSQEPVTL 540  
DB 481 NQILILGVMDVSLDIEKILTRFTLCPNGYFAIDPNGYVLLHNPQKNPKSQEPVTL 540

QY 541 DFLDALENDIKVEIRNKMIDGESGKERTLVKSQDERYIDKGNRTYTWTPVNGTDSL 600  
DB 541 DFLDALENDIKVEIRNKMIDGESGKERTLVKSQDERYIDKGNRTYTWTPVNGTDSL 600

QY 601 ALVLPYTFYIYKAKLEETITQARSKKGMKDSSETLKPDPNFESGYTFIAPRDYCNLKI 660  
DB 601 ALVLPYTFYIYKAKLEETITQARSKKGMKDSSETLKPDPNFESGYTFIAPRDYCNLKI 660

QY 661 SDNTEFLNFEFIDRKTNPNSCNTDLINRVLLDAGFTNVLQVYWSKQKNIKGVKAR 720  
DB 661 SDNTEFLNFEFIDRKTNPNSCNTDLINRVLLDAGFTNVLQVYWSKQKNIKGVKAR 720

QY 721 FVYTDGGITRVYPKEAGENQENPETYEDSFYKRLSDNDNYVFTAPYFNKSGPGAYESGI 780  
DB 721 FVYTDGGITRVYPKEAGENQENPETYEDSFYKRLSDNDNYVFTAPYFNKSGPGAYESGI 780

QY 781 MYSKAVEIYIQGKLLPAVVGKIDVNSWIENFTKTSIRDPKAGPVCDCKRNSDVMDCVI 840  
DB 781 MYSKAVEIYIQGKLLPAVVGKIDVNSWIENFTKTSIRDPKAGPVCDCKRNSDVMDCVI 840

QY 841 LDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLNINSVIAPNKSVDYQSVCEGPAAPKQ 900  
DB 841 LDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLNINSVIAPNKSVDYQSVCEGPAAPKQ 900

QY 901 GAGHRSAVYPSIADILHIGWATAAWSILQQFLLSLTFPRLEAVEMEDDDFTASLSKQ 960  
DB 901 GAGHRSAVYPSIADILHIGWATAAWSILQQFLLSLTFPRLEAVEMEDDDFTASLSKQ 960

QY 961 SCITEQTYFFDNDKSFSGVLDGCGNCSRIHFVEKLMNTNLIFIMVESKGTCPDTRL 1018  
DB 961 SCITEQTYFFDNDKSFSGVLDGCGNCSRIHFVEKLMNTNLIFIMVESKGTCPDTRL 1018

## RESULT 12

AAB62256  
ID AAB62256 standard; Protein; 1018 AA.  
XX AAB62256;  
XX AAB62256;  
DT 11-JUN-2001 (first entry)  
XX Porcine calcium channel alpha2delta subunit.  
XX Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;  
XX nervous system disorder; pain; epilepsy; anxiety; pig.  
OS Sus scrofa.  
XX WO200120336-A2.  
XX 22-MAR-2001.  
XX 18-SEP-2000; 2000WO-EP09136.  
XX 16-SEP-1999; 99US-0397549.  
XX (WARN ) WARNER LAMBERT CO.  
XX Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;  
WPI: 2001-257902/26.  
N-PSDB: AAF57560.  
Competitive binding assay for screening ligands which bind a cerebral  
cortical voltage-dependent calcium channel alpha2delta-1 subunit.  
where the ligands identified are useful for treating disorders of the  
nervous system, including pain -  
Claim 8; Page 129-132; 158pp; English.  
The invention relates to a new method for screening ligands which bind a  
cerebral cortical voltage-dependent calcium channel alpha2delta subunit,  
preferably alpha2delta-1 subunit. The method comprises contacting a  
secreted soluble recombinant alpha2delta-1 subunit with a ligand of  
interest and a labelled compound which binds the subunit, followed by  
measuring the level of binding of the labelled compound to alpha2delta-1  
subunit. The method is useful for screening ligands, preferably  
biologically active products that modulate a nervous system function,  
which bind a cerebral cortical voltage-dependent calcium channel  
alpha2delta-1 subunit. The ligands identified by the method are useful  
for treating disorders of the nervous system, including pain, epilepsy  
and anxiety. The present sequence represents a porcine calcium channel  
alpha2delta subunit.

SQ Sequence 1018 AA;

Query Match 98.9%; Score 5288; DB 22; Length 1018;  
Best Local Similarity 98.8%; Pred. No. 0;  
Matches 1006; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLTQSLILGPSSQEPFSAVITKSWDKMQEDLVTLAKTASGVNQLVDI 60  
DB 1 MAAGCLLALTTLTQSLILGPSSQEPFSAVITKSWDKMQEDLVTLAKTASGVNQLVDI 60

QY 61 YEKYQDLYTVEPNARQLVEIAARDIEKLISNRKALVRLALEAEKVQAAHQRDEFASN 120  
DB 61 YEKYQDLYTVEPNARQLVEIAARDIEKLISNRKALVRLALEAEKVQAAHQRDEFASN 120

QY 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFIIDANFGRQISYQHAHVHPTDIYEGSTIVL 180  
DB 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFIIDANFGRQISYQHAHVHPTDIYEGSTIVL 180

QY 181 NELNWTSAIDVEFKKNEEDPSLLWQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240  
DB 181 NELNWTSAIDVEFKKNEEDPSLLWQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240

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QY 241 RPWYIOGAASPKDMLILVDVSGVSGLTILKLTSTVSEMLETISDDDFVNVASFNSNAQD 300
Db 241 RPWYIOGAASPKDMLILVDVSGVSGLTILKLTSTVSEMLETISDDDFVNVASFNSNAQD 300
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSFAFQOLLNINVRANCNKIIML 360
Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSFAFQOLLNINVRANCNKIIML 360
QY 361 FTDCGEERAQEIFAKYKNDKKVRVFTFSVQGHYDRGPQIOWMACENKGYIYEIPSIGAIR 420
Db 361 FTDCGEERAQEIFAKYKNDKKVRVFTFSVQGHYDRGPQIOWMACENKGYIYEIPSIGAIR 420
QY 421 INTQVEYLDVLRPMVLGAKAKOVQNTVYLDALGLVITGTLPVFNITGQFENKTNLK 480
Db 421 INTQVEYLDVLRPMVLGAKAKOVQNTVYLDALGLVITGTLPVFNITGQFENKTNLK 480
QY 481 NQILGVMGVDSVLEIDIKRLTPRFTLCPNGYFAIDPNCYVLLHNPLOPKPKSEPTVL 540
Db 481 NQILGVMGVDSVLEIDIKRLTPRFTLCPNGYFAIDPNCYVLLHNPLOPKPKSEPTVL 540
QY 541 DFLDAELENDIKVEIRKMKIDGESGKFTPTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600
Db 541 DFLDAELENDIKVEIRKMKIDGESGKFTPTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600
QY 601 ALVLPYTSFYIIKAKTEETITQARSKKGMKDSSETLKPDPNFESGYTFTIAPRDYCNDLKI 660
Db 601 ALVLPYTSFYIIKAKLEETITQARSKKGMKDSSETLKPDPNFESGYTFTIAPRDYCNDLKI 660
QY 661 SDNTEFLNLFNEFIDRKTTPNPNPCNTDLINRVLLDAGFTNELVQYNSKQKNIKGVKAR 720
Db 661 SDNTEFLNLFNEFIDRKTTPNPNPCNTDLINRVLLDAGFTNELVQYNSKQKNIKGVKAR 720
QY 721 FVYTDGGITRVYKPEAGENQENPETIYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
Db 721 FVYTDGGITRVYKPEAGENQENPETIYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
QY 781 MYSKAVEIYIOGKLLAPVVGKIDVNSWTENFTKTSIRDPGAGVPCDCKRNSDVMDCVI 840
Db 781 MYSKAVEIYIOGKLLAPVVGKIDVNSWTENFTKTSIRDPGAGVPCDCKRNSDVMDCVI 840
QY 841 LDGGSFLMANHDDYTNQIGRFFGEIDPSLMRHLNINISYAFNKSVDYQSVCEPGAAPKQ 900
Db 841 LDGGSFLMANHDDYTNQIGRFFGEIDPSLMRHLNINISYAFNKSVDYQSVCEPGAAPKQ 900
QY 901 GAGHRSAYVPSIADILHIGWATAAWSILOQFLSLTPRLLLEAVEMEDDDFTASLSKQ 960
Db 901 GAGHRSAYVPSIADILHIGWATAAWSILOQFLSLTPRLLLEAVEMEDDDFTASLSKQ 960
QY 961 SCITEQTQYFFDNDKSFSGVLDGCGNCSRIHFHVEKLMNTNLFIMVESKGTGCPDCTRL 1018
Db 961 SCITEQTQYFFDNDKSFSGVLDGCGNCSRIHFHVEKLMNTNLFIMVESKGTGCPDCTRL 1018

RESULT 13
ID AAU01033
XX AAU01033 standard; Protein; 1036 AA.
XX AC AAU01033;
XX DT 04-JUL-2001 (first entry)
XX DE Human secreted soluble alpha2delta calcium channel subunit #13 protein.
XX KW Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;
KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;
KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;
KW filter binding assay; wheat germ lectin flashplate assay.
XX OS Homo sapiens.
XX PN WO200119870-A2.
XX

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PD 22-MAR-2001.
PF 18-SEP-2000; 2000WO-EP09137.
PR 16-SEP-1999; 99US-0397550.
PA (WARN ) WARNER LAMBERT CO.
XX Brown JP, Bertelli F;
PI WPI; 2001-235262/24.
DR N-PSDB; AAS01424.
XX
PT Calcium channel alpha2delta subunits, useful in e.g. SPA assays,
PT Flashplate assays, Nickel Flashplate assays, Filter binding assays or
PT Wheat Germ Lectin Flashplate assays -
XX
PS Claim 31; Page 134-137; 160pp; English.
XX
CC The present sequence represents human secreted calcium channel
CC alpha2delta subunit #13 which is soluble and retains the functional
CC characteristics of the full length or wild type alpha2delta subunit
CC (AAU01025) from which it is derived. The invention relates to truncated
CC alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins
CC which retain their affinity for radioactively labelled gabapentin. The
CC alpha2delta subunit is 1 of the components of the heteromultimeric
CC voltage-dependent calcium channel (VDCC) complexes present in neuronal
CC and non-neuronal tissues including heart and skeletal muscle. Numerous
CC soluble forms of the human calcium channel alpha2delta subunits
CC (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the
CC porcine calcium channel alpha2delta subunits (AAU01027-AAU01031) are
CC described. The secreted soluble alpha2delta subunit may be used in assays
CC e.g. scintillation proximity assay (SPA), flashplate, nickel flashplate,
CC filter binding or wheat germ lectin flashplate assays to detect or
CC measure the binding or interaction of a ligand (e.g. gabapentin,
CC L-Norleucine, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Isoleucine,
CC L-Valine, Spermine and/or L-Phenylalanine) of a calcium channel
CC alpha2delta subunit.
XX
SQ Sequence 1036 AA;
Query Match 98.9%; Score 5288; DB 22; Length 1036;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1006; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
QY 1 MAAGCLLALTLTFLQSLIGSSQEPFSAVTIKSWYDKMQEDLVTAKTASGVNQLVDI 60
Db 1 MAAGCLLALTLTFLQSLIGSSQEPFSAVTIKSWYDKMQEDLVTAKTASGVNQLVDI 60
QY 61 YEKYODLYTVEPNAROLVETAAARDIEKLLSNRSKALVRLALEAEKVQAAHQWREDFASN 120
Db 61 YEKYODLYTVEPNAROLVETAAARDIEKLLSNRSKALVRLALEAEKVQAAHQWREDFASN 120
QY 121 EVVYNAKDDLDLPEKNDSEPGSQRIKPVFFIDANFGQISYQAAHVHPTDIYEGSTIVL 180
Db 121 EVVYNAKDDLDLPEKNDSEPGSQRIKPVFFIDANFGQISYQAAHVHPTDIYEGSTIVL 180
QY 181 NELNWTSALEDEVFKKNREEDPSLLWQVFGSATGLARYYPASPPWVNSRTPNKIDLYDVR 240
Db 181 NELNWTSALEDEVFKKNREEDPSLLWQVFGSATGLARYYPASPPWVNSRTPNKIDLYDVR 240
QY 241 RPWYIOGAASPKDMLILVDVSGVSGLTILKLTSTVSEMLETISDDDFVNVASFNSNAQD 300
Db 241 RPWYIOGAASPKDMLILVDVSGVSGLTILKLTSTVSEMLETISDDDFVNVASFNSNAQD 300
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSFAFQOLLNINVRANCNKIIML 360
Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSFAFQOLLNINVRANCNKIIML 360
QY 361 FTDCGEERAQEIFAKYKNDKKVRVFTFSVQGHYDRGPQIOWMACENKGYIYEIPSIGAIR 420
Db 361 FTDCGEERAQEIFAKYKNDKKVRVFTFSVQGHYDRGPQIOWMACENKGYIYEIPSIGAIR 420

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QY 421 INTQEVLDVLRPMVLGADKAKQVQWNTVYLDALGLVITGTLPVFNITGONENKTNLK 480  
 Db 421 INTQEVLDVLRPMVLGADKAKQVQWNTVYLDALGLVITGTLPVFNITGONENKTNLK 480  
 QY 481 NQILGVMGVDSLEDIKRLTPRFTLCPNGYVFAIDPNCYVLLHPNLOPKNPKSOEPVTL 540  
 Db 481 NQILGVMGVDSLEDIKRLTPRFTLCPNGYVFAIDPNCYVLLHPNLOPKNPKSOEPVTL 540  
 QY 541 DFLDAELENDIKVEIRNKMIDGESGEKTRTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
 Db 541 DFLDAELENDIKVEIRNKMIDGESGEKTRTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
 QY 601 ALVLPYTFYIYKAKIETITQARSKKGMKDSKSETLKPDPFESGTYFTIAPRDYCNLDKI 660  
 Db 601 ALVLPYTFYIYKAKIETITQARSKKGMKDSKSETLKPDPFESGTYFTIAPRDYCNLDKI 660  
 QY 661 SDNTEFLNFEFIDRKTPNPNPCNTDLINRVLLDAGFTNVLVQNSKQKNIKGVKAR 720  
 Db 661 SDNTEFLNFEFIDRKTPNPNPCNTDLINRVLLDAGFTNVLVQNSKQKNIKGVKAR 720  
 QY 721 FVYTDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
 Db 721 FVYTDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
 QY 781 MYSKAVEIYLOGLLPAVVGKIDVNSWIENFTKTSIRDPACAGVCDCKRNSDVMDCVI 840  
 Db 781 MYSKAVEIYLOGLLPAVVGKIDVNSWIENFTKTSIRDPACAGVCDCKRNSDVMDCVI 840  
 QY 841 LDGSGFLMANHDDYTNQIGRFFGEIDPSLMRHLNYSVYAFNKSVDYQSVCEPGAAPKQ 900  
 Db 841 LDGSGFLMANHDDYTNQIGRFFGEIDPSLMRHLNYSVYAFNKSVDYQSVCEPGAAPKQ 900  
 QY 901 GAGHSAYVPSADIILHIGWATAAWSILOQFLLSLTPRLLLEAVEMEDDDFTASLSKQ 960  
 Db 901 GAGHSAYVPSADIILHIGWATAAWSILOQFLLSLTPRLLLEAVEMEDDDFTASLSKQ 960  
 QY 961 SCITEQTOFFDNDKSFSGVLDCGNCRIFFHVEKLMNTNLFIIMVESKGTCPDTRL 1018  
 Db 961 SCITEQTOFFDNDKSFSGVLDCGNCRIFFHVEKLMNTNLFIIMVESKGTCPDTRL 1018

RESULT 14  
 AAB62257  
 ID AAB62257 standard; Protein; 1036 AA.  
 XX  
 AC AAB62257;  
 XX  
 DT 11-JUN-2001 (first entry)  
 XX  
 DE Porcine calcium channel alpha2delta subunit.  
 XX  
 KW Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;  
 KW nervous system disorder; pain; epilepsy; anxiety; pig.  
 XX  
 OS Sus scrofa.  
 XX  
 PN W0200120336-A2.  
 XX  
 PD 22-MAR-2001.  
 XX  
 PF 18-SEP-2000; 2000WO-EP09136.  
 XX  
 PR 16-SEP-1999; 99US-0397549.  
 XX  
 PA (WARN ) WARNER LAMBERT CO.  
 XX  
 PI Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;  
 XX  
 DR WPI; 2001-257902/26.  
 DR N-PSDB; AAF57561.  
 XX  
 PT Competitive binding assay for screening ligands which bind a cerebral  
 PT cortical voltage-dependent calcium channel alpha2delta-1 subunit,

where the ligands identified are useful for treating disorders of the nervous system, including pain -  
 Claim 8; Page 132-135; 158pp; English.

The invention relates to a new method for screening ligands which bind a cerebral cortical voltage-dependent calcium channel alpha2delta subunit, preferably alpha2delta-1 subunit. The method comprises contacting a secreted soluble recombinant alpha2delta-1 subunit with a ligand of interest and a labelled compound which binds the subunit, followed by measuring the level of binding of the labelled compound to alpha2delta-1 subunit. The method is useful for screening ligands, preferably biologically active products that modulate a nervous system function, which bind a cerebral cortical voltage-dependent calcium channel alpha2delta-1 subunit. The ligands identified by the method are useful for treating disorders of the nervous system, including pain, epilepsy and anxiety. The present sequence represents a porcine calcium channel alpha2delta subunit.

Sequence 1036 AA;

Query Match 98.9%; Score 5288; DB 22; Length 1036;  
 Best Local Similarity 98.8%; Pred. No. 0;  
 Matches 1006; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MAAGCLLATLTTLFQSLIGSPSPPPSAVTIKSWDKMOEDLTAKTASGVNQLVDI 60  
 Db 1 MAAGCLLATLTTLFQSLIGSPSPPPSAVTIKSWDKMOEDLTAKTASGVNQLVDI 60

Qy 61 YEKQDLYTVEPNARQVLEIAARDIEKLLNSRKALVRLALEAEKVQAAHQWREDFASN 120  
 Db 61 YEKQDLYTVEPNARQVLEIAARDIEKLLNSRKALVRLALEAEKVQAAHQWREDFASN 120

Qy 121 EWTYNAKDDLDPEKNDSEPGSQRIKPVFIIDANFGROIYSQHAHVHTPTDIYEGSTIVL 180  
 Db 121 EWTYNAKDDLDPEKNDSEPGSQRIKPVFIIDANFGROIYSQHAHVHTPTDIYEGSTIVL 180

Qy 181 NELNWTSALEDFVFKNREEDPSLLWQVFGSATGLARYYPASPWDNSTRPNKIDLYDVR 240  
 Db 181 NELNWTSALEDFVFKNREEDPSLLWQVFGSATGLARYYPASPWDNSTRPNKIDLYDVR 240

Qy 241 RPWYIOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETLDSDDFVNVASNSNAQD 300  
 Db 241 RPWYIOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETLDSDDFVNVASNSNAQD 300

Qy 301 VSCFOHLVQANVRNKKVLDKAVNNITAKITDYKKGFSFAFEQLLNYSRANCNKIIML 360  
 Db 301 VSCFOHLVQANVRNKKVLDKAVNNITAKITDYKKGFSFAFEQLLNYSRANCNKIIML 360

Qy 361 FTDGGEERAQEIFAKYNNKDKKVRVFTFSVGQHNTRYDRGPIOMMACENKGYEIPISGAIR 420  
 Db 361 FTDGGEERAQEIFAKYNNKDKKVRVFTFSVGQHNTRYDRGPIOMMACENKGYEIPISGAIR 420

Qy 421 INTQEVLDVLRPMVLGADKAKQVQWNTVYLDALGLVITGTLPVFNITGONENKTNLK 480  
 Db 421 INTQEVLDVLRPMVLGADKAKQVQWNTVYLDALGLVITGTLPVFNITGONENKTNLK 480

Qy 481 NQILGVMGVDSLEDIKRLTPRFTLCPNGYVFAIDPNCYVLLHPNLOPKNPKSOEPVTL 540  
 Db 481 NQILGVMGVDSLEDIKRLTPRFTLCPNGYVFAIDPNCYVLLHPNLOPKNPKSOEPVTL 540

Qy 541 DFLDAELENDIKVEIRNKMIDGESGEKTRTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
 Db 541 DFLDAELENDIKVEIRNKMIDGESGEKTRTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600

Qy 601 ALVLPYTFYIYKAKIETITQARSKKGMKDSKSETLKPDPFESGTYFTIAPRDYCNLDKI 660  
 Db 601 ALVLPYTFYIYKAKIETITQARSKKGMKDSKSETLKPDPFESGTYFTIAPRDYCNLDKI 660

Qy 661 SDNTEFLNFEFIDRKTPNPNPCNTDLINRVLLDAGFTNVLVQNSKQKNIKGVKAR 720  
 Db 661 SDNTEFLNFEFIDRKTPNPNPCNTDLINRVLLDAGFTNVLVQNSKQKNIKGVKAR 720

QY 721 FVVTGGITRVYPKEAGENWQENPETEYEDSYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
 Db 721 FVVTGGITRVYPKEAGENWQENPETEYEDSYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
 QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIEFTKTSIRDPKAGPVCDCCKRNSDVMDCVI 840  
 Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIEFTKTSIRDPKAGPVCDCCKRNSDVMDCVI 840  
 QY 841 LDGGFLMANHDDVTNOIGRFFGEIDPSLMRHLVNSVYAFNKSYYQSVCEPGAAPKQ 900  
 Db 841 LDGGFLMANHDDVTNOIGRFFGEIDPSLMRHLVNSVYAFNKSYYQSVCEPGAAPKQ 900  
 QY 901 GAGHSAYVPSVADILQIGWATAAAWILQOFLLSLTFPRLLEAVEEMDDDFASLSKQ 960  
 Db 901 GAGHSAYVPSVADILQIGWATAAAWILQOFLLSLTFPRLLEAVEEMDDDFASLSKQ 960  
 QY 961 SCITBQTOYFFDNDKSFSGVLDGNCNCRIFHVEKLMNTNLFIMVSKGTCPCDTRL 1018  
 Db 961 SCITBQTOYFFDNDKSFSGVLDGNCNCRIFHVEKLMNTNLFIMVSKGTCPCDTRL 1018  
 RESULT 15  
 AAU01034  
 ID AAU01034 standard; Protein; 1063 AA.  
 AC AAU01034;  
 XX  
 DT 04-JUL-2001 (first entry)  
 XX  
 DE Human secreted soluble alpha2delta calcium channel subunit #14 protein.  
 KW Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;  
 KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;  
 KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;  
 KW filter binding assay; wheat germ lectin flashplate assay.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200119870-A2.  
 XX  
 XX 22-MAR-2001.  
 PD  
 PF 18-SEP-2000; 2000WO-EP09137.  
 XX  
 PR 16-SEP-1999; 99US-0397550.  
 XX  
 PA (WARN ) WARNER LAMBERT CO.  
 XX  
 PI Brown JP, Bertelli F;  
 XX  
 DR WPI; 2001-235262/24.  
 XX  
 DR N-PSDB; AAS01425.  
 XX  
 PT Calcium channel alpha2delta subunits, useful in e.g. SPA assays,  
 PT Flashplate assays, Nickel Flashplate assays, Filter binding assays or  
 PT Wheat Germ Lectin Flashplate assays -  
 XX  
 PS Claim 31; Page 137-140; 160pp; English.  
 XX  
 CC The present sequence represents human secreted calcium channel  
 CC alpha2delta subunit #14 which is soluble and retains the functional  
 CC characteristics of the full length or wild type alpha2delta subunit  
 CC (AAU01025) from which it is derived. The invention relates to truncated  
 CC alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins  
 CC which retain their affinity for radioactively labelled gabapentin. The  
 CC alpha2delta subunit is 1 of the components of the heteromultimeric  
 CC voltage-dependent calcium channel (VDCC) complexes present in neuronal  
 CC and non-neuronal tissues including heart and skeletal muscle. Numerous  
 CC soluble forms of the human calcium channel alpha2delta subunits  
 CC (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the  
 CC porcine calcium channel alpha2delta subunits (AAU01027-AAU01031) are  
 CC described. The secreted soluble alpha2delta subunit may be used in assays  
 CC e.g. scintillation proximity assay (SPA), flashplate, nickel flashplate,

CC filter binding or wheat germ lectin flashplate assays to detect or  
 CC measure the binding or interaction of a ligand (e.g. gabapentin,  
 CC L-Norleucine, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Isoleucine,  
 CC L-Valine, Spermine and/or L-Phenylalanine) of a calcium channel  
 CC alpha2delta subunit.  
 XX  
 SQ Sequence 1063 AA;  
 Query Match 98.9%; Score 5288; DB 22; Length 1063;  
 Best Local Similarity 98.8%; Pred. No. 0;  
 Matches 1006; Conservative 5; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 MAACCLLALTLTLFQSLILGPSQEPFSAVTIKSWDKMQEDLVTIAKTASGVNOLVDI 60  
 Db 1 MAAGCCLLALTLTLFQSLILGPSSEEPFSAVTIKSWDKMQEDLVTIAKTASGVNOLVDI 60  
 QY 61 YEKYQDLTYVEPNARQLVEIAARDIEKLLSNRSKALVRLALEAKVQAAHQRDEFASN 120  
 Db 61 YEKYQDLTYVEPNARQLVEIAARDIEKLLSNRSKALVRLALEAKVQAAHQRDEFASN 120  
 QY 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFIDANFGRIQISYQHAHVHIPTDIEGSTIVL 180  
 Db 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRIQISYQHAHVHIPTDIEGSTIVL 180  
 QY 181 NELNWTSAIDVEFKKREEDPSLLMQVFGSATGLARYYPASPVWDNSRTPNKIDLYDVR 240  
 Db 181 NELNWTSAIDVEFKKREEDPSLLMQVFGSATGLARYYPASPVWDNSRTPNKIDLYDVR 240  
 QY 241 RPWYIOGAASPDKMLILVDVSGVSLTLKLTSTVSEMLETLSDDDFVNVASFNSNAOD 300  
 Db 241 RPWYIOGAASPDKMLILVDVSGVSLTLKLTSTVSEMLETLSDDDFVNVASFNSNAOD 300  
 QY 301 VSCFHLVQANVRNKKVLDAVNNTAKGITDYKKGFSFAFOLLNYSRANCNKIIML 360  
 Db 301 VSCFHLVQANVRNKKVLDAVNNTAKGITDYKKGFSFAFOLLNYSRANCNKIIML 360  
 QY 361 FTDGGEERAQEIFAKYNDKKVRFVTFSGOHNNDYDRGPIOWMACENKGYEYELPSIGAIR 420  
 Db 361 FTDGGEERAQEIFAKYNDKKVRFVTFSGOHNNDYDRGPIOWMACENKGYEYELPSIGAIR 420  
 QY 421 INTQEYLDVLGPRMVLGADKAKOVQWNTVYLDALGLVITGTPVFNITGQENKTNLK 480  
 Db 421 INTQEYLDVLGPRMVLGADKAKOVQWNTVYLDALGLVITGTPVFNITGQENKTNLK 480  
 QY 481 NQLILGVMGVDSLEDIKRLTPRFLCPNGYTFADPNQYVLLHPLNPKPKSQEPVTL 540  
 Db 481 NQLILGVMGVDSLEDIKRLTPRFLCPNGYTFADPNQYVLLHPLNPKPKSQEPVTL 540  
 QY 541 DFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSODERYIDKGNRTYTWTPVNGTDYSL 600  
 Db 541 DFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSODERYIDKGNRTYTWTPVNGTDYSL 600  
 QY 601 ALVLPYTFYIYKAKIETITQARSKKGMKDSKSETLKPDNFEEGTYFTIAPRDYCNLDKI 660  
 Db 601 ALVLPYTFYIYKAKIETITQARSKKGMKDSKSETLKPDNFEEGTYFTIAPRDYCNLDKI 660  
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 Db 661 SDNTEFLNFEFIDRKTPNPNPCNTDNLINRVLLDAGFTNELVQNSKQNKIGVKAR 720  
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 Db 721 FVVTGGITRVYPKEAGENWQENPETEYEDSYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
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 QY 841 LDGGFLMANHDDVTNOIGRFFGEIDPSLMRHLVNSVYAFNKSYYQSVCEPGAAPKQ 900  
 Db 841 LDGGFLMANHDDVTNOIGRFFGEIDPSLMRHLVNSVYAFNKSYYQSVCEPGAAPKQ 900  
 QY 901 GAGHSAYVPSVADILQIGWATAAAWILQOFLLSLTFPRLLEAVEEMDDDFASLSKQ 960  
 Db 901 GAGHSAYVPSVADILQIGWATAAAWILQOFLLSLTFPRLLEAVEEMDDDFASLSKQ 960

Db 901 GAGHSAYVPSVADIIQIGWATAAAWSILOQFLSLTFPRLEAVEMEDDDFTASLSKQ 960  
QY 961 SCITEQYFFDNDKSFSGVLDGNCNRIFHVEKLMNTNLIFIMVESKGTCPCDTRL 1018  
Db 961 SCITEQYFFDNDKSFSGVLDGNCNRIFHVEKLMNTNLIFIMVESKGTCPCDTRL 1018

Search completed: February 10, 2003, 14:18:01  
Job time : 38.0366 secs

1. 2. 3. 4. 5. 6. 7. 8. 9. 10. 11. 12. 13. 14. 15. 16. 17. 18. 19. 20. 21. 22. 23. 24. 25. 26. 27. 28. 29. 30. 31. 32. 33. 34. 35. 36. 37. 38. 39. 40. 41. 42. 43. 44. 45. 46. 47. 48. 49. 50. 51. 52. 53. 54. 55. 56. 57. 58. 59. 60. 61. 62. 63. 64. 65. 66. 67. 68. 69. 70. 71. 72. 73. 74. 75. 76. 77. 78. 79. 80. 81. 82. 83. 84. 85. 86. 87. 88. 89. 90. 91. 92. 93. 94. 95. 96. 97. 98. 99. 100.

GenCore version 5.1.3  
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## OM protein - protein search, using sw model

Run on: February 10, 2003, 14:13:55 ; Search time 11.291 Seconds

(without alignments)  
2652.785 Million cell updates/sec

Title: US-10-090-827-6

Perfect score: 5349  
Sequence: 1 MAAGCLLALTLTLPFOSLLIG.....TNLITFWSKGTCPDTRL 1018

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
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4: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID | Description       |
|------------|--------|-------------|--------|-------|-------------------|
| 1          | 5288   | 98.9        | 1091   | 1     | US-07-745-206A-25 |
| 2          | 5288   | 98.9        | 1091   | 1     | US-08-455-543A-52 |
| 3          | 5288   | 98.9        | 1091   | 2     | US-08-223-305C-52 |
| 4          | 5288   | 98.9        | 1091   | 2     | US-08-311-363-25  |
| 5          | 5284   | 98.8        | 1091   | 3     | US-08-713-118-4   |
| 6          | 5284   | 98.8        | 1091   | 4     | US-09-452-007-4   |
| 7          | 5248.5 | 98.1        | 1086   | 1     | US-08-455-543A-54 |
| 8          | 5248.5 | 98.1        | 1086   | 2     | US-08-223-305C-54 |
| 9          | 5231.5 | 97.8        | 1084   | 1     | US-08-455-543A-56 |
| 10         | 5231.5 | 97.8        | 1084   | 2     | US-08-223-305C-56 |
| 11         | 5212   | 97.4        | 1103   | 1     | US-08-455-543A-53 |
| 12         | 5212   | 97.4        | 1103   | 2     | US-08-223-305C-53 |
| 13         | 5192   | 97.1        | 1079   | 1     | US-08-455-543A-55 |
| 14         | 5192   | 97.1        | 1079   | 2     | US-08-223-305C-55 |
| 15         | 5161.5 | 96.5        | 1106   | 1     | US-08-435-675B-5  |
| 16         | 5143.5 | 96.2        | 1106   | 1     | US-08-336-257A-8  |
| 17         | 4937   | 92.3        | 1086   | 6     | 5386025-8         |
| 18         | 2887.5 | 54.0        | 1145   | 4     | US-09-470-443-2   |
| 19         | 2887.5 | 54.0        | 1145   | 4     | US-09-470-443-4   |
| 20         | 2866.5 | 53.6        | 1076   | 4     | US-09-470-443-6   |
| 21         | 2563.5 | 47.9        | 508    | 1     | US-08-435-675B-6  |
| 22         | 185    | 3.5         | 885    | 3     | US-09-074-579-5   |
| 23         | 185    | 3.5         | 885    | 4     | US-09-388-774-5   |
| 24         | 164.5  | 3.1         | 789    | 1     | US-08-471-033-32  |
| 25         | 164.5  | 3.1         | 789    | 1     | US-08-471-044-32  |
| 26         | 164.5  | 3.1         | 789    | 2     | US-08-463-483A-32 |
| 27         | 164.5  | 3.1         | 789    | 2     | US-08-471-046A-32 |

|    |       |     |     |   |                   |                   |
|----|-------|-----|-----|---|-------------------|-------------------|
| 28 | 164.5 | 3.1 | 789 | 2 | US-08-470-566B-32 | Sequence 32, Appl |
| 29 | 164.5 | 3.1 | 789 | 2 | US-08-838-219B-4  | Sequence 4, Appl  |
| 30 | 164.5 | 3.1 | 789 | 2 | US-08-469-334-32  | Sequence 32, Appl |
| 31 | 164.5 | 3.1 | 789 | 3 | US-09-300-529-32  | Sequence 32, Appl |
| 32 | 164.5 | 3.1 | 789 | 3 | US-09-233-336A-4  | Sequence 4, Appl  |
| 33 | 164.5 | 3.1 | 789 | 4 | US-09-233-336A-4  | Sequence 4, Appl  |
| 34 | 164.5 | 3.1 | 789 | 4 | US-09-402-036-4   | Sequence 4, Appl  |
| 35 | 164.5 | 3.1 | 789 | 4 | US-09-402-036-4   | Sequence 4, Appl  |
| 36 | 161.5 | 3.0 | 746 | 2 | US-08-838-219B-6  | Sequence 6, Appl  |
| 37 | 161.5 | 3.0 | 746 | 3 | US-09-233-336A-6  | Sequence 6, Appl  |
| 38 | 161.5 | 3.0 | 746 | 4 | US-09-233-336A-6  | Sequence 6, Appl  |
| 39 | 161.5 | 3.0 | 746 | 4 | US-09-402-036-6   | Sequence 6, Appl  |
| 40 | 161.5 | 3.0 | 746 | 4 | US-09-402-036-6   | Sequence 6, Appl  |
| 41 | 160.5 | 3.0 | 790 | 4 | US-08-960-780-4   | Sequence 4, Appl  |
| 42 | 160.5 | 3.0 | 790 | 4 | US-09-073-898-4   | Sequence 4, Appl  |
| 43 | 160.5 | 3.0 | 946 | 3 | US-09-074-579-3   | Sequence 3, Appl  |
| 44 | 160.5 | 3.0 | 946 | 4 | US-09-388-774-3   | Sequence 3, Appl  |
| 45 | 157.5 | 2.9 | 789 | 4 | US-08-960-780-6   | Sequence 6, Appl  |

## ALIGNMENTS

RESULT 1  
US-07-745-206A-25Sequence 25, Application US/07745206A  
Patent No. 5429921

## GENERAL INFORMATION:

APPLICANT: Harpold, Michael

APPLICANT: Ellis, Steven

APPLICANT: Williams, Mark

APPLICANT: McCue, Ann

TITLE OF INVENTION: Feldman, Daniel

TITLE OF INVENTION: Human Calcium Channel Compositions and

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSER: Fitch, Even, Tabin &amp; Flannery

STREET: 135 S. LaSalle

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/745,206A

FILING DATE: 19910815

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Feder, Scott B

REFERENCE/DOCKET NUMBER: 51504

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-372-7842

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 1091 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-745-206A-25

Query Match 98.9%; Score 5288; DB 1; Length 1091;  
Best Local Similarity 98.8%; Pred. No. 0;  
Matches 1006; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLTLPFOSLLIGPSSEPPSAVTKSMVDMQEDVTLAKTASGVNQVLDI 60  
DB 1 MAAGCLLALTLTLPFOSLLIGPSSEPPSAVTKSMVDMQEDVTLAKTASGVNQVLDI 60

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QY 61 YEKYODLYTEVPNNARQVEIAARDIEKLISNSRSKALVRLALEAEKVOAAHOMREDFASN 120
    |||||||
DB 61 YEKYODLYTEVPNNARQVEIAARDIEKLISNSRSKALVRLALEAEKVOAAHOMREDFASN 120
QY 121 EYVYIYNAKDIDPEKNDSPEGSORIKKPYFTIDANFGROISTQHAAYHLPDIYEGSTIVL 180
    |||||||
DB 121 EYVYIYNAKDIDPEKNDSPEGSORIKKPYFTIDANFGROISTQHAAYHLPDIYEGSTIVL 180
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DB 181 NELNMTSLADIEVFKKNNREDESSLIMOVGSGATGLARYPASPWNDSTPKIDLYVRR 240
QY 241 RPYWYIQAASPKMDLIVDVGSGVSGTLTKLIRTSVSEMEETLSDDDFVNVAESPNSAOD 300
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DB 241 RPYWYIQAASPKMDLIVDVGSGVSGTLTKLIRTSVSEMEETLSDDDFVNVAESPNSAOD 300
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DB 301 VSCFQHLVQAVNRKKVYLKDAVNNITAKGIDYKKGSFAFEQLLNVSANCNKTIIML 360
QY 361 FPDGGEERAQELFNKYNDKKVYRFTPSVGOHNDRCPIOMACENKGYEIPISGAIR 420
    |||||||
DB 361 FPDGGEERAQELFNKYNDKKVYRFTPSVGOHNDRCPIOMACENKGYEIPISGAIR 420
QY 421 INFOEYLDVLRPMVLAGDKAKQVOMTVYLDALGLVITGTLPEVNITGQENKTNLK 480
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DB 421 INFOEYLDVLRPMVLAGDKAKQVOMTVYLDALGLVITGTLPEVNITGQENKTNLK 480
QY 481 NOLIGVGVSVSLIEDIKRLPRFLCPNGYFPAIDPBGVYLLHPNLOPKMKQDEPTL 540
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DB 481 NOLIGVGVSVSLIEDIKRLPRFLCPNGYFPAIDPBGVYLLHPNLOPKMKQDEPTL 540
QY 541 DELDAELENDIKVEIRNMKINGESEGETFRLVKSODERYIDKGNRTWTWPNVGTQVSL 600
    |||||||
DB 541 DELDAELENDIKVEIRNMKINGESEGETFRLVKSODERYIDKGNRTWTWPNVGTQVSL 600
QY 601 ALVLPYGYFYIKAKIETITQANSKKGKMKDSEFLKPDNEESGYTPIAPRDYCNLDKI 660
    |||||||
DB 601 ALVLPYGYFYIKAKIETITQANSKKGKMKDSEFLKPDNEESGYTPIAPRDYCNLDKI 660
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    |||||||
DB 661 SONNTEFLNNEFTDRKTPNNPSCNPTDLINRVILDACTNEIYONVSKKNIKGVYAR 720
QY 721 FVYTDGCTIRVYPKRAGENNMOENPETYEDSEFYKSLDNDNVETAPYFNKSGPGAYESGI 780
    |||||||
DB 721 FVYTDGCTIRVYPKRAGENNMOENPETYEDSEFYKSLDNDNVETAPYFNKSGPGAYESGI 780
QY 781 MYSKAVEIYIIGKLLKPAVVGKIDVNSWIENFTKTSIRDPACAGPYCDCKRNSDVMCVI 840
    |||||||
DB 781 MYSKAVEIYIIGKLLKPAVVGKIDVNSWIENFTKTSIRDPACAGPYCDCKRNSDVMCVI 840
QY 841 LDDGGEFLMANHDDYTNIGRFGFIDSLMRHLVNIYVAFNKSYSYDQSCFEGAAPKQ 900
    |||||||
DB 841 LDDGGEFLMANHDDYTNIGRFGFIDSLMRHLVNIYVAFNKSYSYDQSCFEGAAPKQ 900
QY 901 GAGHSAAVYPSIADILHIGWATAAAMSILQOFLSLTFPRULAEVEMEDDFTASLSKQ 960
    |||||||
DB 901 GAGHSAAVYPSIADILHIGWATAAAMSILQOFLSLTFPRULAEVEMEDDFTASLSKQ 960
QY 961 SCITQOTQYFPDNDKSSSGVLDGCGCRIFRIVEKIMNTNLIFTVYESKGTGCPDTRL 1018
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DB 961 SCITQOTQYFPDNDKSSSGVLDGCGCRIFRIVEKIMNTNLIFTVYESKGTGCPDTRL 1018

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## RESULT 2

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US-08-455-543A-52
; Sequence 52, Application US/08455543A
; Patent No. 5792846
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark

```

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APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESS: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
FILING DATE: May 31, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-455-543A-52
Query Match 98.9%; Score 5288; DB 1; length 1091;
Best local similarity 98.8%; Pred. No. 0;
Matches 1006; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

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DB 241 RPWYIGGAASPKDMLTLVVGSGVSGSLTKLIRTSVSEMLFTLSDDEFFVNAVSFNSMAD 300
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DB 301 VSCFOHLVQANVRANKVLDKAVNNITAKITDYKKGFSAFEOLLNTYNSRANCKIIML 360
QY 361 FTDGGERAOEITFAKYNKCKKRVFESVGOHNDYRGPLOMACENKGYEIPSTIGAIR 420
DB 361 FTDGGERAOEITFAKYNKCKKRVFESVGOHNDYRGPLOMACENKGYEIPSTIGAIR 420
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DB 421 INTQETLDVLRGPRVLADGKAKOVMTNYYLDALDELGLVITGTLVFNITGQENKNTMLK 480
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DB 481 NOLITGVNGVDVSLIEDIRLTPRFLCNGYFFAIDPMGYVLLHPNLOPKNPKSOEPTVL 540
QY 541 DELDAELENDDIKVEIRNKMIDGESGEKTFRTLVKSODERYIDKGRYTWMPVNTDLSL 600
DB 541 DELDAELENDDIKVEIRNKMIDGESGEKTFRTLVKSODERYIDKGRYTWMPVNTDLSL 600
QY 601 ALVLTYSFYIYKAKIETITQARSKKGMKDESLTKPDNFEESGYTPPIAPRDYCNLDKI 660
DB 601 ALVLTYSFYIYKAKIETITQARSKKGMKDESLTKPDNFEESGYTPPIAPRDYCNLDKI 660
QY 661 SDNTEFLNTEFLNTEFLNTEFLNTEFLNTEFLNTEFLNTEFLNTEFLNTEFLNTEFLN 720
DB 661 SDNTEFLNTEFLNTEFLNTEFLNTEFLNTEFLNTEFLNTEFLNTEFLNTEFLNTEFLN 720
QY 721 FVVTGIGITRYVPEKAGENMOENPEYEDSFYKRSILDNDNVFTAPYFNKSGPAYESGI 780
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DB 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNISSVAFNKSSTYOSVCEGGAAPKQ 900
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DB 901 GAGHRSAYVPSIADILHIGWATAAANSIIQOFLSLTFRLLTAVEMEDDFTASLSKQ 960
QY 961 SCIEQOYFPPDNKSKFSFGVLDGNCRSIFVHEKIMNTNLIPIVMSKGTCPDTRL 1018
DB 961 SCIEQOYFPPDNKSKFSFGVLDGNCRSIFVHEKIMNTNLIPIVMSKGTCPDTRL 1018

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RESULT 3
US-08-223-305C-52
; Sequence 52, Application US/08223305C
; Patent No. 5851824
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert

```

```

TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/223,305C
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 52516 (P519739)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0062
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-223-305C-52

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Query Match 98.9%; Score 5288; DB 2; Length 1091;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1006; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
QY 1 MAAGCLLALTLTIFOSLIGPSSQEPFSAVITKSWDKMOEDLVTLAKTASGVNQLVDI 60
DB 1 MAAGCLLALTLTIFOSLIGPSSQEPFSAVITKSWDKMOEDLVTLAKTASGVNQLVDI 60
QY 61 YEKYODLYVEPNAROLVEIARDEKLSNRKALVLALEAKRYQAAHQWREDFASN 120
DB 61 YEKYODLYVEPNAROLVEIARDEKLSNRKALVLALEAKRYQAAHQWREDFASN 120
QY 121 EYVYNAKDDLDPEKNDSEPGSORIKPVETIDANFGROIISYQAAVHIPTDIYEGSTIVL 180
DB 121 EYVYNAKDDLDPEKNDSEPGSORIKPVETIDANFGROIISYQAAVHIPTDIYEGSTIVL 180
QY 181 NELNMTSALDEYFKKRNREDDPSLIMQVGSATGLARIYPASFWNDSRTPKNKIDLYDVR 240
DB 181 NELNMTSALDEYFKKRNREDDPSLIMQVGSATGLARIYPASFWNDSRTPKNKIDLYDVR 240

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181 NEIWMTSALDEVEKRNKNEEDPSILMOVFGSATGLARYPASPVWDSRTPNKIDLDYVR 240
241 RPYWIOGAASPKDMLILVDVSGSVSGITLKLIRTSVSEMLETISDDDFVNVASFNMAOD 300
241 RPYWIOGAASPKDMLILVDVSGSVSGITLKLIRTSVSEMLETISDDDFVNVASFNMAOD 300
301 VSCFOHLVOANVRNKKVLAOVANNITAKGTTDYKKGFSFAEQLNYSRANCKIIML 360
301 VSCFOHLVOANVRNKKVLAOVANNITAKGTTDYKKGFSFAEQLNYSRANCKIIML 360
361 FTDSGEERAOEIFAKYKDKKVRFFSVGOHNDRGPIDOMMACENKGYEIPISGAIR 420
361 FTDSGEERAOEIFAKYKDKKVRFFSVGOHNDRGPIDOMMACENKGYEIPISGAIR 420
421 INFOEYLDVIGRPMVLAAGDKAKOVQWNTNYLDALGLVITGLPVFNITGQENKTNLK 480
421 INFOEYLDVIGRPMVLAAGDKAKOVQWNTNYLDALGLVITGLPVFNITGQENKTNLK 480
481 NQILIGWGVDSLEDIKRLTPRTLCPNGYFAIDPNGVYLHPNLOPKNPSQEPVTL 540
481 NQILIGWGVDSLEDIKRLTPRTLCPNGYFAIDPNGVYLHPNLOPKNPSQEPVTL 540
541 DELAELENDIKVEIRNKMIDEGSEKFTFLVKSODERYIDKGNRTYTWPVNGTDSL 600
541 DELAELENDIKVEIRNKMIDEGSEKFTFLVKSODERYIDKGNRTYTWPVNGTDSL 600
601 ALVLPYTSFYIKAKIEETITQARSKKGKMDSETLKPNEESGYFFIARPDYCNLDKI 660
601 ALVLPYTSFYIKAKIEETITQARSKKGKMDSETLKPNEESGYFFIARPDYCNLDKI 660
661 SDNTEFLTNNEFTDRKTPNPNPCNDLIRVYLLDAGFTLQVONWSKOKNKGVAR 720
661 SDNTEFLTNNEFTDRKTPNPNPCNDLIRVYLLDAGFTLQVONWSKOKNKGVAR 720
721 FVYTDGIGITRYYPKEAGENQENPETYEDSFYKRSILDNDNVYTAIFYNKSGBPAYSIGI 780
721 FVYTDGIGITRYYPKEAGENQENPETYEDSFYKRSILDNDNVYTAIFYNKSGBPAYSIGI 780
781 MYSKAVEIYIOGKILKRAVNGIKIDVNSWIEFNFTKSTRDCAGPYCDCKRNSVMOCVI 840
781 MYSKAVEIYIOGKILKRAVNGIKIDVNSWIEFNFTKSTRDCAGPYCDCKRNSVMOCVI 840
841 LDDGFFLLMANHDDYTNOIGRFGSIDPSLMRLHVNISVYAFNKSUYDQSVCEGAAPKQ 900
841 LDDGFFLLMANHDDYTNOIGRFGSIDPSLMRLHVNISVYAFNKSUYDQSVCEGAAPKQ 900
901 GAGRSAYVPSIADILHIGWATAAASILQOFLISTFPRLLEAVEEMEDDFTASLSKQ 960
901 GAGRSAYVPSIADILHIGWATAAASILQOFLISTFPRLLEAVEEMEDDFTASLSKQ 960
961 SCITROTOTFFPNDKSPSGVLDGNCGRIFHEKIMNTNLIIFIVESKGTCPDTRL 1018
961 SCITROTOTFFPNDKSPSGVLDGNCGRIFHEKIMNTNLIIFIVESKGTCPDTRL 1018

```

## RESULT 4

US-08-311-363-25

Sequence 25, Application US/08311363

Patent No. 5678958

GENERAL INFORMATION:

APPLICANT: Harpold, Michael

APPLICANT: Ellis, Steven

APPLICANT: Williams, Mark

APPLICANT: Feldman, Daniel

APPLICANT: McCue, Ann

APPLICANT: Brenner, Robert

TITLE OF INVENTION: Human Calcium Channel Compositions and

METHODS

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller &amp; McClain

STREET: 1660 Union Street

```

CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,363
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-51506
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-311-363-25

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Query Match 98.9%; Score 5288; DB 2; Length 1091;
Best local similarity 98.8%; Pred. No. 0;
Matches 1006; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

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1 MAAGCLLALTLTFOSSLIGPSSQEPFSAVITKSWVDKMOEDVYLAFTASGVNOVDI 60
1 MAAGCLLALTLTFOSSLIGPSSQEPFSAVITKSWVDKMOEDVYLAFTASGVNOVDI 60
61 YEKYODLYTEPNNAOLVEIARDIEKLISNRKALVLALEAEKVQAHOHREDFASN 120
61 YEKYODLYTEPNNAOLVEIARDIEKLISNRKALVLALEAEKVQAHOHREDFASN 120
121 EYVYNAKDLDEPKNDSEPGSORIKPVFIIDANPEROISYQAAVHPTDLYEGSTYL 180
121 EYVYNAKDLDEPKNDSEPGSORIKPVFIIDANPEROISYQAAVHPTDLYEGSTYL 180
181 NEIWMTSALDEVEKRNKNEEDPSILMOVFGSATGLARYPASPVWDSRTPNKIDLDYVR 240
181 NEIWMTSALDEVEKRNKNEEDPSILMOVFGSATGLARYPASPVWDSRTPNKIDLDYVR 240
241 RPYWIOGAASPKDMLILVDVSGSVSGITLKLIRTSVSEMLETISDDDFVNVASFNMAOD 300
241 RPYWIOGAASPKDMLILVDVSGSVSGITLKLIRTSVSEMLETISDDDFVNVASFNMAOD 300
301 VSCFOHLVOANVRNKKVLAOVANNITAKGTTDYKKGFSFAEQLNYSRANCKIIML 360
301 VSCFOHLVOANVRNKKVLAOVANNITAKGTTDYKKGFSFAEQLNYSRANCKIIML 360
361 FTDSGEERAOEIFAKYKDKKVRFFSVGOHNDRGPIDOMMACENKGYEIPISGAIR 420
361 FTDSGEERAOEIFAKYKDKKVRFFSVGOHNDRGPIDOMMACENKGYEIPISGAIR 420
421 INFOEYLDVIGRPMVLAAGDKAKOVQWNTNYLDALGLVITGLPVFNITGQENKTNLK 480
421 INFOEYLDVIGRPMVLAAGDKAKOVQWNTNYLDALGLVITGLPVFNITGQENKTNLK 480
481 NQILIGWGVDSLEDIKRLTPRTLCPNGYFAIDPNGVYLHPNLOPKNPSQEPVTL 540
481 NQILIGWGVDSLEDIKRLTPRTLCPNGYFAIDPNGVYLHPNLOPKNPSQEPVTL 540
541 DELAELENDIKVEIRNKMIDEGSEKFTFLVKSODERYIDKGNRTYTWPVNGTDSL 600
541 DELAELENDIKVEIRNKMIDEGSEKFTFLVKSODERYIDKGNRTYTWPVNGTDSL 600

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QY 601 ALVPTYSFYIYIKAKIEETITQANSKKGKMKDSETLKPDNFEESGYTPIAPDYCNDLKI 660
DB 601 ALVPTYSFYIYIKAKIEETITQANSKKGKMKDSETLKPDNFEESGYTPIAPDYCNDLKI 660
QY 661 SDNTEFLNNEFLNDRTPNPNPCNDLIRVLLDAGFTNELVQNTWSKKNIKGYKAR 720
DB 661 SDNTEFLNNEFLNDRTPNPNPCNDLIRVLLDAGFTNELVQNTWSKKNIKGYKAR 720
QY 721 FVYTDGITRYPRKAGENMOENPEYEDSFYKRSILDNDNYVTAPEFNKSGPAYESGI 780
DB 721 FVYTDGITRYPRKAGENMOENPEYEDSFYKRSILDNDNYVTAPEFNKSGPAYESGI 780
QY 781 MYSKAVEIYIOGKLKPAVVGIKIDVNSWIEFTKTSIRDPACAPVDCCKRNSDVMCVI 840
DB 781 MYSKAVEIYIOGKLKPAVVGIKIDVNSWIEFTKTSIRDPACAPVDCCKRNSDVMCVI 840
QY 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNSVAFNKSXYQSVCEPGAAPKQ 900
DB 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNSVAFNKSXYQSVCEPGAAPKQ 900
QY 901 GAGHRSAYVPSIADILHIGMWATAAAMSILOQFLSLTFPRLLEAVEMEDDDFTASLSKQ 960
DB 901 GAGHRSAYVPSIADILHIGMWATAAAMSILOQFLSLTFPRLLEAVEMEDDDFTASLSKQ 960
QY 961 SCITEOTGYFFDNDKSFSGVLDGNCGRIFHEVEKLMNTLIFTWESKGTCPDTRL 1018
DB 961 SCITEOTGYFFDNDKSFSGVLDGNCGRIFHEVEKLMNTLIFTWESKGTCPDTRL 1018

```

## RESULT 5

```

US-08-713-118-4
Sequence 4, Application US/08713118
Patent No. 6040436
GENERAL INFORMATION:
APPLICANT: Franco, Rodrigo
APPLICANT: Sun Chen, Ai Ru
APPLICANT: Suey, David J.
TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713, 118
FILING DATE: 16-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mata, Elizabeth W.
REGISTRATION NUMBER: 38,236
REFERENCE/DOCKET NUMBER: ACC96-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-713-118-4

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Query Match 98.8%; Score 5284; DB 3; Length 1091;

Best Local Similarity 98.7%; Pred. No. 0;  
Matches 1005; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

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QY 1 MAAGCLLALTLTLFOSLLIPSSQEPSPAVTIKSWDKQEDVTLATASGVNOLDVI 60
DB 1 MAAGCLLALTLTLFOSLLIPSSQEPSPAVTIKSWDKQEDVTLATASGVNOLDVI 60
QY 61 YEKYODLYTEPPNAROLVETIARDIEKLSNSKALVLAELAEVQAHOHREFPASN 120
DB 61 YEKYODLYTEPPNAROLVETIARDIEKLSNSKALVLAELAEVQAHOHREFPASN 120
QY 121 EYVYNAKDLDPEKNDSEPGSORIKPVFTIDANFGRQISYQAAVHPTDIYEGSTIYL 180
DB 121 EYVYNAKDLDPEKNDSEPGSORIKPVFTIDANFGRQISYQAAVHPTDIYEGSTIYL 180
QY 181 NELNMTSALDEVEKKNREEDPSILMQVFGSATGLARYPASPWNDSRTPNKIDLYDVR 240
DB 181 NELNMTSALDEVEKKNREEDPSILMQVFGSATGLARYPASPWNDSRTPNKIDLYDVR 240
QY 241 RPYVIGGAAPKMLILVYSGSVGLTLKLTPTSVSEMLETLSDDDFYNVASFNSNAD 300
DB 241 RPYVIGGAAPKMLILVYSGSVGLTLKLTPTSVSEMLETLSDDDFYNVASFNSNAD 300
QY 301 VSCFOHLVQANVRNKKVLDVANNITAKGITYKKGSFAFQDLNLYNSRANCKIIML 360
DB 301 VSCFOHLVQANVRNKKVLDVANNITAKGITYKKGSFAFQDLNLYNSRANCKIIML 360
QY 361 FTDGGEEBAQELFAKYNKCKKRVFFSVGOHNYDRPIOMMACENKGYEIPISGAIR 420
DB 361 FTDGGEEBAQELFAKYNKCKKRVFFSVGOHNYDRPIOMMACENKGYEIPISGAIR 420
QY 421 INTOEYLDVLRPMVLVAGRAKQOVNTNYLDALDELGLVITGTLPENTTGNENKNTNK 480
DB 421 INTOEYLDVLRPMVLVAGRAKQOVNTNYLDALDELGLVITGTLPENTTGNENKNTNK 480
QY 481 NOLILGVMDVSLIEDIKRLTPFTLCPNGYFAIDPNCYVLLHPNLOPKNKSQEPYTL 540
DB 481 NOLILGVMDVSLIEDIKRLTPFTLCPNGYFAIDPNCYVLLHPNLOPKNKSQEPYTL 540
QY 541 DFLDALDELNDIWEIENKKNIDSESGKTPRTLYKSODEXYIRKGNRTYTWTPVNGTDSL 600
DB 541 DFLDALDELNDIWEIENKKNIDSESGKTPRTLYKSODEXYIRKGNRTYTWTPVNGTDSL 600
QY 601 ALVPTYSFYIYIKAKIEETITQANSKKGKMKDSETLKPDNFEESGYTPIAPDYCNDLKI 660
DB 601 ALVPTYSFYIYIKAKIEETITQANSKKGKMKDSETLKPDNFEESGYTPIAPDYCNDLKI 660
QY 661 SDNTEFLNNEFLNDRTPNPNPCNDLIRVLLDAGFTNELVQNTWSKKNIKGYKAR 720
DB 661 SDNTEFLNNEFLNDRTPNPNPCNDLIRVLLDAGFTNELVQNTWSKKNIKGYKAR 720
QY 721 FVYTDGITRYPRKAGENMOENPEYEDSFYKRSILDNDNYVTAPEFNKSGPAYESGI 780
DB 721 FVYTDGITRYPRKAGENMOENPEYEDSFYKRSILDNDNYVTAPEFNKSGPAYESGI 780
QY 781 MYSKAVEIYIOGKLKPAVVGIKIDVNSWIEFTKTSIRDPACAPVDCCKRNSDVMCVI 840
DB 781 MYSKAVEIYIOGKLKPAVVGIKIDVNSWIEFTKTSIRDPACAPVDCCKRNSDVMCVI 840
QY 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNSVAFNKSXYQSVCEPGAAPKQ 900
DB 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNSVAFNKSXYQSVCEPGAAPKQ 900
QY 901 GAGHRSAYVPSIADILHIGMWATAAAMSILOQFLSLTFPRLLEAVEMEDDDFTASLSKQ 960
DB 901 GAGHRSAYVPSIADILHIGMWATAAAMSILOQFLSLTFPRLLEAVEMEDDDFTASLSKQ 960
QY 961 SCITEOTGYFFDNDKSFSGVLDGNCGRIFHEVEKLMNTLIFTWESKGTCPDTRL 1018
DB 961 SCITEOTGYFFDNDKSFSGVLDGNCGRIFHEVEKLMNTLIFTWESKGTCPDTRL 1018

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RESULT 6

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US-09-452-007-4
: Sequence 4, Application US/09452007
: Patent No. 6140485
: GENERAL INFORMATION:
: APPLICANT: Franco, Rodrigo
: APPLICANT: Sun Chen, Ai Ru
: APPLICANT: Suey, David J.
: TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL
: TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P. C.
: STREET: Two Militia Drive
: CITY: Lexington
: STATE: MA
: COUNTRY: USA
: ZIP: 02173-4799
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/452,007
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/713,118
: FILING DATE: 16-SEP-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Mala, Elizabeth W.
: REGISTRATION NUMBER: 38,236
: REFERENCE/DOCKET NUMBER: ACC96-01
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-861-6240
: TELEFAX: 617-861-9540
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1091 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
:
US-09-452-007-4
Query Match 98.8%; Score 5284; DB 4; Length 1091;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1005; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

```

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DB 361 FTDGGEERAQELFAKYNKDKKRVFTFSVGOHNDRGFIOMMACENKGYEISIGAIR 420
OY 421 INTQEVLDVLRPMVLGAGKAKOVONTVYLDALFLGLVITGTLPPVFNITGONEKNTLK 480
DB 421 INTQEVLDVLRPMVLGAGKAKOVONTVYLDALFLGLVITGTLPPVFNITGONEKNTLK 480
OY 481 NOLLIGMGVDVSLDIDKRLPRFTLCPNGYFFAIDPNGYVLLHPNLOPKNPKSGEPTL 540
DB 481 NOLLIGMGVDVSLDIDKRLPRFTLCPNGYFFAIDPNGYVLLHPNLOPKNPKSGEPTL 540
OY 541 DFLDALENDIVEIRKMKMIDGSEBKTFRILVKSODERYIDKGRITWTVPVNGTDSL 600
DB 541 DFLDALENDIVEIRKMKMIDGSEBKTFRILVKSODERYIDKGRITWTVPVNGTDSL 600
OY 601 ALVLPYTSFYIYIKAKIEETITQARSKGKMDSETLKPDNPEESGYTFLAPDYCNLDKI 660
DB 601 ALVLPYTSFYIYIKAKIEETITQARSKGKMDSETLKPDNPEESGYTFLAPDYCNLDKI 660
OY 661 SDNTEFLINFEFIDRKTPNPNPCNTDLINRVLDAFTNELVONYMSKONIKGVAR 720
DB 661 SDNTEFLINFEFIDRKTPNPNPCNTDLINRVLDAFTNELVONYMSKONIKGVAR 720
OY 721 FVYTDGGITRVYPRKAGEWQENPETYEDSFYKSLDNDNYFTAPYKNSGPGAYESGI 780
DB 721 FVYTDGGITRVYPRKAGEWQENPETYEDSFYKSLDNDNYFTAPYKNSGPGAYESGI 780
OY 781 MYSKAVEIYIOGKLKPAVVGKIDVNSWIENFTKTSIRDPCAGVCCCKRSDVMDCVI 840
DB 781 MYSKAVEIYIOGKLKPAVVGKIDVNSWIENFTKTSIRDPCAGVCCCKRSDVMDCVI 840
OY 841 LDDGFLMANHDDYNTQIGREFGEIDPSLMRLVNI SYAFNKSYDYOSVCEPAABKQ 900
DB 841 LDDGFLMANHDDYNTQIGREFGEIDPSLMRLVNI SYAFNKSYDYOSVCEPAABKQ 900
OY 901 GAGHRSAIYVPSIDILHITGMATAAWSLLOOPLSLTPRLLEAVEMDDFTSLSKQ 960
DB 901 GAGHRSAIYVPSIDILHITGMATAAWSLLOOPLSLTPRLLEAVEMDDFTSLSKQ 960
OY 961 SCITTEOTYFFNDSSFSGVLDCCGNCRIPIHYEKLMTNLFIIVESKGTGCPDTRL 1018
DB 961 SCITTEOTYFFNDSSFSGVLDCCGNCRIPIHYEKLMTNLFIIVESKGTGCPDTRL 1018

RESULT 7
US-08-455-543A-54
: Sequence 54, Application US/0845543A
: Patent No. 5792846
: GENERAL INFORMATION:
: APPLICANT: Harpold, Michael
: APPLICANT: Ellis, Steven
: APPLICANT: Williams, Mark
: APPLICANT: Feldman, Daniel
: APPLICANT: McCue, Ann
: TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
: TITLE OF INVENTION: METHODS
: NUMBER OF SEQUENCES: 57
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Brown, Martin, Haller & McClain
: STREET: 1660 Union Street
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92101-2926
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq Version 1.5
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/455,543A
: FILING DATE: May 31, 1995

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PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/223,305  
 FILING DATE: April 4, 1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/868,354  
 FILING DATE: April 10, 1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/745,206  
 FILING DATE: 15-AUG-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/620,250  
 FILING DATE: 30-NOV-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/482,384  
 FILING DATE: 20-FEB-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/603,751  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/US89/01408  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/176,899  
 FILING DATE: 04-APR-1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie L.  
 REGISTRATION NUMBER: 33,779  
 REFERENCE/DOCKET NUMBER: 6362-52517  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619)238-0999  
 TELEFAX: (619)238-0062  
 INFORMATION FOR SEQ ID NO: 54:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1086 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-435-543a-54

Query Match 98.1%; Score 5248.5; DB 1; Length 1086;  
 Best Local Similarity 98.3%; Pred. No. 0;  
 Matches 1001; Conservative 5; Mismatches 7; Indels 5; Gaps 1;

QY 1 MAAGCLLALFLTLFQSLIGPSSQEPPEPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60  
 DB 1 MAAGCLLALFLTLFQSLIGPSSQEPPEPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60  
 QY 61 YEKQDLYTEPNNAKQVLVIAARDIEKLSSNSKALVRLALEAKVQAAHQWREDFASN 120  
 DB 61 YEKQDLYTEPNNAKQVLVIAARDIEKLSSNSKALVRLALEAKVQAAHQWREDFASN 120  
 QY 121 EYVYNAKDDLDPEKNDSESGSRIKPFVITDANFGQISYQAAVHIPIIDIEGSTIYL 180  
 DB 121 EYVYNAKDDLDPEKNDSESGSRIKPFVITDANFGQISYQAAVHIPIIDIEGSTIYL 180  
 QY 181 NELNMTSALDVEFKKNEEDPSILMQVFGSATGLARYPPASPMWDSRTPNKIDLYDVR 240  
 DB 181 NELNMTSALDVEFKKNEEDPSILMQVFGSATGLARYPPASPMWDSRTPNKIDLYDVR 240  
 QY 241 RPYWIOGAASPKMLITLVDSGSVSGITLKITVSSEMLETISDDDFVAVAFNSNAOD 300  
 DB 241 RPYWIOGAASPKMLITLVDSGSVSGITLKITVSSEMLETISDDDFVAVAFNSNAOD 300  
 QY 301 VSCFOHLVQANVRNKVYLKDAVNNITAKGITYKKGFSFAFEOLLNVNVRACNKIIML 360  
 DB 301 VSCFOHLVQANVRNKVYLKDAVNNITAKGITYKKGFSFAFEOLLNVNVRACNKIIML 360  
 QY 361 FTDGGERRADEFIRAKTKKKVRYVTFSGOHNYDRQPIOMMACENKGYEYIPISIGAIR 420  
 DB 361 FTDGGERRADEFIRAKTKKKVRYVTFSGOHNYDRQPIOMMACENKGYEYIPISIGAIR 420

QY 421 INTQEYLDVLRGPMVLADGKAKOVONTNYYLDALDELGITLTLPYFNITGQENKNTLK 480  
 DB 421 INTQEYLDVLRGPMVLADGKAKOVONTNYYLDALDELGITLTLPYFNITGQENKNTLK 480  
 QY 481 NOILIGMVDVSLIEDIKRLTPFTLCIPNGYIFAIDPNQVYLHPMLQPKNSQBPVTL 540  
 DB 481 NOILIGMVDVSLIEDIKRLTPFTLCIPNGYIFAIDPNQVYLHPMLQPKNSQBPVTL 540  
 QY 541 DFLDAELENDIKVEIRNKMDIGESGKPTRTLKSDSEYIDKGNNTYWPVNGDVL 600  
 DB 541 DFLDAELENDIKVEIRNKMDIGESGKPTRTLKSDSEYIDKGNNTYWPVNGDVL 600  
 QY 601 ALVLPYSEFYIKAKIETITQARSKKGMKDETLKPNFEESGYTFIAPDYCNDLKI 660  
 DB 601 ALVLPYSEFYIKAKIETITQARSKKGMKDETLKPNFEESGYTFIAPDYCNDLKI 660  
 QY 661 SDNTEFLNENFTDRKTPNPNPSCWTDLINRYLDAGTNNELVONYSKQNKIKGVAR 720  
 DB 661 SDNTEFLNENFTDRKTPNPNPSCWTDLINRYLDAGTNNELVONYSKQNKIKGVAR 720  
 QY 721 FVYTDGITRVYPKFAGEKMOENPETEDSFYKRSIDNDNNTVFTAPYFKSGPGAYESGI 780  
 DB 721 FVYTDGITRVYPKFAGEKMOENPETEDSFYKRSIDNDNNTVFTAPYFKSGPGAYESGI 780  
 QY 776 MSKAVEIYIQGKLKPAVVGIRKIDVNSWIEFTKTSIRDPCAGPYCDCKRSDVMDCVI 840  
 DB 776 MSKAVEIYIQGKLKPAVVGIRKIDVNSWIEFTKTSIRDPCAGPYCDCKRSDVMDCVI 840  
 QY 841 LDGGLFLMANHDYTNQGRFGEIDPSLMRLVNI SYAANKSYDIQSVCEPAAPRO 900  
 DB 841 LDGGLFLMANHDYTNQGRFGEIDPSLMRLVNI SYAANKSYDIQSVCEPAAPRO 900  
 QY 901 GAGHRSAVYPSIADILHIGMATAAAMSILOQFLSLFPRLLEAVEMDDDFTSLSKQ 960  
 DB 901 GAGHRSAVYPSIADILHIGMATAAAMSILOQFLSLFPRLLEAVEMDDDFTSLSKQ 960  
 QY 961 SCTTEOTQTFPNDKSGSEGVLDGCGNSRIFFVEKIMNTLFIWESKGTGCPDTRL 1018  
 DB 961 SCTTEOTQTFPNDKSGSEGVLDGCGNSRIFFVEKIMNTLFIWESKGTGCPDTRL 1018

RESULT 8  
 US-08-223-305C-54  
 Sequence 54, Application US/08223305C  
 Patent No. 5851824  
 GENERAL INFORMATION:  
 APPLICANT: Harpold, Michael  
 APPLICANT: Ellis, Steven  
 APPLICANT: Williams, Mark  
 APPLICANT: Feldman, Daniel  
 APPLICANT: McCue, Ann  
 APPLICANT: Brenner, Robert  
 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
 NUMBER OF SEQUENCES: 57  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Brown, Martin, Haller & McClain  
 STREET: 1660 Union Street  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92101-2926  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/223,305C  
 FILING DATE: April 4, 1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/868,354  
 FILING DATE: April 10, 1992

```

: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/745,206
: FILING DATE: 15-AUG-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/620,250
: FILING DATE: 30-NOV-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/482,384
: FILING DATE: 20-FEB-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/603,751
: FILING DATE: 04-APR-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO PCT/US89/01408
: FILING DATE: 04-APR-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/176,899
: FILING DATE: 04-APR-1988
: ATTORNEY/AGENT INFORMATION:
: NAME: Seidman, Stephanie L.
: REGISTRATION NUMBER: 33,779
: REFERENCE/DOCKET NUMBER: 52516 (P519739)
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619)238-0999
: TELEFAX: (619)238-0062
: INFORMATION FOR SEQ ID NO: 54:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1086 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FRAGMENT TYPE: internal
: US-08-223-305C-54

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Query Match      98.1%; Score 5248.5; DB 2; Length 1086;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 1001; Conservative 5; Mismatches 7; Indels 5; Gaps 1;

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QY 1 MAGGCLATLTFLFOSLLTIGSSOEPSPSAVTRKSMVNMKMODLVTLAKTSGVQNLVDI 60
DB 1 MAGGCLATLTFLFOSLLTIGSSOEPSPSAVTRKSMVNMKMODLVTLAKTSGVQNLVDI 60
QY 61 YEKYODLVTEBPNNARQVLEIARDIEKLNSRKALVRLAEAKVQAHHQWRDPASN 120
DB 61 YEKYODLVTEBPNNARQVLEIARDIEKLNSRKALVRLAEAKVQAHHQWRDPASN 120
QY 121 EYVYTNAKDDLPKNDSPGSGQRIRKPFVIDANFGROIYQHAHVHPTDIYEGSTYVL 180
DB 121 EYVYTNAKDDLPKNDSPGSGQRIRKPFVIDANFGROIYQHAHVHPTDIYEGSTYVL 180
QY 181 NELNMTSAIDVEYFKNRREDPSLIMOVPGSATGLARYVPASPVWVNSRPNKIDLYDVR 240
DB 181 NELNMTSAIDVEYFKNRREDPSLIMOVPGSATGLARYVPASPVWVNSRPNKIDLYDVR 240
QY 241 RFWYIIGAASPKDMLILVDVSGSVSGLTLLKLRISVSEKLETLSDDFVNVASFNSMAD 300
DB 241 RFWYIIGAASPKDMLILVDVSGSVSGLTLLKLRISVSEKLETLSDDFVNVASFNSMAD 300
QY 301 VSCFQHLVQANRNKRVKLVLDANNITAKGITYKKGFSAFQQLNINVSRAKCKIIML 360
DB 301 VSCFQHLVQANRNKRVKLVLDANNITAKGITYKKGFSAFQQLNINVSRAKCKIIML 360
QY 361 FIDGGERAEQELFAKYNKDKKRVFFSVGOHNYRGPLOMACENKGYYPISGAIR 420
DB 361 FIDGGERAEQELFAKYNKDKKRVFFSVGOHNYRGPLOMACENKGYYPISGAIR 420
QY 421 INTQEVLDVLRPMVLASGAKAQOVQWNTVYLDALGLVITGTLPEVNTIGNENKTNLK 480
DB 421 INTQEVLDVLRPMVLASGAKAQOVQWNTVYLDALGLVITGTLPEVNTIGNENKTNLK 480
QY 481 NQIITGVKAVDVSLDIKRLTPRFILCPNGYFAIDPNKYVLLHNNLPKKNKSEPTVL 540
DB 481 NQIITGVKAVDVSLDIKRLTPRFILCPNGYFAIDPNKYVLLHNNLPKKNKSEPTVL 540

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DB 481 NQIITGVKAVDVSLDIKRLTPRFILCPNGYFAIDPNKYVLLHNNLPKKNKSEPTVL 540
QY 541 DFLDAELNDIKVEIRKMKIDGESGEKTFRTLVKSODERIDKGNFTYMTVPNGVDYSL 600
DB 536 DFLDAELNDIKVEIRKMKIDGESGEKTFRTLVKSODERIDKGNFTYMTVPNGVDYSL 595
QY 601 ALVLPYSFYIRAKIETITTOARSKKKKKKDSSETLKPONFEESGYTFLAPRDYCNLDKI 660
DB 596 ALVLPYSFYIRAKIETITTOARSKKKKKKDSSETLKPONFEESGYTFLAPRDYCNLDKI 655
QY 661 SDNTEFLNPFNEIDRKTPNPNSCNTDLINRYLDAGFTNELVQWYMSKONIKGVKAR 720
DB 656 SDNTEFLNPFNEIDRKTPNPNSCNTDLINRYLDAGFTNELVQWYMSKONIKGVKAR 715
QY 721 FVYTDGITRYVPRKAEENQENPEYEDSFYRSIDNDNYVTATAYFNKSGGAESEGI 780
DB 716 FVYTDGITRYVPRKAEENQENPEYEDSFYRSIDNDNYVTATAYFNKSGGAESEGI 775
QY 781 MVSRAVEIYIQGKLKPAVVGIRKIDVNSWLENFTKTSIRDPACGAPYCDCKRNSVDVCYI 840
DB 776 MVSRAVEIYIQGKLKPAVVGIRKIDVNSWLENFTKTSIRDPACGAPYCDCKRNSVDVCYI 835
QY 841 LDDGGLMANHDDYTNQITRPFGEIDPSLMRLVNI SYAFNKSTDYOSVCEPGAAPRO 900
DB 836 LDDGGLMANHDDYTNQITRPFGEIDPSLMRLVNI SYAFNKSTDYOSVCEPGAAPRO 895
QY 901 GAGHRSAVPSIADILHIGMWATAAAMSIIQOFLSLTLPRLLEAVEMEDDPTASLSKO 960
DB 896 GAGHRSAVPSIADILHIGMWATAAAMSIIQOFLSLTLPRLLEAVEMEDDPTASLSKO 955
QY 961 SCITEOTYFEDNDKSKFSFVLDGNCSTRIFHEKIMNTNLIPIVWESKGTCPCDTRL 1018
DB 956 SCITEOTYFEDNDKSKFSFVLDGNCSTRIFHEKIMNTNLIPIVWESKGTCPCDTRL 1013

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RESULT 9
US-08-455-543A-56
: Sequence 56, Application US/08455543A
: Patent No. 5792846
: GENERAL INFORMATION:
: APPLICANT: Harpold, Michael
: APPLICANT: Ellis, Steven
: APPLICANT: Williams, Mark
: APPLICANT: Feldman, Daniel
: APPLICANT: McCue, Ann
: TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
: NUMBER OF SEQUENCES: 57
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Brown, Martin, Haller & McClain
: STREET: 1660 Union Street
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92101-2926
: COMPUTER READABLE FORM:
: MEDIUM TYPE: diskette
: OPERATING SYSTEM: IBM compatible
: SOFTWARE: FASTSEQ Version 1.5
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/455,543A
: FILING DATE: May 31, 1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/223,305
: FILING DATE: April 4, 1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/868,354
: FILING DATE: April 10, 1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/745,206
: FILING DATE: 15-AUG-1991

```

```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: MO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 1084 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-455-543A-56

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Query Match 97.8%; Score 5231.5; DB 1; Length 1084;  
Best Local Similarity 98.0%; Pred. No. 0;

Matches 998; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

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QY 1 MAAGCLLTLTLFOSLLIGPSOPEPPSAVATKSMVWKMOMEDLVTLAKTASGVNQLVDI 60
DB 1 MAGGLLTLTLFOSLLIGPSSEPPPSAVATKSMVWKMOMEDLVTLAKTASGVNQLVDI 60
QY 61 YEKYODLVTEPNNAKQLEIAARDIEKLNSRKALVRLALEKQVQAHOHREDFASN 120
DB 61 YEKYODLVTEPNNAKQLEIAARDIEKLNSRKALVRLALEKQVQAHOHREDFASN 120
QY 121 EYVYNAKDDLDPEKNSEPSORIKPFITDANFGROISYQHAHVIPTDIYEGSTIVL 180
DB 121 EYVYNAKDDLDPEKNSEPSORIKPFITDANFGROISYQHAHVIPTDIYEGSTIVL 180
QY 181 NELNMTSALDEVFKNREDEPSLLMOVGSATGLARYYPASPVWNSRTPKIDLYVRR 240
DB 181 NELNMTSALDEVFKNREDEPSLLMOVGSATGLARYYPASPVWNSRTPKIDLYVRR 240
QY 241 RPWYIQGASPKMLLVDSVSGSLTKLIRTSVSEMLETSSDDDFVNVASFNNAOD 300
DB 241 RPWYIQGASPKMLLVDSVSGSLTKLIRTSVSEMLETSSDDDFVNVASFNNAOD 300
QY 301 VSCFOHLYQAVNRKTKLDAVNNITAKGTIDYKKGSPAFEOILLNVSRANCKITIML 360
DB 301 VSCFOHLYQAVNRKTKLDAVNNITAKGTIDYKKGSPAFEOILLNVSRANCKITIML 360
QY 361 FTDOGEERAOIEFNKYKDKKRVFTFSVGOHNYDRGPIOMMACENKGYEIPISGAIR 420
DB 361 FTDOGEERAOIEFNKYKDKKRVFTFSVGOHNYDRGPIOMMACENKGYEIPISGAIR 420
QY 421 INTQEYLDVGRPMVNLGDKAKOVOMNNVYLDALDELGLVITGILPVFNITGOENKTNLK 480
DB 421 INTQEYLDVGRPMVNLGDKAKOVOMNNVYLDALDELGLVITGILPVFNITGOENKTNLK 480
QY 481 NQLLIGVAGVDSLEDIKRLTPRETLCPNGYFAIDPNGYVLLHPNLOPKNPISOEPVYL 540
DB 481 NQLLIGVAGVDSLEDIKRLTPRETLCPNGYFAIDPNGYVLLHPNLOPKNPISOEPVYL 540
QY 541 DFLDAELENDIKVEIRKMKIDGSEGETFRTLVKSODERYIDKGNRTYTWPVNGTDYSL 600

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DB 541 DFLDAELENDIKVEIRKMKIDGSEGETFRTLVKSODERYIDKGNRTYTWPVNGTDYSL 600
QY 601 ALVLPDYSEFYIYKAKIETITQARSKGKMKDSEITLKPDNFEESGYTFIAPRDVCNDLKI 660
DB 601 ALVLPDYSEFYIYKAKIETITQARSKGKMKDSEITLKPDNFEESGYTFIAPRDVCNDLKI 660
QY 661 SDNNTIEFLNNEFIDRKTNNPNSCNDLIRVLLDAGFTNELVQNTWWSKOKNIKGVKAR 720
DB 661 SDNNTIEFLNNEFIDRKTNNPNSCNDLIRVLLDAGFTNELVQNTWWSKOKNIKGVKAR 720
QY 721 FVTDGGLITRYPKRAGENMOENPETYDSFKRSNDNDNVFPAFPNNSGPGAYESGI 780
DB 721 FVTDGGLITRYPKRAGENMOENPETYDSFKRSNDNDNVFPAFPNNSGPGAYESGI 780
QY 774 MYSRAVEIYIOGKLLKPAVGIKIDVNSWIENFTKTSIRPFCAGPVDCCKRNSVYMCVI 833
DB 774 MYSRAVEIYIOGKLLKPAVGIKIDVNSWIENFTKTSIRPFCAGPVDCCKRNSVYMCVI 833
QY 841 LDDGGLTMAHDDYTNOIGRFEIDPSLMRLVNI SVAFNKSVDYOSVCEPGAAPKQ 900
DB 841 LDDGGLTMAHDDYTNOIGRFEIDPSLMRLVNI SVAFNKSVDYOSVCEPGAAPKQ 900
QY 901 GAGHRSAYVPSIADILHIGWMTAAANSILQOFLISLTPRLLEAVEMEDDFTASLSKO 960
DB 901 GAGHRSAYVPSIADILHIGWMTAAANSILQOFLISLTPRLLEAVEMEDDFTASLSKO 960
QY 961 SCITEQOYFFDNDKSFSGVLDGNCSTRIFHVEKLMNTLIFIMWSKGTCCDTRL 1018
DB 961 SCITEQOYFFDNDKSFSGVLDGNCSTRIFHVEKLMNTLIFIMWSKGTCCDTRL 1018

```

RESULT 10

US-08-223-305C-56  
Sequence 56: Application US/08223305C

Patent No. 5851824

GENERAL INFORMATION:

APPLICANT: Harpold, Michael

APPLICANT: Ellis, Steven

APPLICANT: Williams, Mark

APPLICANT: Feldman, Daniel

APPLICANT: McCre, Ann

APPLICANT: Brenner, Robert

TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

TITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller & McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/223,305C

FILING DATE: April 4, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/868,354

FILING DATE: April 10, 1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/745,206

FILING DATE: 15-AUG-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/620,250

FILING DATE: 30-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/482,384

FILING DATE: 20-FEB-1990

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/603,751  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/US89/01408  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/176,899  
 FILING DATE: 04-APR-1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie L.  
 REGISTRATION NUMBER: 33,779  
 REFERENCE/DOCKET NUMBER: 52516 (P519739)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619)238-0999  
 TELEFAX: (619)238-0062  
 INFORMATION FOR SEQ ID NO: 56:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1084 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-223-305C-56

Query Match 97.8%; Score 5231.5; DB 2; Length 1084;  
 Best Local Similarity 98.0%; Pred. No. 0;  
 Matches 998; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 1 MAACGLATLTTLFQSLILIGPSSEPPSAVITKSWVDKMQEDLVTLAKTASGVNQLVDI 60  
 DB 1 MAACGLATLTTLFQSLILIGPSSEPPSAVITKSWVDKMQEDLVTLAKTASGVNQLVDI 60  
 QY 61 YEKYQDLYTPVPPNAROLVETLAADIEKLNSKALVRLALEKXQAAHQWEDDASN 120  
 DB 61 YEKYQDLYTPVPPNAROLVETLAADIEKLNSKALVRLALEKXQAAHQWEDDASN 120  
 QY 121 EYVYVNAKDDDPKNDSEPPSQRIRPFIDANFGROI SYQAAVH1PTDIYEGSTIVL 180  
 DB 121 EYVYVNAKDDDPKNDSEPPSQRIRPFIDANFGROI SYQAAVH1PTDIYEGSTIVL 180  
 QY 121 EYVYVNAKDDDPKNDSEPPSQRIRPFIDANFGROI SYQAAVH1PTDIYEGSTIVL 180  
 DB 121 EYVYVNAKDDDPKNDSEPPSQRIRPFIDANFGROI SYQAAVH1PTDIYEGSTIVL 180  
 QY 181 NELNMTSALDEVFKKNREDEPSLLMOVFGSATGLARIYPASPVWVNSHTPKIDLYVRR 240  
 DB 181 NELNMTSALDEVFKKNREDEPSLLMOVFGSATGLARIYPASPVWVNSHTPKIDLYVRR 240  
 QY 241 RPYVYOGAASPKMDLIVDVGSGVSGTLKLTISVSEMLETLLSDDDPVNVAFSNSAOD 300  
 DB 241 RPYVYOGAASPKMDLIVDVGSGVSGTLKLTISVSEMLETLLSDDDPVNVAFSNSAOD 300  
 QY 301 VSCFOHLYOVANRNKVKLDAVNNITAKGIDYKKGFSFAEQLLNVNSRANCKIIML 360  
 DB 301 VSCFOHLYOVANRNKVKLDAVNNITAKGIDYKKGFSFAEQLLNVNSRANCKIIML 360  
 QY 301 VSCFOHLYOVANRNKVKLDAVNNITAKGIDYKKGFSFAEQLLNVNSRANCKIIML 360  
 DB 301 VSCFOHLYOVANRNKVKLDAVNNITAKGIDYKKGFSFAEQLLNVNSRANCKIIML 360  
 QY 361 FTDDGEEBAQELFFAKYNDKRVVTPSVGQANDRGCIOMACENKXYEITISGAR 420  
 DB 361 FTDDGEEBAQELFFAKYNDKRVVTPSVGQANDRGCIOMACENKXYEITISGAR 420  
 QY 421 INTQETLVNIGRPVLAGKAKOVONTNVDALDELGLVITGTLVPEVITQONENKTMK 480  
 DB 421 INTQETLVNIGRPVLAGKAKOVONTNVDALDELGLVITGTLVPEVITQONENKTMK 480  
 QY 481 NOLILGVNGVDSLEDIRLTPRTFLCNGYFAIDPNGVYLLHPNLOPKNPKSOEPTVL 540  
 DB 481 NOLILGVNGVDSLEDIRLTPRTFLCNGYFAIDPNGVYLLHPNLOPKNPKSOEPTVL 540  
 QY 541 DPLDALENDIKVETRNKMIIDSESEKTPRTVKSODERTYIDKGRRTYTWPNVNGTDSL 600  
 DB 541 DPLDALENDIKVETRNKMIIDSESEKTPRTVKSODERTYIDKGRRTYTWPNVNGTDSL 600  
 QY 601 ATVLPTYSYIYIKAKIEETITQARSKGKMKDSEFLKPDNFESEGYTIAIPDYCNLDKI 660  
 DB 601 ATVLPTYSYIYIKAKIEETITQARSKGKMKDSEFLKPDNFESEGYTIAIPDYCNLDKI 660  
 \*DB 601 ATVLPTYSYIYIKAKIEETITQARSKGKMKDSEFLKPDNFESEGYTIAIPDYCNLDKI 660

QY 661 SDNTEFLNENETDRKTPNNPSCNTDLINRVLLDAGFTNELVQNYWWSKOKNIKGVKAR 720  
 DB 654 SDNTEFLNENETDRKTPNNPSCNTDLINRVLLDAGFTNELVQNYWWSKOKNIKGVKAR 713  
 QY 721 FVYVTDGITRYVPRKAGENWOBNETYDSSYKNSLNDNTVFFAPYFNKSGPAPYSGI 780  
 DB 714 FVYVTDGITRYVPRKAGENWOBNETYDSSYKNSLNDNTVFFAPYFNKSGPAPYSGI 773  
 QY 781 MYSKAVEITIOGKLKPAVVGKIDVNSWINTFTKTSIRDCAGPVCCKRNSVIMCVI 840  
 DB 774 MYSKAVEITIOGKLKPAVVGKIDVNSWINTFTKTSIRDCAGPVCCKRNSVIMCVI 833  
 QY 841 LDDGFFLMAHNDYTNQIGREFGEIDPSLMRHLVNI SYVAFNKSXYDYQVCEPGAAPKQ 900  
 DB 834 LDDGFFLMAHNDYTNQIGREFGEIDPSLMRHLVNI SYVAFNKSXYDYQVCEPGAAPKQ 893  
 QY 901 GAGHSAYVPSIADLIHIGWMTAAWSTLQOFLJLTFPRLLEAVEHEDDFTASLSKQ 960  
 DB 894 GAGHSAYVPSIADLIHIGWMTAAWSTLQOFLJLTFPRLLEAVEHEDDFTASLSKQ 953  
 QY 961 SCITEOTYFPPNDKSFSGVLDGNCGRIFPVEKLTMTNLIIFIVESKGTCPDTRL 1018  
 DB 954 SCITEOTYFPPNDKSFSGVLDGNCGRIFPVEKLTMTNLIIFIVESKGTCPDTRL 1011

RESULT 11  
 US-08-455-543A-53  
 Sequence 53, Application US/08455543A  
 Patent No. 5792846  
 GENERAL INFORMATION:  
 APPLICANT: Harpold, Michael  
 APPLICANT: Ellis, Steven  
 APPLICANT: Williams, Mark  
 APPLICANT: Feldman, Daniel  
 APPLICANT: McCue, Ann  
 APPLICANT: Brenner, Robert  
 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
 NUMBER OF SEQUENCES: 57  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Brown, Martin, Haller & McClain  
 STREET: 1660 Union Street  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92101-2926  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/455,543A  
 FILING DATE: May 31, 1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/223,305  
 FILING DATE: April 4, 1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/868,354  
 FILING DATE: April 10, 1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/745,206  
 FILING DATE: 15-AUG-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/620,250  
 FILING DATE: 30-NOV-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/482,384  
 FILING DATE: 20-FEB-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/603,751  
 FILING DATE: 04-APR-1989



PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/US89/01408  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/176,899  
 FILING DATE: 04-APR-1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie L.  
 REGISTRATION NUMBER: 33,779  
 REFERENCE/DOCKET NUMBER: 6362-52517  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619)238-0999  
 TELEFAX: (619)238-0062  
 INFORMATION FOR SEQ ID NO: 53:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1103 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-455-543A-53

Query Match 97.4%; Score 5212; DB 1; Length 1103;  
 Best Local Similarity 96.2%; Pred. No. 0;  
 Matches 998; Conservative 5; Mismatches 8; Indels 26; Gaps 2;

QY 1 MAAGCLLALTLTLFQSLIGPSSQRPSPAVTISKWDKMOEDLVTLAKTASGVNQLVDI 60  
 DB 1 MAGAGCLLALTLTLFQSLIGPSSQRPSPAVTISKWDKMOEDLVTLAKTASGVNQLVDI 60  
 QY 61 YEKYODLVYEPNNARQVETAAARDIEKLNSKALVRLALEKYOAAHOMREDFASN 120  
 DB 61 YEKYODLVYEPNNARQVETAAARDIEKLNSKALVRLALEKYOAAHOMREDFASN 120  
 QY 121 EYVYNNAKDDLDPEKNDESPGSORIKPFVIDANFGROIISYQAAVHPIDYEGSTIVL 180  
 DB 121 EYVYNNAKDDLDPEKNDESPGSORIKPFVIDANFGROIISYQAAVHPIDYEGSTIVL 180  
 QY 121 EYVYNNAKDDLDPEKNDESPGSORIKPFVIDANFGROIISYQAAVHPIDYEGSTIVL 180  
 DB 121 EYVYNNAKDDLDPEKNDESPGSORIKPFVIDANFGROIISYQAAVHPIDYEGSTIVL 180  
 QY 181 NELNMTSALDEYFKKRNEDPSLMOYVGSATGLARYPASPWVNDNRTPNKIDLYDVR 240  
 DB 181 NELNMTSALDEYFKKRNEDPSLMOYVGSATGLARYPASPWVNDNRTPNKIDLYDVR 240  
 QY 241 RFWYIOGAASPKMDLIVDVGSGVSGTLKIRTSVSEMLETSSDDPFVAVFNSNAOD 300  
 DB 241 RFWYIOGAASPKMDLIVDVGSGVSGTLKIRTSVSEMLETSSDDPFVAVFNSNAOD 300  
 QY 301 VSCFOHLVQAVNRKKVYLKDAVNNITAKGIDYKKGFSAFEQLLNVNSRANCKIIML 360  
 DB 301 VSCFOHLVQAVNRKKVYLKDAVNNITAKGIDYKKGFSAFEQLLNVNSRANCKIIML 360  
 QY 361 FTDGGEERAOEIFAKYNNKDKVRFETPSVGOHNDRGPIDMACENKGYEETPSIGAIR 420  
 DB 361 FTDGGEERAOEIFAKYNNKDKVRFETPSVGOHNDRGPIDMACENKGYEETPSIGAIR 420  
 QY 421 INFOEYLDVLRPMYLAGDRAKQVOMTVNYLDALELGLVITGLTPYFNITGOENKTNK 480  
 DB 421 INFOEYLDVLRPMYLAGDRAKQVOMTVNYLDALELGLVITGLTPYFNITGOENKTNK 480  
 QY 481 NQILIGWGVYVSLIEDIKRLTPRTLCPPNGYFAIDPNGVLLHPILQPK----- 530  
 DB 481 NQILIGWGVYVSLIEDIKRLTPRTLCPPNGYFAIDPNGVLLHPILQPK----- 530  
 QY 531 -----NPKSOEPTLDFLDALELNDIKVEIRNKMIDGESGEKTFPIVKSQOERI 581  
 DB 541 LRRKRPINQNPKSGEPYTLDFLDALELNDIKVEIRNKMIDGESGEKTFPIVKSQOERI 600  
 QY 582 DKGRITTTVPNGTDSALVLPYSSFYIKAKIETITTOASKKGKMDSETILKPNDF 641  
 DB 601 DKGRITTTVPNGTDSALVLPYSSFYIKAKIETITTOASKKGKMDSETILKPNDF 653  
 QY 642 EESGYTIAARDYCNDAKISDNTTEFLNNEFDIKTRNNNSCNTDLINRYLLDAGFTN 701  
 DB 642 EESGYTIAARDYCNDAKISDNTTEFLNNEFDIKTRNNNSCNTDLINRYLLDAGFTN 701

DB 654 EESGYTIAARDYCNDAKISDNTTEFLNNEFDIKTRNNNSCNTDLINRYLLDAGFTN 713  
 QY 702 ELVONTWSKOKNIKGVAKARVYVDGIRTVYPRKEGEMNOENPETEEDSEFYKSLDNDNY 761  
 DB 714 ELVONTWSKOKNIKGVAKARVYVDGIRTVYPRKEGEMNOENPETEEDSEFYKSLDNDNY 773  
 QY 762 VFTAPYFNKSGPAAVSGIMVSKAVEITYOGKLLRPAYVGIKIDVNSIENFTKTSIRDP 821  
 DB 774 VFTAPYFNKSGPAAVSGIMVSKAVEITYOGKLLRPAYVGIKIDVNSIENFTKTSIRDP 833  
 QY 822 CAGPVDCCKRNSDVMDCVILDDGFLMANHDDYTNQIGRFGELIDPMLHNLVNSIYA 881  
 DB 834 CAGPVDCCKRNSDVMDCVILDDGFLMANHDDYTNQIGRFGELIDPMLHNLVNSIYA 893  
 QY 882 FNSSTYOSVCEGGAAPKOGAGHRSAYVPSIADILHIGMATAAAMSILQOFLSLTFPR 941  
 DB 894 FNSSTYOSVCEGGAAPKOGAGHRSAYVPSIADILHIGMATAAAMSILQOFLSLTFPR 953  
 QY 942 LLEAVEMEDDFTASLSKSCITBOTOFEDNDKSFSGVILDCGCSRIHYEKLANTNL 1001  
 DB 954 LLEAVEMEDDFTASLSKSCITBOTOFEDNDKSFSGVILDCGCSRIHYEKLANTNL 1013  
 QY 1002 IFIMVSKGTCPDTRL 1018  
 DB 1014 IFIMVSKGTCPDTRL 1030

RESULT 12  
 US-08-223-305C-53  
 Sequence 53, Application US/08223305C  
 Patent No. 5851824  
 GENERAL INFORMATION:  
 APPLICANT: Harpold, Michael  
 APPLICANT: Ellis, Steven  
 APPLICANT: Williams, Mark  
 APPLICANT: Feldman, Daniel  
 APPLICANT: McCue, Ann  
 APPLICANT: Brenner, Robert  
 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
 TITLE OF INVENTION: METHODS  
 NUMBER OF SEQUENCES: 57  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Brown, Martin, Haller & McCain  
 STREET: 1660 Union Street  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92101-2926  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSP version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/223,305C  
 FILING DATE: April 4, 1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/868,354  
 FILING DATE: April 10, 1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/745,206  
 FILING DATE: 15-AUG-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/620,250  
 FILING DATE: 30-NOV-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/482,384  
 FILING DATE: 20-FEB-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/603,751  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/US89/01408

FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA: US 07/176,899  
 APPLICATION NUMBER: 04-APR-1988  
 FILING DATE: 04-APR-1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie L.  
 REGISTRATION NUMBER: 33,779  
 REFERENCE/DOCKET NUMBER: 52516 (P519739)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619)238-0999  
 TELEFAX: (619)238-0062  
 INFORMATION FOR SEQ ID NO: 53:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1103 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-223-305C-53

Query Match 97.4%; Score 5212; DB 2; Length 1103;  
 Best Local Similarity 96.2%; Pred. No. 0;  
 Matches 998; Conservative 5; Mismatches 8; Indels 26; Gaps 2;

QY 1 MAAGCLALTLTLFQSLIGSPSQEPSPSAVTIKSWVDKMOEDLVTLAKTASGVNQLVDI 60  
 DB 1 MAAGCLALTLTLFQSLIGSPSQEPSPSAVTIKSWVDKMOEDLVTLAKTASGVNQLVDI 60  
 QY 61 YEKIOTLYTTPNNARQVETAAADIEKLSNRKALVRLALEKQVQAQHQWEDPASN 120  
 DB 61 YEKIOTLYTTPNNARQVETAAADIEKLSNRKALVRLALEKQVQAQHQWEDPASN 120  
 QY 121 EYVYNAKDDIDPEKNDSEPSQRIKPFIDANFGROIYQHAQVHPTDIYEGSTVL 180  
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 DB 121 EYVYNAKDDIDPEKNDSEPSQRIKPFIDANFGROIYQHAQVHPTDIYEGSTVL 180  
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 DB 181 NELNNTSALDEVEFKKNEEDPSLMOVYGSATGLARIYPASPVWDNSTPKIDLYVRR 240  
 QY 241 RPYTQGAAPKMDILVDYSGVSGTLKIRTSVSEMLTSLDDDEPVNVAFSNSNAD 300  
 DB 241 RPYTQGAAPKMDILVDYSGVSGTLKIRTSVSEMLTSLDDDEPVNVAFSNSNAD 300  
 QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKITDYKKGSFAFEQLINYSRANCKIIML 360  
 DB 301 VSCFQHLVQANVRNKKVLDKAVNNITAKITDYKKGSFAFEQLINYSRANCKIIML 360  
 QY 361 FTDGEERAQELFAKYNKDKRVRFVSQHNDRGPIOMACENKGYEIRISGAR 420  
 DB 361 FTDGEERAQELFAKYNKDKRVRFVSQHNDRGPIOMACENKGYEIRISGAR 420  
 QY 421 INFOEYLDVLRPNVLADGKAKQVQWTVVYDALELGLVITGLPVENITQONENKNTLK 480  
 DB 421 INFOEYLDVLRPNVLADGKAKQVQWTVVYDALELGLVITGLPVENITQONENKNTLK 480  
 QY 481 NOLIGVGVDSLEIDIKRLPRFLPCNGYFFAIDPNGYVLLHNNLOPK----- 530  
 DB 481 NOLIGVGVDSLEIDIKRLPRFLPCNGYFFAIDPNGYVLLHNNLOPK----- 530  
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 DB 531 -----NPKSQEPVTLDFDALENDIKVEIRNKKMIDGSEKTRPTLVKSODERYI 581  
 QY 582 DKGNRTYTWTPVNGTDSYSLALVPTYSFYIKAKIETITQARSKKGMKDETLKPNF 641  
 DB 582 DKGNRTYTWTPVNGTDSYSLALVPTYSFYIKAKIETITQARSKKGMKDETLKPNF 641  
 QY 601 DKGNRTYTWTPVNGTDSYSLALVPTYSFYIKAKIETITQARSKKGMKDETLKPNF 653  
 DB 601 DKGNRTYTWTPVNGTDSYSLALVPTYSFYIKAKIETITQARSKKGMKDETLKPNF 653  
 QY 642 EESGTYFIAPROYCNDKISDNNTFELNENFIDRKTPNPNNSCWTDLINRVLDAAGTIN 701  
 DB 642 EESGTYFIAPROYCNDKISDNNTFELNENFIDRKTPNPNNSCWTDLINRVLDAAGTIN 701  
 QY 654 EESGTYFIAPROYCNDKISDNNTFELNENFIDRKTPNPNNSCWTDLINRVLDAAGTIN 713  
 DB 654 EESGTYFIAPROYCNDKISDNNTFELNENFIDRKTPNPNNSCWTDLINRVLDAAGTIN 713

QY 702 ELVONWMSKOKNIKGVKAFVTTDGTITRVYPKEAGENMOENPETEEDSFYKRSILDNDY 761  
 DB 714 ELVONWMSKOKNIKGVKAFVTTDGTITRVYPKEAGENMOENPETEEDSFYKRSILDNDY 773  
 QY 762 VTPAPYFNKSGGAYESGIMWSKAVEIYIOGKLLKPAVVGKIKIDVNSIMEPTKSTIDP 821  
 DB 774 VTPAPYFNKSGGAYESGIMWSKAVEIYIOGKLLKPAVVGKIKIDVNSIMEPTKSTIDP 833  
 QY 822 CAGPVCDCRNSDVMDCVLLDGGFLLMANHDDYTNQIGRFFGEIDPISLMLHVNISYVA 881  
 DB 834 CAGPVCDCRNSDVMDCVLLDGGFLLMANHDDYTNQIGRFFGEIDPISLMLHVNISYVA 893  
 QY 882 FNKSYDQSGCEGAAPKQAGHRSAYVPSIADLIHIGMATAAASLQGFUSLTFPR 941  
 DB 894 FNKSYDQSGCEGAAPKQAGHRSAYVPSIADLIHIGMATAAASLQGFUSLTFPR 953  
 QY 942 LLEAVEMEDDFTASLSKSCITEOTQYFENDSKSFSGVLDGCSRFHEKLMNTNL 1001  
 DB 954 LLEAVEMEDDFTASLSKSCITEOTQYFENDSKSFSGVLDGCSRFHEKLMNTNL 1013  
 QY 1002 IFIMVSKGTCPDPTL 1018  
 DB 1014 IFIMVSKGTCPDPTL 1030

RESULT 13  
 US-08-455-543A-55  
 Sequence 55, Application US/08455543A  
 Patent No. 5792846

GENERAL INFORMATION:  
 APPLICANT: Harpold, Michael  
 APPLICANT: Ellis, Steven  
 APPLICANT: Williams, Mark  
 APPLICANT: Feldman, Daniel  
 APPLICANT: McCue, Ann  
 APPLICANT: Brenner, Robert  
 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
 NUMBER OF SEQUENCES: 57  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Brown, Martin, Haller & McClain  
 STREET: 1660 Union Street  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92101-2926

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ Version 1.5

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/455,543A  
 FILING DATE: May 31, 1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/223,305  
 FILING DATE: April 4, 1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/868,354  
 FILING DATE: April 10, 1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/745,206  
 FILING DATE: 15-AUG-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/620,250  
 FILING DATE: 30-NOV-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/482,384  
 FILING DATE: 20-FEB-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/603,751  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:

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APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/176, 899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-455-543A-55

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Query Match          97.1%; Score 5192; DB 1; Length 1079;
Best Local Similarity 97.5%; Pred. No. 0;
Matches 993; Conservative 5; Mismatches 8; Indels 12; Gaps 2;

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QY 1 MAAGGLALTLTQLSLLIGSSQPPPSAVTISWDMKQEDLVTLAKTASGVNQLVDI 60
DB 1 MAAGGLALTLTQLSLLIGSSQPPPSAVTISWDMKQEDLVTLAKTASGVNQLVDI 60
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DB 61 YEKYODLVTPENNAQRLVEIAARDIEKLSNRSKALVRLALEAKQOAAQWEDPASN 120
QY 121 EYVYINAKDLDPEKNDSEPSQRIKPFVIDANFGRQISYQHAHVHPTDIYEGSTIVL 180
DB 121 EYVYINAKDLDPEKNDSEPSQRIKPFVIDANFGRQISYQHAHVHPTDIYEGSTIVL 180
QY 121 EYVYINAKDLDPEKNDSEPSQRIKPFVIDANFGRQISYQHAHVHPTDIYEGSTIVL 180
DB 121 EYVYINAKDLDPEKNDSEPSQRIKPFVIDANFGRQISYQHAHVHPTDIYEGSTIVL 180
QY 181 NELNMTSLDVEFKKNREDESSLMOVGSGTGLARYYPASPMWVNSRTPKIDLYVRR 240
DB 181 NELNMTSLDVEFKKNREDESSLMOVGSGTGLARYYPASPMWVNSRTPKIDLYVRR 240
QY 241 RPYVIOGAASPKDMLLVDSVSGVSLTLKLTFTSVSEMETLSDDDPFVNVASPNNAOD 300
DB 241 RPYVIOGAASPKDMLLVDSVSGVSLTLKLTFTSVSEMETLSDDDPFVNVASPNNAOD 300
QY 301 VSCQOHLVQAVNRKRYLAKDAVNNITAKGTDYKGFSAFEQLLNVNSRANCKLIML 360
DB 301 VSCQOHLVQAVNRKRYLAKDAVNNITAKGTDYKGFSAFEQLLNVNSRANCKLIML 360
QY 361 FTDGGERAEIIFAKYKNDKRVFTFSGVGHNDRGPIOMMACENKGYEYETPSIAIR 420
DB 361 FTDGGERAEIIFAKYKNDKRVFTFSGVGHNDRGPIOMMACENKGYEYETPSIAIR 420
QY 421 INTQEIYDLVGRPVNLAGRAKQVQWNTNYLDALGLVITGLTPVNTIGQENKTNLK 480
DB 421 INTQEIYDLVGRPVNLAGRAKQVQWNTNYLDALGLVITGLTPVNTIGQENKTNLK 480
QY 481 NQTLIGWGVDSLEDKRLPRPTLCRPNKYTPAIDPNGVYLLHPNLOPK-----EYVTL 540
DB 481 NQTLIGWGVDSLEDKRLPRPTLCRPNKYTPAIDPNGVYLLHPNLOPK-----EYVTL 540
QY 541 DFLDAELNDIKVEIRKMDIGSGEFTFLVKSODERTIDKGNRTYTPVNGTDYSL 600
DB 541 DFLDAELNDIKVEIRKMDIGSGEFTFLVKSODERTIDKGNRTYTPVNGTDYSL 600
QY 601 ALVPTPSFYIYAKIETTTQARSKKGKKKDESLKPDNFEESGYTFLAPRDYCDLKI 660
DB 601 ALVPTPSFYIYAKIETTTQARSKKGKKKDESLKPDNFEESGYTFLAPRDYCDLKI 660
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QY 649 SDNTEFLNFEIDKTPNNNSCNTDLINRYLLDAGFNEIYVQWWSOKIKGVYKAR 708
DB 649 SDNTEFLNFEIDKTPNNNSCNTDLINRYLLDAGFNEIYVQWWSOKIKGVYKAR 708

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QY 721 FVYTDGITRYPKKAGENQENPEYEDSFYKRSKSLNDNVYFAPYFNKSGCAVESGI 780
DB 709 FVYTDGITRYPKKAGENQENPEYEDSFYKRSKSLNDNVYFAPYFNKSGCAVESGI 768
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIEFNFKTSIRPDCAGPVDCRNSDVMCVI 840
DB 769 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIEFNFKTSIRPDCAGPVDCRNSDVMCVI 828
QY 841 LDDGFLMANHDDYTNQIGRFEIGIDPSLMRLVNI SYVAFNKSXYQSGCEGAPKQ 900
DB 829 LDDGFLMANHDDYTNQIGRFEIGIDPSLMRLVNI SYVAFNKSXYQSGCEGAPKQ 888
QY 901 GAGHRSAYVPSIADILHGMWATAAASIIQOFLSTLTPRLLAEVMEDDPTASLSKQ 960
DB 889 GAGHRSAYVPSIADILHGMWATAAASIIQOFLSTLTPRLLAEVMEDDPTASLSKQ 948
QY 961 SCITEQTYEFENDSKSFGVLDGNCSTRIFHEKLMNTMLIFLWYSKGTCTCDTRL 1018
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RESULT 14
US-08-223-305C-55
Sequence 55, Application US/08223305C
Patent No. 5851824

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GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/223,305C
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/668,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
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APPLICATION NUMBER: WO PCT/US89/01408
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:

```

NAME: Seidman, Stephanie L.  
 REGISTRATION NUMBER: 33,779  
 REFERENCE/DOCKET NUMBER: 52516 (P519739)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619)238-0999  
 TELEFAX: (619)238-0062  
 INFORMATION FOR SEO ID NO: 55:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1079 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-223-305C-55

Query Match 97.1%; Score 5192; DB 2; Length 1079;

Best Local Similarity 97.5%; Pred. No. 0;

Matches 993; Conservative 5; Mismatches 8; Indels 12; Gaps 2;

QY 1 MAACGLALITLTLFQSLIGSSQEPSPAVTIKSWYDKMOEDLVTLAKTASGVNQLYDI 60  
 DB 1 MAACGLALITLTLFQSLIGSSQEPSPAVTIKSWYDKMOEDLVTLAKTASGVNQLYDI 60  
 QY 61 YEKYODLYTPNNAROLVETIARDIEKLNSRSKALVRLALEAKYQAAHOMREDFASN 120  
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 QY 121 EYVYVYNAKDDLDPEKNDSEPSQRIKVEYFIDANFGQISYQAAVHIPDIYEGSTIVL 180  
 DB 121 EYVYVYNAKDDLDPEKNDSEPSQRIKVEYFIDANFGQISYQAAVHIPDIYEGSTIVL 180  
 QY 181 NELMWTSLADVEFKNREDEPSILMOYFGSATGLARYPPASPWNDKRTPKIDLYVYR 240  
 DB 181 NELMWTSLADVEFKNREDEPSILMOYFGSATGLARYPPASPWNDKRTPKIDLYVYR 240  
 QY 241 RPWTYOGAASPKDMLIYDVGSGVSGITLKLIRTSVSEMETLSDDDFVNVAEFSNAOD 300  
 DB 241 RPWTYOGAASPKDMLIYDVGSGVSGITLKLIRTSVSEMETLSDDDFVNVAEFSNAOD 300  
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 DB 301 VSCFQHLVQAVNRKRYKLDVANNITAKGITDYKKGFSFAEQLLANNVNSANCKTIML 360  
 QY 361 FTDDGEERAQELFKYNNCKKVRFTFSVGOHNDRGPIDMACENKGYEIEISIAIR 420  
 DB 361 FTDDGEERAQELFKYNNCKKVRFTFSVGOHNDRGPIDMACENKGYEIEISIAIR 420  
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 DB 421 INFOEYLDVIGRPVYLAGDKAKQVQWNTNVYLDALGLVITGTLVPENITGQENKTNLK 480  
 QY 481 NOLLIGWGVNVSLEDIKRLPRFTLCPNGYFAIDPRGYLLHPNIOPKPKQOEPTVL 540  
 DB 481 NOLLIGWGVNVSLEDIKRLPRFTLCPNGYFAIDPRGYLLHPNIOPKPKQOEPTVL 540  
 QY 541 DFLDAELENDIKVEIRNMKIDGSEGEKFRILVKSODERYIDKGNRTYTWTVPNGDTYSL 600  
 DB 541 DFLDAELENDIKVEIRNMKIDGSEGEKFRILVKSODERYIDKGNRTYTWTVPNGDTYSL 600  
 QY 596 ALVLPYSPFYIYKAKLEETITQARY-----SETLPKDNFEESGYFIAIPDYCNDIKI 648  
 DB 596 ALVLPYSPFYIYKAKLEETITQARY-----SETLPKDNFEESGYFIAIPDYCNDIKI 648  
 QY 661 SONNTEFLINFEETIDRKTNNPNSCNTDLIRVILLDAGTEBLVQYNSKOKNKGVAR 720  
 DB 661 SONNTEFLINFEETIDRKTNNPNSCNTDLIRVILLDAGTEBLVQYNSKOKNKGVAR 720  
 QY 721 FVYTDGGITRVYKKEAGENWQENPETYEDSFYKRSILDNDNVETAPYFNKSGPGAYESGI 780  
 DB 721 FVYTDGGITRVYKKEAGENWQENPETYEDSFYKRSILDNDNVETAPYFNKSGPGAYESGI 780  
 QY 781 MWSKAVEIYIOGKLKPAVVGIKIDVNSMIENFTKTSIRDPACAGVYCCCKRNSDVMDCVI 840

DB 769 MWSKAVEIYIOGKLKPAVVGIKIDVNSMIENFTKTSIRDPACAGVYCCCKRNSDVMDCVI 828  
 QY 841 LDDGGFILMANDDVTNOIGRFFGEIDPSLRHVNISVYAFNKSXYQASCEGAPKQ 900  
 DB 829 LDDGGFILMANDDVTNOIGRFFGEIDPSLRHVNISVYAFNKSXYQASCEGAPKQ 888  
 QY 901 GAGHSAYVPSIADILHIGWMTAAWSILQOFLSLTFPRLLRAVEMEDDDFTASLSKQ 960  
 DB 889 GAGHSAYVPSIADILHIGWMTAAWSILQOFLSLTFPRLLRAVEMEDDDFTASLSKQ 948  
 QY 961 SCITEOTOFYFENDSKSPSGVLDGNCGRIRIHEVKLMTNLIETWESKGTCPDTRL 1018  
 DB 949 SCITEOTOFYFENDSKSPSGVLDGNCGRIRIHEVKLMTNLIETWESKGTCPDTRL 1006

RESULT 15

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Sequence 5, Application US/08435675B

Patent No. 5710250

GENERAL INFORMATION:

APPLICANT: Ellis, Steven Bradley

APPLICANT: Williams, Mark E.

APPLICANT: Harpold, Michael Miller

APPLICANT: Schwartz, Arnold

APPLICANT: Brenner, Robert

TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller & McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: CA

COUNTRY: USA

ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/435,675B

FILING DATE: 05-MAY-1995

CLASSIFICATION: 435

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APPLICATION NUMBER: US 08/314,083

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INFORMATION FOR SEO ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1106 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

US-08-435-675B-5

Query Match 96.5%; Score 5161.5; DB 1; Length 1106;

Best Local Similarity 95.4%; Pred. No. 0;

Matches 992; Conservative 10; Mismatches 9; Indels 29; Gaps 4;

QY 1 MAACCLATLTLTLEFOS--LLIGSSQEPFSAVTIKSWDKMODVLTLAKTASGVNOLV 58  
1 MAARPLAMTLTLTMOALILIGPSSEPFPSAVTIKSWDKMODVLTLAKTASGVNOLV 60  
QY 59 DIYEKODLYTVEPNNAQLEIAARDIEKLSRSKALVRLALEAKVOAHOHREDFA 118  
61 DIYEKODLYTVEPNNAQLEIAARDIEKLSRSKALVRLALEAKVOAHOHREDFA 120  
QY 119 SNEVYVYNAKODLDPEKNDESPGSQRIKPYEIDANFGRQISYOHAAVHIPTDIYEGSTI 178  
121 SNEVYVYNAKODLDPEKNDESPGSQRIKPYEIDANFGRQISYOHAAVHIPTDIYEGSTI 180  
QY 179 VLNEIMNTSALDEYFKKRNREDEPSLLIMOVGSAFGTGLARYYPASPWNDSRTPKIDLVDV 238  
181 VLNEIMNTSALDEYFKKRNREDEPSLLIMOVGSAFGTGLARYYPASPWNDSRTPKIDLVDV 240  
QY 239 RRRPWTIIOGAASPKDMLLVDSVSGVGLTLKLRISVSEMLETLSDDDFVNAVASFNSNA 298  
241 RRRPWTIIOGAASPKDMLLVDSVSGVGLTLKLRISVSEMLETLSDDDFVNAVASFNSNA 300  
QY 299 ODVSCFOHLYOANVRKKATYLKDAVNNITAKGIDYKKGFSFAFEQLLNVNSRANCNKII 358  
301 ODVSCFOHLYOANVRKKATYLKDAVNNITAKGIDYKKGFSFAFEQLLNVNSRANCNKII 360  
QY 359 MLETTDGERRAOEIEFAKYNNKDKKVRVFTFSVGOHNDGRPIOMMACENKGYEYELPSIGA 418  
361 MLETTDGERRAOEIEFAKYNNKDKKVRVFTFSVGOHNDGRPIOMMACENKGYEYELPSIGA 420  
QY 419 IRTNTOEYIDVYGRPWTLADGRKAKOVMTNYYLDALEGLVITGTLPVFNITGONENKTN 478  
421 IRTNTOEYIDVYGRPWTLADGRKAKOVMTNYYLDALEGLVITGTLPVFNITGONENKTN 480  
QY 479 LKNOLLIGVAGVDSLEDKRLTPRETLCPNGYFYAIDPNGVYLLHPNLOPK----- 530  
481 LKNOLLIGVAGVDSLEDKRLTPRETLCPNGYFYAIDPNGVYLLHPNLOPK----- 540  
QY 531 -----NPKSQEPVTLDFDALELNDIKVEIRNNKIDGSEGEKTFRLVKSODER 579  
541 INLRRRRPVPONPKSQEPVTLDFDALELNDIKVEIRNNKIDGSEGEKTFRLVKSODER 600  
QY 580 YIDKGNRTYTPVNGTGY-STALVLPYTSFYIYAKIETITTOARSKKGMKDSSETLKP 638  
601 YIDKGNRTYTPVNGTGY-STALVLPYTSFYIYAKIETITTOARSKKGMKDSSETLKP 653  
QY 639 DNEESGYTFIAPRDYCNLDKISDNTEFLNFEFIDRKTNNPNSCNTDLINRYLIDAG 698  
654 DNEESGYTFIAPRDYCNLDKISDNTEFLNFEFIDRKTNNPNSCNTDLINRYLIDAG 713  
QY 699 FTNELVQYNSKOKNIKGVKARFVYTDGTRVYPRKAGENMOENPETEYEDSFYKRSIDN 758  
714 FTNELVQYNSKOKNIKGVKARFVYTDGTRVYPRKAGENMOENPETEYEDSFYKRSIDN 773  
QY 759 DNYVFTAPYFNKSGPAGVESGIMVSKAVEIYIOGKRLKPAVVGIKIDVNSWIENTFTYTSI 818  
774 DNYVFTAPYFNKSGPAGVESGIMVSKAVEIYIOGKRLKPAVVGIKIDVNSWIENTFTYTSI 833  
QY 819 RDPGAGPYCDCKRNSDVMDCVIILDDGGFLMANHDDYTNOIGRFFGEIDPSIMRHLVNIS 876  
834 RDPGAGPYCDCKRNSDVMDCVIILDDGGFLMANHDDYTNOIGRFFGEIDPSIMRHLVNIS 893  
QY 879 VYAFNKSYDVOSVCEPAGAPROGAGHRSAYVPSIADLIHIGWATAAAMSILOOFLILST 938  
894 VYAFNKSYDVOSVCEPAGAPROGAGHRSAYVPSIADLIHIGWATAAAMSILOOFLILST 953  
QY 939 FPRILLEAVEMEDDFTASLSKOSCTEQTOYFENDSKSFSGYLDGNCGRIFHVEKLMN 998  
954 FPRILLEAVEMEDDFTASLSKOSCTEQTOYFENDSKSFSGYLDGNCGRIFHVEKLMN 1013  
QY 999 TNLIFIVESKGTGRCPTRL 1018  
1014 TNLIFIVESKGTGRCPTRL 1033

Search completed: February 10, 2003, 14:23:08  
Job time : 17.291 secs

